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<p>(21) International Application Number: PCT/US98/04493 (22) International Filing Date: 6 March 1998 (06.03.98) (30) Priority Data: <table border="0"> <tr><td>60/040,162</td><td>7 March 1997 (07.03.97)</td><td>US</td></tr> <tr><td>60/040,333</td><td>7 March 1997 (07.03.97)</td><td>US</td></tr> <tr><td>60/038,621</td><td>7 March 1997 (07.03.97)</td><td>US</td></tr> <tr><td>60/040,161</td><td>7 March 1997 (07.03.97)</td><td>US</td></tr> <tr><td>60/040,626</td><td>7 March 1997 (07.03.97)</td><td>US</td></tr> <tr><td>60/040,334</td><td>7 March 1997 (07.03.97)</td><td>US</td></tr> <tr><td>60/040,336</td><td>7 March 1997 (07.03.97)</td><td>US</td></tr> <tr><td>60/040,163</td><td>7 March 1997 (07.03.97)</td><td>US</td></tr> <tr><td>60/043,580</td><td>11 April 1997 (11.04.97)</td><td>US</td></tr> <tr><td>60/043,568</td><td>11 April 1997 (11.04.97)</td><td>US</td></tr> </table> <p>(Continued on the following page) (71) Applicant (for all designated States except US): HUMAN GENOME SCIENCES, INC. [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): RUBEN, Steven, M. [US/US]; 18528 Heritage Hills Drive, Olney, MD 20832 (US). ROSEN, Craig, A. [US/US]; 22400 Rolling Hills Road, Laytonsville, MD 20882 (US). FISCHER, Carrie, L. [US/US]; 5810 Hall Street, Burke, VA 22015 (US). SOPPET, Daniel, R. [US/US]; 15050 Stillfield, Place, Centreville, VA 22020 (US). CARTER, Kenneth, C. [US/US]; 11601 Brandy Hall Lane, North Potomac, MD 20878 (US). BEDNARIK, Daniel, P. [US/US]; 8822 Blue Sea Drive, Columbia, MD 21046 (US). ENDRESS, Gregory, A. [US/US]; 9729 Clagett Farm Drive, Potomac, MD 20854 (US). YU, Guo-Liang [CN/US]; 13524 Straw Bale Lane, Darnestown, MD 20878 (US). NI, Jian [CN/US]; 5502 Manorfield Road, Rockville, MD 20853 (US). FENG, Ping [CN/US]; 4 Relda Court, Gaithersburg, MD 20878 (US). YOUNG, Paul, E. [US/US]; 122 Beckwith Street, Gaithersburg, MD 20878 (US). GREENE, John, M. [US/US]; 872 Diamond Drive, Gaithersburg, MD 20878 (US). FERRIE, Ann, M. [US/US]; 13203 L Astoria Hill Court, Germantown,</p> </p>		60/040,162	7 March 1997 (07.03.97)	US	60/040,333	7 March 1997 (07.03.97)	US	60/038,621	7 March 1997 (07.03.97)	US	60/040,161	7 March 1997 (07.03.97)	US	60/040,626	7 March 1997 (07.03.97)	US	60/040,334	7 March 1997 (07.03.97)	US	60/040,336	7 March 1997 (07.03.97)	US	60/040,163	7 March 1997 (07.03.97)	US	60/043,580	11 April 1997 (11.04.97)	US	60/043,568	11 April 1997 (11.04.97)	US	<p>MD 20874 (US). DUAN, Roxanne [US/US]; 4541 Fairfield Drive, Bethesda, MD 20814 (US). HU, Jing-Shan [CN/US]; 1247 Lakeside Drive #3034, Sunnyvale, CA 94086 (US). FLORENCE, Kimberly, A. [US/US]; 12805 Atlantic Avenue, Rockville, MD 20851 (US). OLSEN, Henrik, S. [DK/US]; 182 Kendrick Place #24, Gaithersburg, MD 20878 (US). EBNER, Reinhard [DE/US]; 9906 Shelburne Terrace #316, Gaithersburg, MD 20878 (US). BREWER, Laurie, A. [US/US]; 14920 Mount Nebo Road, Poolesville, MD 20837 (US). MOORE, Paul, A. [GB/US]; Apartment #104, 1908 Holly Ridge Drive, McLean, VA 22102 (US). SHI, Yanggu [CN/US]; 437 West Side Drive, Gaithersburg, MD 20878 (US). LAFLEUR, David, W. [US/US]; 1615 Q Street, N.W. #807, Washington, DC 20009 (US). LI, Yi [CN/US]; 1247 Lakeside Drive #3034, Sunnyvale, CA 94086 (US). ZENG, Zhizhen [CN/US]; 13950 Saddleview Drive, Gaithersburg, MD 20878 (US). KYAW, Hla [BU/US]; 520 Sugarbush Circle, Frederick, MD 21703 (US). (74) Agents: BROOKES, Anders, A. et al.; Human Genome Sciences, Inc., 9410 Key West Avenue, Rockville, MD 10850 (US). (81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).</p>
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<p>(54) Title: 186 HUMAN SECRETED PROTEINS (57) Abstract The present invention relates to 186 novel human secreted proteins and isolated nucleic acids containing the coding regions of the genes encoding such proteins. Also provided are vectors, host cells, antibodies, and recombinant methods for producing human secreted proteins. The invention further relates to diagnostic and therapeutic methods useful for diagnosing and treating disorders related to these novel human secreted proteins.</p>																																

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186 Human Secreted Proteins

Field of the Invention

This invention relates to newly identified polynucleotides and the polypeptides encoded by these polynucleotides, uses of such polynucleotides and polypeptides, and
5 their production.

Background of the Invention

Unlike bacterium, which exist as a single compartment surrounded by a membrane, human cells and other eucaryotes are subdivided by membranes into many functionally distinct compartments. Each membrane-bounded compartment, or
10 organelle, contains different proteins essential for the function of the organelle. The cell uses "sorting signals," which are amino acid motifs located within the protein, to target proteins to particular cellular organelles.

One type of sorting signal, called a signal sequence, a signal peptide, or a leader sequence, directs a class of proteins to an organelle called the endoplasmic reticulum
15 (ER). The ER separates the membrane-bounded proteins from all other types of proteins. Once localized to the ER, both groups of proteins can be further directed to another organelle called the Golgi apparatus. Here, the Golgi distributes the proteins to vesicles, including secretory vesicles, the cell membrane, lysosomes, and the other organelles.

20 Proteins targeted to the ER by a signal sequence can be released into the extracellular space as a secreted protein. For example, vesicles containing secreted proteins can fuse with the cell membrane and release their contents into the extracellular space - a process called exocytosis. Exocytosis can occur constitutively or after receipt of a triggering signal. In the latter case, the proteins are stored in secretory vesicles (or
25 secretory granules) until exocytosis is triggered. Similarly, proteins residing on the cell membrane can also be secreted into the extracellular space by proteolytic cleavage of a "linker" holding the protein to the membrane.

Despite the great progress made in recent years, only a small number of genes encoding human secreted proteins have been identified. These secreted proteins include
30 the commercially valuable human insulin, interferon, Factor VIII, human growth hormone, tissue plasminogen activator, and erythropoietin. Thus, in light of the pervasive role of secreted proteins in human physiology, a need exists for identifying and characterizing novel human secreted proteins and the genes that encode them. This knowledge will allow one to detect, to treat, and to prevent medical disorders by using
35 secreted proteins or the genes that encode them.

Summary of the Invention

The present invention relates to novel polynucleotides and the encoded polypeptides. Moreover, the present invention relates to vectors, host cells, antibodies, and recombinant methods for producing the polypeptides and polynucleotides. Also provided are diagnostic methods for detecting disorders related to the polypeptides, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying binding partners of the polypeptides.

Detailed Description

Definitions

The following definitions are provided to facilitate understanding of certain terms used throughout this specification.

In the present invention, "isolated" refers to material removed from its original environment (e.g., the natural environment if it is naturally occurring), and thus is altered "by the hand of man" from its natural state. For example, an isolated polynucleotide could be part of a vector or a composition of matter, or could be contained within a cell, and still be "isolated" because that vector, composition of matter, or particular cell is not the original environment of the polynucleotide.

In the present invention, a "secreted" protein refers to those proteins capable of being directed to the ER, secretory vesicles, or the extracellular space as a result of a signal sequence, as well as those proteins released into the extracellular space without necessarily containing a signal sequence. If the secreted protein is released into the extracellular space, the secreted protein can undergo extracellular processing to produce a "mature" protein. Release into the extracellular space can occur by many mechanisms, including exocytosis and proteolytic cleavage.

As used herein, a "polynucleotide" refers to a molecule having a nucleic acid sequence contained in SEQ ID NO:X or the cDNA contained within the clone deposited with the ATCC. For example, the polynucleotide can contain the nucleotide sequence of the full length cDNA sequence, including the 5' and 3' untranslated sequences, the coding region, with or without the signal sequence, the secreted protein coding region, as well as fragments, epitopes, domains, and variants of the nucleic acid sequence. Moreover, as used herein, a "polypeptide" refers to a molecule having the translated amino acid sequence generated from the polynucleotide as broadly defined.

In the present invention, the full length sequence identified as SEQ ID NO:X was often generated by overlapping sequences contained in multiple clones (contig

analysis). A representative clone containing all or most of the sequence for SEQ ID NO:X was deposited with the American Type Culture Collection ("ATCC"). As shown in Table 1, each clone is identified by a cDNA Clone ID (Identifier) and the ATCC Deposit Number. The ATCC is located at 12301 Park Lawn Drive, Rockville,
5 Maryland 20852, USA. The ATCC deposit was made pursuant to the terms of the Budapest Treaty on the international recognition of the deposit of microorganisms for purposes of patent procedure.

A "polynucleotide" of the present invention also includes those polynucleotides capable of hybridizing, under stringent hybridization conditions, to sequences contained
10 in SEQ ID NO:X, the complement thereof, or the cDNA contained within the clone deposited with the ATCC. "Stringent hybridization conditions" refers to an overnight incubation at 42° C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM sodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed
15 by washing the filters in 0.1x SSC at about 65°C.

Also contemplated are nucleic acid molecules that hybridize to the polynucleotides of the present invention at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages
20 of formamide result in lowered stringency); salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37°C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH₂PO₄; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 µg/ml salmon sperm blocking DNA; followed by washes at 50°C with 1XSSPE, 0.1% SDS. In addition, to achieve even
25 lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include
30 Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

Of course, a polynucleotide which hybridizes only to polyA+ sequences (such
35 as any 3' terminal polyA+ tract of a cDNA shown in the sequence listing), or to a

complementary stretch of T (or U) residues, would not be included in the definition of "polynucleotide," since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically any double-stranded cDNA clone).

5 The polynucleotide of the present invention can be composed of any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and
10 double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A polynucleotide may also contain one or more modified bases or DNA or RNA backbones modified for stability
15 or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications can be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.

 The polypeptide of the present invention can be composed of amino acids joined
20 to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres, and may contain amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more detailed monographs,
25 as well as in a voluminous research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be
30 branched, for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic polypeptides may result from posttranslation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a
35 nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine,

formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. (See, for instance, PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth Enzymol 182:626-646 (1990); Rattan et al., Ann NY Acad Sci 663:48-62 (1992).)

"SEQ ID NO:X" refers to a polynucleotide sequence while "SEQ ID NO:Y" refers to a polypeptide sequence, both sequences identified by an integer specified in Table 1.

"A polypeptide having biological activity" refers to polypeptides exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. In the case where dose dependency does exist, it need not be identical to that of the polypeptide, but rather substantially similar to the dose-dependence in a given activity as compared to the polypeptide of the present invention (i.e., the candidate polypeptide will exhibit greater activity or not more than about 25-fold less and, preferably, not more than about tenfold less activity, and most preferably, not more than about three-fold less activity relative to the polypeptide of the present invention.)

25 Polynucleotides and Polypeptides of the Invention

FEATURES OF PROTEIN ENCODED BY GENE NO: 1

This gene is expressed primarily in testes tumor and to a lesser extent in fetal brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer particularly of the testes, and defects of the central nervous system such as seizure and neurodegenerative disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly cancer of the testes and central nervous system,

expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., testes and other reproductive tissue, brain and other tissue of the nervous system, and blood cells, and spleen, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of testicular cancer and treatment of central nervous system disorders since this gene is primarily expressed in the testes tumor and developing brain.

FEATURES OF PROTEIN ENCODED BY GENE NO: 2

This gene is expressed primarily in cancer tissues, such as breast cancer and Wilm's tumor, and to a lesser extent in fetal tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, and/or tumors, particularly, those found in the breast, and developmental abnormalities or disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the glandular tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., mammary tissue, and fetal tissue and, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 314 as residues: Pro-11 to Thr-18, Leu-43 to Pro-50, Gly-64 to Leu-72, and Leu-81 to Lys-86.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of cancers and/or tumors, particularly, those found in the breast since expression is mainly in cancer/tumor tissues. May serve as therapeutic proteins for proliferation/differentiation of fetal tissues.

FEATURES OF PROTEIN ENCODED BY GENE NO: 3

This gene is expressed primarily in CD34 depleted buffy coat and to a lesser extent in spleen, chronic lymphocytic leukemia.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: blood disorders or leukemias, diseases of the immune system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for
10 differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and spleen, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or
15 cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of blood disorders or
20 leukemias, diseases of the immune system since expression is in tissues related to immune function.

FEATURES OF PROTEIN ENCODED BY GENE NO: 4

This gene is expressed primarily in CD34 depleted buffy coat.

25 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: blood disorders or lymphocytic diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification
30 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual
35 having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of blood disorders since expression is in tissues related to immune function.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 5

This gene is expressed primarily in CD34 depleted buffy coat.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: blood or immune
10 diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and cancerous
15 and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 317 as residues:
20 Pro-13 to Lys-21.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of blood disorders since expression is in tissues related to immune function.

25 FEATURES OF PROTEIN ENCODED BY GENE NO: 6

This gene is expressed primarily in CD34 depleted buffy coat.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: blood or immune
30 diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., and blood cells, and
35 cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level

in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 318 as residues: Lys-31 to Lys-39.

5 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of blood diseases since it is expressed in tissues related to immune function.

FEATURES OF PROTEIN ENCODED BY GENE NO: 7

10 This gene is expressed primarily in CD34 depleted buffy coat and to a lesser extent in pineal gland.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: diseases of the immune system and brain associated diseases. Similarly, polypeptides and antibodies directed to
15 these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and pineal gland, and cancerous and wounded tissues) or
20 bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

25 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of blood disorders, immune diseases or brain associated diseases (specifically of the pineal gland) since expression is in tissues related to immune function.

FEATURES OF PROTEIN ENCODED BY GENE NO: 8

30 The translation product of this gene shares sequence homology with an organic cation transporter which is thought to be important in organic cation uptake in the kidney and liver. (See Accession No. 2343059.) Preferred polypeptide fragments comprise the amino acid sequence ITIAIQMICLVNXELYPTFVRNXGVMVCSSLCDIGGIPT
FIVFRLREVWQALPLILFAVLGLLAAGVTLLLPETKGVALPETMKDAENLGRKAKPKENTIYLK
35 VQTSEPSGT (SEQ ID NO: 615) or TMKDAENLGRKAKPKENT (SEQ ID NO: 616) as well as N-terminal and C-terminal deletions of these fragments. Also preferred are polynucleotide fragments encoding these polypeptide fragments.

This gene is expressed primarily in liver.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: hepatic and renal diseases where drug elimination/cation exchange (organic cation uptake) in the liver and kidney are problematic. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hepatic or renal system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., kidney and liver, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 320 as residues: Asn-64 to Asn-74, and Gln-81 to Gly-87.

The tissue distribution and homology to organic cation transporter indicate that polynucleotides and polypeptides corresponding to this gene are useful as a polyspecific transporter that is important for drug elimination in the liver (and possibly kidney) since expression is found in the liver.

FEATURES OF PROTEIN ENCODED BY GENE NO: 9

This gene is expressed primarily in eosinophil induced with IL-5 and to a lesser extent in fetal liver and spleen. This gene also maps to chromosome 15, and therefore can be used in linkage analysis as a marker for chromosome 15.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: diseases of the immune system, particularly allergies or asthma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, liver, and spleen, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the

standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating/diagnosis of diseases involving eosinophil reactions since expression seems to be concentrated in eosinophils and other tissues involved in immunity such as the liver and spleen.

FEATURES OF PROTEIN ENCODED BY GENE NO: 10

This gene is expressed primarily in tissues of hematopoietic lineage and to a lesser extent in Hodgkins lymphoma. Any frame shifts in this sequence can easily be clarified using known molecular biology techniques.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, and immune deficiency or dysfunction. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., hematopoietic cells, lymphoid and reticuloendothelial tissues, and cancerous tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/ diagnosis for lymphomas or immune dysfunction or as a therapeutic protein useful in immune modulation based on expression in anergic T-cells and lymphomas.

30 FEATURES OF PROTEIN ENCODED BY GENE NO: 11

This gene is expressed primarily in neutrophils and to a lesser extent in activated lymphoid cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the cell type present in a biological sample and for diagnosis of diseases and conditions: inflammation. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders

of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells and lymphoid tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another
5 tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 323 as residues: Glu-40 to Lys-46.

The tissue distribution indicates that polynucleotides and polypeptides
10 corresponding to this gene are useful for modulation of an immune reaction or as a growth factor for the differentiation or proliferation of neutrophils for the treatment of neutropenia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 12

15 This gene is expressed primarily in brain and to a lesser extent in activated T-cells. It is likely that the open reading frame containing the predicted signal peptide continues in the 5' direction. Preferred polypeptide fragments comprise the amino acid sequence PRVRNSPEDLGLSLTGDSCKL (SEQ ID NO:617).

Therefore, polynucleotides and polypeptides of the invention are useful as
20 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neurodegenerative disorders including ischemic shock, alzheimers and cognitive disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a
25 number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and brain, and other tissue of the nervous system and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from
30 an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 324 as residues: Ser-5 to Glu-14, Ile-21 to Pro-35, Ser-65 to Asp-81, Cys-89 to Val-96, Lys-136 to Ser-145, Ile-152 to Met-169, and Arg-189 to Lys-196.

35 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnostic/treatment for cancers of the given tissue or in the treatment of neurological disorders of the CNS.

FEATURES OF PROTEIN ENCODED BY GENE NO: 13

This gene was also recently cloned by other groups, naming this calcium-activated potassium channel gene, hKCa4. (See Accession No. AF033021, see also, Accession
 5 No. 2584866.) This gene is mapped to human chromosome 19q13.2. A second signal sequence likely exists upstream from the predicted signal sequence as described in Table 1. Preferred polypeptide fragments comprise: QADDLQATVAALCVLRGGGPWAG SWLSPKTPGAMGGDLVLGLGALRRRKRL (SEQ NO: 618); or EQEKSLAGWALVLAXXGIGL MVLHAEMLWFGGCSAVNATGHLSDTLWLIPITFLTIGYGDVVPGMTWVGKIVCLCTGVMGVCC
 10 TALLVAVVARKLEFNKAEKHVHNFMMDIQYTKEMKESAAARVLQEAWMFYKHTRRKESHAAR XHQRXLLAAINAFRQVRLKHKRLREQVNSMVDISKMHMILYDLQQLSSSHRALEKQIDTLAG KLDALTELLSTALGPRQLPEPSQQSK (SEQ ID NO: 619), as well as N-terminal and C-terminal deletions. Also preferred are polynucleotide fragments encoding these polypeptide fragments.

15 This gene is expressed primarily in breast lymph node and T-cells, and to a lesser extent in placenta.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: hematologic and
 20 immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., lymphoid
 25 tissue, blood cells and placenta, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a
 30 sequence shown in SEQ ID NO. 325 as residues: Arg-13 to Lys-23.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment/diagnosis of hematologic and diseases involving immune modulation based on distribution in the lymph node and T-cells.

FEATURES OF PROTEIN ENCODED BY GENE NO: 14

This gene was recently cloned by another group, calling it PAPS synthase. (See Accession No. e1204135.) Preferred polypeptide fragments comprise the amino acid sequence YQAHHVSRNKRQVVGTRGGFRGCTVWLTGLSGAGK (SEQ ID NO: 620).

5 Also preferred are the polynucleotide fragments encoding this polypeptide fragment.

It has been discovered that this gene is expressed primarily in benign prostate hyperplasia, Human Umbilical Vein Endothelial Cells and to a lesser extent in smooth muscle and Human endometrial stromal cells-treated with estradiol.

Therefore, polynucleotides and polypeptides of the invention are useful as
10 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: inflammation, ischemia, and restenosis, based on endothelial cell and smooth muscle cell expression, and prostate diseases such as benign prostate hyperplasia or prostate cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing
15 immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the prostate or vessels of the circulatory system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., prostate, endothelial cells, smooth muscle, and endometrium, and cancerous and wounded tissues) or bodily
20 fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 326 as residues: Arg-21 to Asp-26, Lys-35 to Lys-44,
25 Glu-49 to Asn-58.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating/diagnosing diseases or conditions where the endothelial cell lining of the veins and arteries of underlying smooth muscle are involved.

30

FEATURES OF PROTEIN ENCODED BY GENE NO: 15

This gene is expressed primarily in human 6 week embryo and to a lesser extent in placenta.

Therefore, polynucleotides and polypeptides of the invention are useful as
35 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: developmental anomalies or fetal deficiencies. Similarly, polypeptides and antibodies directed to these

polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly developmental in nature, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., embryonic tissue, and placenta, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 327 as residues Lys-50 to Glu-57.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for detection of developmental abnormalities.

FEATURES OF PROTEIN ENCODED BY GENE NO: 16

This gene is expressed primarily in kidney and amygdala and to a lesser extent in fetal tissues. This gene is mapped to chromosome 14, and therefore is useful in linkage analysis as a marker for chromosome 14.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) present in a biological sample and for diagnosis of diseases and conditions: kidney diseases, neurological disorders and developmental abnormalities. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s). For a number of disorders of the above tissues, particularly of the renal system or developing fetal tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., kidney, amygdala, and fetal tissues, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment or diagnosis of conditions affecting the brain, kidneys and fetal development.

FEATURES OF PROTEIN ENCODED BY GENE NO: 17

This gene is expressed primarily in ovarian cancer.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: solid tumors similar to ovarian cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., ovarian and other reproductive tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 329 as residues Ser-51 to Val-56.
- The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment of solid tumors of the reproductive system such as ovarian cancer.

FEATURES OF PROTEIN ENCODED BY GENE NO: 18

This gene is expressed primarily in brain medulloblastoma. Preferred polypeptide fragments comprise the amino acid sequence: IRHEQHPNFSLEMHSGSSLLFLPQL ILILPVCAHLHEELNC (SEQ ID NO: 643) and SFFISEEKGHLLLQAERHPWVAGALVGVSGLTLTTCSGPTEKPATKNYFLKRLQLQEMHIRAN (SEQ ID NO: 644), as well as N-terminal and C-terminal deletions. Also preferred are polynucleotide fragments encoding these polypeptide fragments.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumors particularly of the CNS or. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the Central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene

expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating medulloblastoma or similar tumors.

5

FEATURES OF PROTEIN ENCODED BY GENE NO: 19

This gene is expressed primarily in adipocytes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: obesity. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the adipose tissues expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., adipocytes and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating obesity by regulating the function and number of adipocytes

FEATURES OF PROTEIN ENCODED BY GENE NO: 20

This gene is expressed primarily in B cell lymphoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, of the immune system with an emphasis on B cell lymphoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the tumors of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and lymphoid tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,

the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of B cell derived tumors based on its expression in b cell lymphomas

FEATURES OF PROTEIN ENCODED BY GENE NO: 21

This gene is expressed primarily in immune cells and to a lesser extent in fetal tissues

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: inflammatory diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., cells of the immune system, and fetal tissues, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:333 as residues Asp-10 to Pro-19, Ser-74 to Tyr-79, Glu-95 to Lys-110.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of diseases involving alterations in T cell activity.

FEATURES OF PROTEIN ENCODED BY GENE NO: 22

It has been discovered that this gene is expressed primarily in ovarian tumor.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumors particularly of the ovary. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of tumors of the reproductive organs. expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., ovarian

and other reproductive tissue and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 334 as residues: Leu-22 to Gln-27.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of ovarian tumors as it has only been identified in ovarian tumors.

FEATURES OF PROTEIN ENCODED BY GENE NO: 23

It has been discovered that this gene is expressed primarily in fetal tissues and to a lesser extent in osteoclastoma cell line

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: osteoporosis or arthritis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skeletal expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone cells, and fetal tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of conditions of abnormal bone remodeling due to enhanced activity of osteoclasts. This may be useful as a specific marker for malignancies derived from osteoclasts or their precursors.

FEATURES OF PROTEIN ENCODED BY GENE NO: 24

The translation product of this gene shares sequence homology with a periplasmic ribonuclease which is thought to be important in degrading extracellular polynucleotides

It has been discovered that this gene is expressed primarily in serum treated smooth muscle cells

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: vascular disease such as restenosis. Similarly, polypeptides and antibodies directed to these polypeptides are
5 useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the vasculature expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., smooth muscle, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or
10 spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 336 as residues: Gln-30 to Lys-36, and Pro-41 to Arg-48.

15 The tissue distribution and homology to ribonucleases indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment of pathological conditions of smooth muscle associated with bacterial or viral infiltration

FEATURES OF PROTEIN ENCODED BY GENE NO: 25

20 This gene is expressed primarily in Early Stage Human Brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: human brain development and related diseases. Similarly, polypeptides and antibodies directed to
25 these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the human brain development and related diseases, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and
30 cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to this gene indicate that polynucleotides
35 and polypeptides corresponding to this gene are useful for diagnosis and treatment of diseases affecting human brain development and related diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 26

It has been discovered that this gene is expressed primarily in human brain tissue.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: human brain diseases and other diseases related to brain diseases, which may be caused by brain diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in
10 providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the human brain diseases, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum,
15 plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

 The tissue distribution and homology to the gene indicate that polynucleotides
20 and polypeptides corresponding to this gene are useful for diagnosis and treatment of human brain diseases and other diseases related.

FEATURES OF PROTEIN ENCODED BY GENE NO: 27

It has been discovered that this gene is expressed primarily in Anergic T-cells.

25 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immune diseases, inflammatory diseases and diseases related to T lymph cells. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological
30 probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune diseases, inflammatory diseases and diseases related to T lymph cells, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and cancerous and wounded tissues) or bodily fluids (e.g.,
35 serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene

expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to the gene indicate that polynucleotides and polypeptides corresponding to this gene are useful for immune diseases,
5 inflammatory diseases and diseases related to T lymph cells.

FEATURES OF PROTEIN ENCODED BY GENE NO: 28

The translation product of this gene shares sequence homology with *Shigella flexneri* positive transcriptional regulator CriR (criR) gene which is thought to be
10 important in regulation of gene expression.

This gene is expressed primarily in human synovial sarcoma and normal human brain tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
15 biological sample and for diagnosis of diseases and conditions: human brain diseases particularly sarcomas of the synovium. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the human brain and synovium and other related human
20 brain diseases, expression of this gene at significantly higher or lower levels may be routinely detected in certain (e.g., synovial tissue, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,
25 the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of human synovial sarcoma and other related human brain diseases.

30

FEATURES OF PROTEIN ENCODED BY GENE NO: 29

This gene is expressed in bone marrow, infant brain, fetal liver and spleen, prostate and to a lesser extent in pineal gland, adipose tissue, kidney, adrenal gland, umbilical vein endothelial cells, and T cells.

35 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: diseases related to bone marrow or

hematoplastic tissues, prostate, kidney, adrenal gland, and cardiovascular tissue or organs. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the diseases related to hematoplastic tissues, immune system, prostate, kidney, adrenal gland, and cardiovascular tissue or organs, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone marrow, hematopoietic cells, pineal gland, adipose tissue, kidney, adrenal gland, endothelial cells, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to the gene indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of diseases related to hematoplastic tissues, immune system, prostate, kidney, adrenal gland, and cardiovascular tissue or organs.

FEATURES OF PROTEIN ENCODED BY GENE NO: 30

This gene is expressed primarily in meningea and to a lesser extent in breast and adult brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: Diseases of the meningea and related brain diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the meningea and related brain diseases, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., meningea, mammary tissue, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of diseases of the meningea and related brain diseases.

5 **FEATURES OF PROTEIN ENCODED BY GENE NO: 31**

This gene is expressed in meningea, fetal spleen, osteoblast and to a lesser extent in activated T-cells, endometrial stromal cells, fetal lung, HL-60, thymus, testis and endothelial cells.

Therefore, polynucleotides and polypeptides of the invention are useful as
10 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: meningeal disease, osteoporosis, immune diseases, and hematoplastic diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for identification of the tissue(s) or cell type(s). For a number of disorders of the
15 above tissues or cells, particularly of the meningeal diseases, osteoporosis, immune diseases, and hematoplastic diseases, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, endometrium, lung, thymus, testis, and endothelial cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal
20 fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to gene indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of
25 meningeal, osteoporosis, immune diseases, hematoplastic diseases, testis diseases and lung diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 32

This gene is expressed primarily in human thymus and to a much lesser extent
30 in infant brain, T-cells, smooth muscle, endothelial cells, bone marrow, human ovarian tumor and keratinocytes testes, osteoclastoma, breast, and tonsils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: Diseases involving the
35 thymus, particularly thymic cancer and diseases involving T-cell maturation. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a

number of disorders of the above tissues or cells, particularly of the thymus, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., thymus, brain, and other tissue of the nervous system, blood cells, bone marrow, ovaries, and testes, and other reproductive tissue, mammary
5 tissue, tonsils, melanocytes and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

10 The tissue distribution and homology to gene indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of diseases of the thymus particularly thymic cancer and diseases involving T-cell maturation.

15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 33**

This gene is expressed primarily in human tonsils, and placenta, and to a lesser extent in adipocytes, melanocyte, and infant brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
20 biological sample and for diagnosis of diseases and conditions: inflammatory diseases, immune diseases, and obesity. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the inflammatory diseases, immune diseases, and obesity, expression of
25 this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., tonsils, placenta, adipocytes, melanocytes, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard
30 gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to this gene indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of diseases such as inflammation, immune diseases, and obesity.

35

FEATURES OF PROTEIN ENCODED BY GENE NO: 34

This gene is expressed in activated T cells, and to a lesser extent in pituitary, testis, and breast lymph node.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: diseases relating to T cells. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the disorders of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., pituitary, testes and other reproductive tissue, mammary tissue, and lymphoid tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of immune disorders.

20 FEATURES OF PROTEIN ENCODED BY GENE NO: 35

This gene is expressed primarily in infant brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neurological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the diseases relating to neurological disorders, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain, and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of neurological disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 36

This gene is expressed primarily in infant brain.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions: neurological disorders.
Similarly, polypeptides and antibodies directed to these polypeptides are useful in
providing immunological probes for differential identification of the tissue(s) or cell
10 type(s). For a number of disorders of the above tissues or cells, particularly of the
diseases relating to neurological disorders, expression of this gene at significantly
higher or lower levels may be routinely detected in certain tissues and cell types (e.g.,
brain and other tissue of the nervous system, and cancerous and wounded tissues) or
bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another
15 tissue or cell sample taken from an individual having such a disorder, relative to the
standard gene expression level, i.e., the expression level in healthy tissue or bodily
fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
corresponding to this gene are useful for diagnosis and treatment of neurological
20 disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 37

This gene is expressed primarily in human ovary.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
25 biological sample and for diagnosis of diseases and conditions: ovarian cancer.
Similarly, polypeptides and antibodies directed to these polypeptides are useful in
providing immunological probes for differential identification of the tissue(s) or cell
type(s). For a number of disorders of the above tissues or cells, particularly of the
ovarian disorders such as those involving germ cells, ovarian follicles, stromal cells,
30 expression of this gene at significantly higher or lower levels may be routinely detected
in certain tissues and cell types (e.g., ovary and other reproductive tissue, and
cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial
fluid or spinal fluid) or another tissue or cell sample taken from an individual having
such a disorder, relative to the standard gene expression level, i.e., the expression level
35 in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
corresponding to this gene are useful for diagnosis and treatment of ovarioathy.

FEATURES OF PROTEIN ENCODED BY GENE NO: 38

This gene is expressed primarily in lymph node breast cancer.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions: breast cancer. Similarly,
polypeptides and antibodies directed to these polypeptides are useful in providing
immunological probes for differential identification of the tissue(s) or cell type(s). For a
number of disorders of the above tissues or cells, particularly of the breast cancer,
10 expression of this gene at significantly higher or lower levels may be routinely detected
in certain tissues and cell types (e.g., mammary tissue and lymphoid tissue, and
cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial
fluid or spinal fluid) or another tissue or cell sample taken from an individual having
such a disorder, relative to the standard gene expression level, i.e., the expression level
15 in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
corresponding to this gene are useful for used as a diagnostic marker for breast cancer.

FEATURES OF PROTEIN ENCODED BY GENE NO: 39

20 This gene is expressed primarily in brain and to a lesser extent in other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions: neuronal disorders such
as trauma, brain degeneration, and brain tumor. Similarly, polypeptides and antibodies
25 directed to these polypeptides are useful in providing immunological probes for
differential identification of the tissue(s) or cell type(s). For a number of disorders of
the above tissues or cells, particularly of the brain, expression of this gene at
significantly higher or lower levels may be routinely detected in certain tissues and cell
types (e.g., brain and other tissue of the nervous system, and cancerous and wounded
30 tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or
another tissue or cell sample taken from an individual having such a disorder, relative to
the standard gene expression level, i.e., the expression level in healthy tissue or bodily
fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
35 corresponding to this gene are useful for diagnosis and therapeutic treatment of
neuronal disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 40

5 This gene is expressed in early stage human embryo, adrenal gland tumor, and immune tissues such as fetal liver, fetal spleen, T-cell, and myeloid progenitor cell line and to a lesser extent in ovary, colon cancer, and a few other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumorigenesis including
10 adrenal gland tumor, colon cancer and various other tumors, developmental and immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the cancer tissues, early stage human tissues, and immune system,
15 expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, spleen, blood cells, bone marrow, ovary and other reproductive tissue, and colon, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard
20 gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and therapeutic treatment of immune and developmental disorders, and tumorigenesis.

25

FEATURES OF PROTEIN ENCODED BY GENE NO: 41

This gene is expressed primarily in fetal lung, endothelial cells, liver, thymus and a few other immune tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as
30 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immune disorders such as immune deficiency and autoimmune diseases, pulmonary diseases, liver diseases, and tumor matasis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification
35 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the fetal lung, liver, endothelial cells, and immune tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain

tissues and cell types (e.g., lung, endothelial cells, liver, thymus, and other tissue of the immune system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,
5 the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis of immune disorders and pulmonary and hepatic diseases. Its promoter may also be used for immune system and lung-
10 specific gene therapies. The expression of this gene in endothelial cells indicates that it may also involve in angiogenesis which therefore may play role in tumor matasis.

FEATURES OF PROTEIN ENCODED BY GENE NO: 42

This gene is expressed primarily in liver, thyroid, parathyroid and to a lesser
15 extent in fetal lung, stomach and early embryos.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: metabolic regulation, obesity, hepatic failure, hepatocellular tumors or thyroiditis and thyroid tumors. Similarly,
20 polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the digestive/endocrine system expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, thyroid, parathyroid, lung,
25 stomach, and embryonic tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

30 The tissue distribution and the extracellular locations indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection and treatment of digestive/endocrine disorders, including metabolic regulation, hepatic failure, malabsorption, gastritis and neoplasms.

FEATURES OF PROTEIN ENCODED BY GENE NO: 43

This gene is expressed primarily in Schizophrenic adult brain, pituitary, front cortex, hypothalamus and to a lesser extent in retina, adipose and stomach cancer and placenta.

- 5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: schizophrenia and other neurological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification
- 10 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nerve system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., retinal tissue, adipose, stomach, and placenta, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or
- 15 cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful in treatment/detection of disorders in the nerve
- 20 system, including schizophrenia, neurodegeneration, and neoplasia. Additionally, a secreted protein in brain may serve as an endocrine.

FEATURES OF PROTEIN ENCODED BY GENE NO: 44

- The translation product of this gene shares sequence homology with GTP
- 25 binding proteins which are thought to be important in signal transduction and protein transport.

This gene is expressed primarily in umbilical vein and microvascular endothelial cells, GM-CSF treated macrophage, anergic T cells, osteoblast, osteoclast, CD34+ cells and to a lesser extent in gall bladder.

- 30 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: bone formation and growth, osteonecrosis, osteoporosis, angiogenesis and/or hematopoiesis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing
- 35 immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skeletal and hematopoiesis systems, expression of this gene at significantly higher or lower levels

may be routinely detected in certain tissues and cell types (e.g., endothelial cells, blood cells, bone, and gall bladder, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to GTP binding proteins indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment/detection of bone formation and growth, osteonecrosis, osteoporosis, and/or hematopoiesis because its involvement in the growth signaling or angiogenesis.

FEATURES OF PROTEIN ENCODED BY GENE NO: 45

The translation product of this gene shares sequence homology with signal sequence receptor gamma subunit which is thought to be important in protein translocation on endoplasmic reticulum.

This gene is expressed primarily in adrenal gland, salivary gland, prostate, and to a lesser extent in endothelial cells and smooth muscle.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: protein secretion. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the secretory organs, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., adrenal gland, salivary gland, prostate, endothelial cells, and smooth muscle, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to SSR gamma subunit indicate that polynucleotides and polypeptides corresponding to this gene are useful for endocrine disorders, prostate cancer, xerostomia or sialorrhea.

35 FEATURES OF PROTEIN ENCODED BY GENE NO: 46

This gene is expressed primarily in osteoclastoma cells and to a lesser extent in melanocyte, amygdala, brain, and stomach..

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: ossification, osteoporosis, fracture, osteonecrosis, osteosarcoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skeletal systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., melanocytes, amygdala, brain and other tissue of the nervous system, and stomach, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful in intervention of ossification, osteoporosis, fracture, osteonecrosis and osteosarcoma.

FEATURES OF PROTEIN ENCODED BY GENE NO: 48

The translation product of this gene shares sequence homology with proline rich proteins which is thought to be important in protein-protein interaction.

This gene is expressed primarily in brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neurological and psychological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nerve system and endocrine system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to proline-rich proteins indicate that polynucleotides and polypeptides corresponding to this gene are useful in intervention

and detection of neurological diseases, including trauma, neoplasia, degenerative or metabolic conditions in the central nerve system. Additionally, the gene product may be secreted by the brain as an endocrine.

5 **FEATURES OF PROTEIN ENCODED BY GENE NO: 49**

The translation product of this gene shares sequence homology with the AOCB gene from *Aspergillus nidulans* which is important in asexual development.

This gene is expressed primarily in infant brain and to a lesser extent in the developing embryo, trachea tumors, B-cell lymphoma and synovial sarcoma.

10 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neurodegenerative diseases, leukemia and sarcoma's. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential
15 identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain and immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., embryonic tissue, blood cells, trachea, and synovial tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or
20 spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in infant brain and sarcoma's and homology to a gene involved in a key step of eukaryotic development (fungal spore formation) indicates
25 that the protein product of this clone could play a role in neurological diseases such as schizophrenia, particularly in infants. The existence of the gene in a B-cell lymphoma indicates the gene may be used in the treatment and detection of leukemia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 50

30 This gene is expressed primarily in fetal lung.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: pulmonary disorders including lung cancer. Similarly, polypeptides and antibodies directed to these
35 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the pulmonary system, expression of this gene at significantly higher or

lower levels may be routinely detected in certain tissues and cell types (e.g., lung, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution of this gene only in fetal lung indicates that it plays a key role in development of the pulmonary system. This would suggest that misregulation of the expression of this protein product in the adult could lead to lymphoma or sarcoma formation, particularly in the lung. It may also be involved in predisposition to certain pulmonary defects such as pulmonary edema and embolism, bronchitis and cystic fibrosis.

FEATURES OF PROTEIN ENCODED BY GENE NO: 51

This gene is expressed primarily in hematopoietic cell types and fetal cells and to a lesser extent in all tissue types.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects in the immune system and hematopoiesis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., hematopoietic cells, and fetal tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution of this gene predominantly in hematopoietic cells and in the developing embryo indicates that polynucleotides and polypeptides corresponding to this gene are useful for detection and treatment of lymphomas and disease states affecting the immune system or hematopoiesis disorders such as leukemia, AIDS, arthritis and asthma..

FEATURES OF PROTEIN ENCODED BY GENE NO: 52

This gene is expressed primarily in prostate and to a lesser extent in fetal spleen, fetal liver, infant brain and T cell leukemias.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: prostate disorders, prostate cancer, leukemia. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, and/or prostate gland expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., thymus, spleen, liver, brain and other tissue of the nervous system, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution of this gene in prostate indicates that polynucleotides and polypeptides corresponding to this gene are useful for detection or treatment of prostate disorders or prostate cancer. Its distribution in fetal liver and fetal spleen indicates it may play a role in the immune system and its misregulation could lead to immune disorders such as leukemia, arthritis and asthma.

20

FEATURES OF PROTEIN ENCODED BY GENE NO: 53

The translation product of this gene shares sequence homology with dynein.

This gene is expressed primarily in brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neuro-degenerative diseases of the brain. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly neuro-degenerative diseases expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The predominant tissue distribution in the brain and homology to dynein, a microtubule motor protein involved in the positioning of cellular organelles and molecules indicates that polynucleotides and polypeptides corresponding to this gene are useful for detection/treatment of neurodegenerative diseases, such as Alzheimers, 5 Huntingtons, Parkinsons diseases and shizophrenia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 54

The translation product of this gene shares sequence homology with ubiquitin-conjugation protein, an enzyme which is thought to be important in the processing of 10 the Huntingtons Disease causing gene.

This gene is expressed primarily in brain and to a lesser extent in activated macrophages.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a 15 biological sample and for diagnosis of diseases and conditions: neurodegenerative disease states including Huntington's disease. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of brain tissues. For a number of disorders of the above tissues or cells, particularly of the neurological systems expression of this gene at 20 significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level 25 in healthy tissue or bodily fluid from an individual not having the disorder.

The predominant tissue distribution of this gene in the brain and its homology to a Huntington interacting protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for the regulation of the expression of the 30 Huntington disease gene and other neurodegenerative diseases including spinocerebellar ataxia types I and III, dentatorubropallidoluysian and spinal bulbar muscular atrophy. In addition, the existence of elevated levels of free ubiquitin pools in Alzheimer's disease, Parkinson's disease and amyotrophic lateral sclerosis indicates that the ubiquitin pathway of protein degradation plays a role in these disease states. Thus, considering the gene described here is homologous to a ubiquitin-conjugation 35 protein it may play a general role in neurodegenerative conditions.

FEATURES OF PROTEIN ENCODED BY GENE NO: 56

This gene is expressed primarily in T-cells (anergic T-cells, resting T-Cells, apoptotic T-cells) and lymph node (breast), as well as brain (hypothalamus, hippocampus, pituitary, infant brain, early-stage brain).

- 5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immune (e.g. immunodeficiencies, autoimmunities, inflammation, leukemias & lymphomas) and neurological (e.g. Alzheimer's disease, dementia, schizophrenia) disorders. Similarly,
- 10 polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous, hematopoietic and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood
- 15 cells, lymphoid tissue, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.
- 20 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful in the intervention or detection of pathologies associated with the hematopoietic and immune systems, such as anemias (leukemias). In addition, the expression in brain (including fetal) might suggest a role in developmental brain defects, neuro-degenerative diseases or behavioral abnormalities
- 25 (e.g. schizophrenia, Alzheimer's, dementia, depression, etc.).

FEATURES OF PROTEIN ENCODED BY GENE NO: 57

This gene is expressed primarily in lung, and to a lesser extent in a variety of other hematological cell types (e.g. Raji cells, bone marrow cell line, activated

30 monocytes).

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: pulmonary and/or hematological dysfunction. Similarly, polypeptides and antibodies directed to these
- 35 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the vasculo-pulmonary and hematopoietic systems, expression of this

gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., lung and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful in the intervention and detection of pathologies associated with the vasculo-pulmonary system. In addition the expression of this gene in a variety of leukocytic cell types and a bone marrow cell line might suggest a role in hematopoietic and immune system disorders, such as leukemias & lymphomas, inflammation, immunodeficiencies and autoimmunities.

FEATURES OF PROTEIN ENCODED BY GENE NO: 58

The translation product of this gene shares sequence homology with adenylate kinase isozyme 3 (gil163528 GTP:AMP phosphotransferase (EC 2.7.4.10) [Bos taurus]), which is thought to be important in catalyzing the phosphorylation of AMP to ADP in the presence of ATP or inorganic triphosphate.

This gene is expressed primarily in fetal liver, heart and placenta, and to a lesser extent in many other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: hepatic, cardiovascular or reproductive disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hepatic, cardiovascular and reproductive systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, heart, and placenta, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of conditions related to hepatic function and pathogenesis, in particular, those dealing with liver development and the differentiation of hepatocyte progenitor cells.

FEATURES OF PROTEIN ENCODED BY GENE NO: 59

This gene is expressed primarily in CD34 positive cells (Cord Blood).

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions: hematopoietic
differentiation and immune disorders. Similarly, polypeptides and antibodies directed to
these polypeptides are useful in providing immunological probes for differential
10 identification of the tissue(s) or cell type(s). For a number of disorders of the above
tissues or cells, particularly of hematopoietic and immune systems, expression of this
gene at significantly higher or lower levels may be routinely detected in certain tissues
and cell types (e.g., hematopoietic cells, and blood cells, and cancerous and wounded
tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or
15 another tissue or cell sample taken from an individual having such a disorder, relative to
the standard gene expression level, i.e., the expression level in healthy tissue or bodily
fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
corresponding to this gene are useful in the detection and treatment of conditions
associated with CD34-positive cells, and therefore as a marker for cell differentiation in
20 hematopoiesis, as well as immunological disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 60

The translation product of the predicted open reading frame of this contig has
sequence identity to the murine gene designated Insulin-Like Growth Factor-Binding
25 Protein (IGFBP)-1 as described by Lee and colleagues (Hepatology 19 (3), 656-665
(1994)).

This gene is expressed exclusively in hemangiopericytoma.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
30 biological sample and for diagnosis of hemangiopericytoma and other pericyte or
endothelial cell proliferative disorders. Similarly, polypeptides and antibodies directed
to these polypeptides are useful in providing immunological probes for differential
identification of the tissue(s) or cell type(s). For a number of disorders of the above
tissues or cells, particularly of the circulatory and immune systems, expression of this
35 gene at significantly higher or lower levels may routinely be detected in certain tissues
and cell types (e.g., pericyte or endothelial cells, and liver, and cancerous and wounded
tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or

another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Polynucleotides and polypeptides corresponding to this gene are useful as cell growth regulators since IGFBP-1-like molecules function as modulators of insulin-like growth factor activity. In addition, since IGFBP-1 is expressed at high levels following hepatectomy and during fetal liver development, polynucleotides of the present invention may also be used for the diagnosis of developmental disorders. Further, polypeptides of the present invention may be used therapeutically to treat developmental liver disorders as well as to regulate hepatocyte and supporting cell growth following hepatectomy or to treat liver disorders.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of hemangiopericytoma and liver disorders.

15

FEATURES OF PROTEIN ENCODED BY GENE NO: 61

This gene is expressed primarily in schizophrenic frontal cortex.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: nervous system and cognitive disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the frontal cortex and CNS expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study, treatment and diagnosis of frontal cortex, neuro-degenerative and CNS disorders

FEATURES OF PROTEIN ENCODED BY GENE NO: 62

This gene is expressed primarily in human adrenal gland tumor, and to a lesser extent in human kidney, medulla and adult pulmonary tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: metabolic, endocrine disorders. Similarly, polypeptides and antibodies directed to these polypeptides are
5 useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the endocrine and nervous system disorders and neoplasia, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., adrenal gland, kidney, brain and other tissue of the nervous system,
10 pulmonary tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

15 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study, treatment and diagnosis of neurological and endocrine disorders including neoplasia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 63

20 This gene is expressed primarily in human adipocytes, and to a lesser extent in spleen, 12-week old human, and testes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immune, metabolic and
25 growth disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., adipocytes,
30 spleen, and testes and other reproductive tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

35 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study, diagnosis and treatment of immune, developmental and metabolic disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 64

One translated product of this clone is homologous to the mouse zinc finger protein PZF. (See Accession No. 453376; see also Gene 152 (2), 233-238 (1995).) Preferred

5 polypeptide fragments correspond to the highly conserved domains shared between mouse and man. For example, preferred polypeptide fragments comprise the amino acid sequence: LQCEICGFTCRQKASLNWHMKKHDADSFYQFSCNICGKKFEKKDSVVAHKAKSH PEV (SEQ ID NO: 621); ITSTDILGTNPESLTQPSD (SEQ ID NO: 622); NSTSGECLLLEAEGM SKSY (SEQ ID NO: 623); CSGTERVSLMADGKIFVGS GSSGGTEGLVMNSDILGATTEVLIEDSD

10 SAGP (SEQ ID NO: 624); IQYVRCEMEGCGTVLAHPRYLQHIIKYQHLLKKKYVCPHPSCGRLR RLQKQLLRHAKHHT (SEQ ID NO: 625); DQRDYICEYCARAFKSSHNLA VHRMIHTGEK (SEQ ID NO: 626); RSSRTSVSRHRTENTRSSRSKTGSLQLICKSEPNTDQLDY (SEQ ID NO: 627); PFKDDPRDETYKPHLERETPKPRRKS G (SEQ ID NO: 630); QYVRCEMEGCGTVLAHPRYLQ HHIKYQHLLKKKYVCPHPSCGRLR RLQKQLLRHAKHHTD (SEQ ID NO: 629); or residues

15 151-182 of QRDYICEYCARAFKSSHNLA VHRMIHTGEKH Y (SEQ ID NO: 628). Also preferred are polynucleotide fragments encoding these polypeptide fragments.

This gene is expressed primarily in Rhabdomyosarcoma, melanocyte and colon cancer tissue and to a lesser extent in smooth muscle, pancreatic tumor, and apoptotic T-cells.

20 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s)

25 or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and hemopoetic, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., striated muscle, melanocytes, colon, smooth muscle, pancreas, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal

30 fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study, diagnosis and treatment of cancer and

35 hemopoetic disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 65

This gene is expressed primarily in human adipose and salivary gland tissue and to a lesser extent in human bone marrow and fetal kidney.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: metabolic and immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the metabolic and hemopoetic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., adipose, salivary gland, bone marrow, and kidney, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study, diagnosis of metabolic and immune disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 66

This translated product of this gene was recently identified as oxytocinase splice variant 1. (See Accession Nos. 2209276 and d1010078.) Preferred polypeptide fragments comprise the amino acid sequence: EMFDSL SYFKGSSLLMLKTYLSEDFQHAVVLYLHN HSYASIQSDDLWDSFNEVTNQTL DVKRMKTWTLQKGFPLVTVQKKGKELFIQQRFFLNMK PEIQPSDTRYM (SEQ ID NO: 631). Also preferred are polynucleotide fragments encoding this polypeptide fragment.

FEATURES OF PROTEIN ENCODED BY GENE NO: 67

This gene is expressed primarily in hemopoetic cells, particularly apoptotic T-cells, and to lesser extent in primary dendritic cells and adipose tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of apoptotic T-cells, primary dendritic cells, and adipose tissue present in a biological sample and for diagnosis of diseases and conditions: hemopoetic diseases including cancer and general immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell

type(s). For a number of disorders of the above tissues or cells, particularly of the oral and intestinal mucosa as well as hemopoetic and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., hematopoietic cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of diseases of the immune system, including cancer, hemopoetic and infectious diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 68

This gene is expressed primarily in kidney cortex and to a lesser extent in infant brain, heart, uterus, and blood.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of kidney tissue present in a biological sample and for diagnosis of diseases and conditions: soft tissue cancer, inflammation, kidney fibrosis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous and endocrines systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., kidney, brain, and other nervous tissue, heart, uterus, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study and treatment of cancer and fibroses.

FEATURES OF PROTEIN ENCODED BY GENE NO: 69

The translation product of this gene shares strong sequence homology with vertebrate and invertebrate protein tyrosine phosphatases.

This gene is expressed primarily in endometrial tumors, melanocytes, myeloid progenitors and to a lesser extent in infant brain, adipocytes, and several hematopoietic stem cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of transformed hematopoietic and epithelial cells present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, of skin and endometrium, leukemia. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous and hemopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., endometrium, melanocytes, bone marrow, adipocytes, hematopoietic cells, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and sequence similarity with tyrosine phosphatases indicate that polynucleotides and polypeptides corresponding to this gene are useful for study and treatment of cancer and hematopoietic disorders.

20 FEATURES OF PROTEIN ENCODED BY GENE NO: 70

This gene is expressed primarily in osteoclastoma, breast, and infant brain and to a lesser extent in various fetal and transformed bone, ovarian, and neuronal cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: degenerative conditions of the brain and skeleton. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous and skeletal system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone, mammary tissue, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study and treatment of degenerative, neurological and skeletal disorders.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 71

This gene was originally cloned from tumor cell lines. Recently another group has also cloned this gene, calling it the human malignant melanoma metastasis-suppressor (KiSS-1) gene. (See Accession No. U43527.) Preferred polypeptide fragments comprise the amino acid sequence: LEKVASVGNSRPTGQQLESGLLA (SEQ ID NO: 632); VHREEASCYCQAEPSGDL (SEQ ID NO: 633); RPALRQAGGGTREPRQKRWAGL (SEQ ID NO: 634); and AVNFRPQRSQSM (SEQ ID NO: 635). Any frame shifts can easily be resolved using known molecular biology techniques.

This gene is expressed primarily in many types of carcinomas and to a lesser extent in many normal organs.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissues(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer particularly melanomas, and other hyperproliferative disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of transformed organ tissue, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. As a tumor suppressor gene, increase amounts of the polypeptide can be used to treat patients having a particular cancer.

The tissue distribution indicates that this gene and the translated product is useful for diagnosing and study of cancer.

FEATURES OF PROTEIN ENCODED BY GENE NO: 72

This gene is expressed primarily in striatum and to a lesser extent in adipocytes and hemangiopericytoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of striatal cells present in a biological sample and for diagnosis of diseases and conditions: neurological, fat and lysosomal storage

diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., striatal tissue, adipocytes, and vascular tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis, study and treatment of neurodegenerative and growth disorders.

15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 73**

This gene is expressed primarily in bone marrow stromal cells and to a lesser extent in smooth muscle, testes, endothelium, and brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of bone marrow present in a biological sample and for diagnosis of diseases and conditions: connective tissue and hematopoietic diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skeletal and hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone marrow, stromal cells, smooth muscle, testes and other reproductive tissue, endothelium, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study, diagnosis, and treatment of connective tissue and blood diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 74

This gene is expressed primarily in brain, fetal liver and lung and to a lesser extent in retina, spinal chord, activated T-cells and endothelial cells.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of brain and regenerating liver present in a biological sample and for diagnosis of diseases and conditions: CNS and spinal chord injuries, immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells,
10 particularly of the nervous and immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, liver, pulmonary tissue, blood cells, and endothelial cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from
15 an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
corresponding to this gene are useful for study and treatment of hematopoietic and
20 neurological conditions.

FEATURES OF PROTEIN ENCODED BY GENE NO: 75

The translation product of this gene shares sequence homology with GTP binding proteins (intracellular).

25 This gene is expressed primarily in bone marrow, brain, and melanocytes and to a lesser extent in various endocrine and hematopoietic tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: hematopoietic and
30 nervous system conditions. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous and immune, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone
35 marrow, melanocytes, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder,

relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to nucleotide binding factors indicate that polynucleotides and polypeptides corresponding to this gene are useful for study,
5 diagnosis, and treatment of brain degenerative, skin and blood diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 76

This gene is expressed primarily in activated T-cells and to a lesser extent in retina, brain, and fetal bone.

10 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of activated T-cells and developing brain present in a biological sample and for diagnosis of diseases and conditions: immune deficiencies and skeletal and neuronal growth disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes
15 for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous, immune, and skeletomuscular sustems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, brain and other tissue of the nervous system, retinal tissue, and bone, and cancerous and wounded tissues) or
20 bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
25 corresponding to this gene are useful for diagnosis, study and treatment of cancer, urogenital, and brain degenerative diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 77

This gene is expressed primarily in fetal liver, activated monocytes, osteoblasts
30 and to a lesser extent in synovial, brain, and lymphoid tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of myeloid and lymphoid present in a biological sample and for diagnosis of diseases and conditions: inflammation, immune deficiencies, cancer. Similarly, polypeptides and antibodies directed to these
35 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system and skeleton, expression of this gene at significantly

higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, blood cells, bone, synovial tissue, brain and other tissue of the nervous system, and lymphoid tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample
5 taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study, diagnosis, and treatment of lymphoid
10 and mesenchymal cancers and nervous system diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 78

The translation product of this gene shares sequence homology with polymerase polyprotein precursor which is thought to be important in DNA repair and replication

15 This gene is expressed primarily in infant brain and to a lesser extent in tumors and tumor cell lines

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are
20 not limited to, especially of the neural system and developing organs. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the neural system expression of this gene at significantly higher or lower levels may be routinely detected
25 in certain (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

30 The tissue distribution and homology to polymerase polyprotein precursor indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of cancers especially of the neural system and developing organs

35 FEATURES OF PROTEIN ENCODED BY GENE NO: 79

This gene is expressed primarily in muscle and endothelial cells and to a lesser extent in brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: vascular diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the vascular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain (e.g., muscle, endothelial cells, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of disorders of the vascular and neural system including cardiovascular and endothelial.

FEATURES OF PROTEIN ENCODED BY GENE NO: 80

This gene is expressed primarily in placenta and to a lesser extent in fetal liver. Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: developmental disorders and disorder of the haemopoietic system, fetal liver and placenta. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of developmental disorders and disorder of the haemopoietic system, fetal liver and placenta, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., placenta and liver, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of developmental disorders and disorders of the haemopoietic system, fetal liver and placenta.

FEATURES OF PROTEIN ENCODED BY GENE NO: 81

This gene is expressed primarily in bone marrow, placenta and tissues and organs of the hematopoietic system.

- 5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: disorders of the bone and haemopoietic system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification
- 10 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, bone and hematopoietic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone marrow, placenta, and hematopoietic cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal
- 15 fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of disorders of the
- 20 immune, bone and hematopoietic system

FEATURES OF PROTEIN ENCODED BY GENE NO: 82

- The translation product of this gene shares sequence homology with secretory carrier membrane protein which is thought to be important in protein transport and
- 25 export. Any frame shifts in coding sequence can be easily resolved using standard molecular biology techniques. Another group recently cloned this gene, calling it SCAMP. (See Accession No. 2232243.)

This gene is expressed primarily in prostate, breast and spleen, and to a lesser extent in several other tissues and organs.

- 30 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: disorders of the breast prostate and spleen. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification
- 35 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly disorders of the breast prostate and spleen, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell

types (e.g., prostate, mammary tissue, and spleen, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to secretory carrier membrane protein indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of disorders of the breast, prostate and spleen.

10 **FEATURES OF PROTEIN ENCODED BY GENE NO: 83**

This gene is expressed primarily in developing organs and tissue like placenta and infant brain and to a lesser extent in developed organs and tissue like cerebellum and heart.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neurological diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the neural system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., placenta, heart, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of diseases of the neural system including neurological disorders and cancer.

30 **FEATURES OF PROTEIN ENCODED BY GENE NO: 84**

The translation product of this gene shares sequence homology with ATPase 6 in *Trypanosoma brucei* which is thought to be important in metabolism.

This gene is expressed primarily in tumor and fetal tissues and to a lesser extent in melanocytes, kidney cortex, monocytes and ovary.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a

biological sample and for diagnosis of diseases and conditions: metabolism disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the fetal systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., fetal tissues, melanocytes, kidney, blood cells, ovary and other tissue of the reproductive system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to ATPase indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of metabolism disorders, especially in fetal and tumor tissue growth.

15

FEATURES OF PROTEIN ENCODED BY GENE NO: 85

The translation product of this gene shares sequence homology with the immunoglobulin superfamily of proteins which are known to be important in immune response and immunity.

20 This gene is expressed primarily in stromal cells, colon cancer, lung, amygdala, melanocyte and to a lesser extent in a variety of other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects of stromal cell development and cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the stromal cells, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., stromal cells, colon, lung, amygdala, and melanocytes, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

35 The tissue distribution and homology to immunoglobulin indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of immune system disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 86

The translation product of this gene shares sequence homology with transcription initiation factor eIF-4 gamma which is thought to be important in gene transcription.

This gene is expressed primarily in tumor tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumorigenesis.

Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly in tumor tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., endometrium and lung, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to transcription initiation factor eIF-4 gamma indicate that polynucleotides and polypeptides corresponding to this gene are useful for gene regulation in tumorigenesis.

FEATURES OF PROTEIN ENCODED BY GENE NO: 87

The translation product of this gene shares sequence homology at low level in prolines with secreted basic proline-rich peptide II-2 which is thought to be important in protein structure or inhibiting hydroxyapatite formation in vitro.

This gene is expressed primarily in endometrial tumor and fetal lung.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: endometrial tumors. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the muscular/skeletal and reproductive systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., endometrium, and lung, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample

taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

5 The tissue distribution and homology to secreted basic proline-rich peptide II-2 indicate that polynucleotides and polypeptides corresponding to this gene are useful for inhibiting hydroxyapatite formation or establishing cell/tissue structure.

FEATURES OF PROTEIN ENCODED BY GENE NO: 88

10 This gene is expressed primarily in: amniotic cells induced with TNF in culture; and to a lesser extent in colon tissue from a patient with Crohn's Disease; parathyroid tumor; activated T-cells; cells of the human Caco-2 cell line; adenocarcinoma; colon; corpus colosum; fetal kidney; pancreas tumor; fetal brain; early stage brain, and anergic T-cells.

15 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumors. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system; 20 e.g., tumors, expression of this gene at significantly higher or lower levels may be routinely detected in certain (e.g., amniotic cells, colon, kidney, pancreas, parathyroid, brain and other tissue of the nervous system, blood cells, hematopoietic cells, liver, spleen, bone, testes and other reproductive tissue, brain and other tissue of the nervous system, and epithelial cells, and cancerous and wounded tissues) or bodily fluids (e.g., 25 serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

30 The tissue distribution indicates that the protein product of this clone is useful for modulating tumorigenesis and other immune system conditions such as disorders in immune response.

FEATURES OF PROTEIN ENCODED BY GENE NO: 89

35 This gene is expressed primarily in fetal liver/spleen and hematopoietic cells and to a lesser extent in brain, osteosarcoma, and testis tumor.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a

biological sample and for diagnosis of diseases and conditions: leukemia and hematopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., hematopoietic cells, liver, spleen, bone, testes, and other reproductive tissue, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of hematopoietic and immune disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 90

The translation product of this gene shares weak sequence homology with mouse Gcap1 protein which is developmentally regulated in brain.

This gene is expressed primarily in infant and adult brain and fetal liver/spleen and to a lesser extent in smooth muscle, T cells, and a variety of other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neurological or hematopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous, hematopoietic, immune, and endocrine systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, blood cells, liver, spleen, and smooth muscle, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and its homology to Gcap1 protein indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of disorders in neuronal, hematopoietic, immune, and endocrine systems.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 91

This gene is expressed primarily in brain and hematopoietic cells and to a lesser extent in tumor tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
10 biological sample and for diagnosis of diseases and conditions: disorder in nervous, hematopoietic, immune systems and tumorigenesis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous, hematopoietic, immune
15 systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,
20 the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful for diagnosis and treatment of disorders in the nervous, hematopoietic, and immune
25 systems.

FEATURES OF PROTEIN ENCODED BY GENE NO: 92

The translation product of this gene shares sequence homology with neuroendocrine-specific protein A which is thought to be important in neurologic systems.

30 This gene is expressed primarily in brain tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neural disorders and degeneration disease. Similarly, polypeptides and antibodies directed to these
35 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central or peripheral nervous systems, expression of this gene at

significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., hematopoietic cells, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having
5 such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to neuroendocrine-specific protein A indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment or diagnosis of neural disorders and degeneration disease.

10

FEATURES OF PROTEIN ENCODED BY GENE NO: 93

The translation product of this gene shares sequence homology with collagen-like protein and prolin-rich protein which are thought to be important in connective tissue function and tissue structure.

15 This gene is expressed primarily in fetal liver/spleen and brain tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neuronal or hematopoietic disorders. Similarly, polypeptides and antibodies directed to these
20 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous and hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, spleen, and brain and other tissue of the nervous system, and
25 cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to collagen-like protein and proline-rich
30 proteins indicate that polynucleotides and polypeptides corresponding to this gene are useful for supporting brain and hematopoietic tissue function and diagnosis and treatment of disorders in these functions.

FEATURES OF PROTEIN ENCODED BY GENE NO: 94

35 This gene is expressed primarily in embryonic tissues and tumor tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a

biological sample and for diagnosis of diseases and conditions which include, but are not limited to,. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system (e.g., tumors), expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., embryonic tissue and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of cancer.

15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 95**

This gene is expressed primarily in brain tumor, placenta, and melanoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: brain tumor or melanoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain or melanocytes, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, placenta, and melanocytes, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the translation product of this gene is useful in the diagnosis and treatment of brain tumors and melanoma.

FEATURES OF PROTEIN ENCODED BY GENE NO: 96

The translation product of this gene shares sequence homology with a yeast membrane protein, SUR4, which encodes for APA1 that acts on a glucose-signaling pathway that controls the expression of several genes that are transcriptionally regulated by glucose.

This gene is expressed primarily in fetal liver, and to a lesser extent in placenta and breast tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects of fetal liver or defects of glucose-regulated ATPase activities in tissues. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the fetal immune/hematopoietic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, placenta, and mammary tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to yeast SUR4 membrane protein indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of defects of fetal liver or defects of glucose-regulated ATPase activities.

FEATURES OF PROTEIN ENCODED BY GENE NO: 97

This gene is expressed primarily in fetal liver, brain, and amniotic fluid.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects of the fetal immune system and adult brain. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the fetal immune system and adult brain, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., amniotic fluid, serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful for detecting defects of the fetal immune and hematopoietic systems since fetal liver is

the predominant organ responsible for hematopoiesis in the fetus. In addition, the gene product of this gene is thought to be useful for detecting certain neurological defects of the brain.

5 **FEATURES OF PROTEIN ENCODED BY GENE NO: 98**

The translation product of this gene shares sequence homology with an yolk protein precursor, Vitellogenin which is thought to be important in binding lipids such as phosvitin.

This gene is expressed primarily in amniotic cells and fetal liver.

10 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects in amniotic cells, fetal liver development and the fetal immune system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes
15 for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the [insert system where a related disease state is likely, e.g., immune], expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., amniotic cells, and liver, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma,
20 urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

25 The tissue distribution and homology to vitellogenin indicate that the protein product of this clone is useful for treatment and diagnosis of defects in amniotic cells, fetal liver development and the fetal immune system.

FEATURES OF PROTEIN ENCODED BY GENE NO: 99

30 This gene is expressed primarily in placenta, endometrial tumor, osteosarcoma and stromal cells.

 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumor of the endometrium or bone, and osteosarcoma. Similarly, polypeptides and antibodies
35 directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the obstetric system (e.g. placenta,

endometrium) and the bones, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., placenta, endometrium, bone, and stromal cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of tumors and abnormalities of the endometrium, and the bones because of its abundance in the aforementioned tissues..

FEATURES OF PROTEIN ENCODED BY GENE NO: 100

This gene is expressed primarily in hepatocellular tumor.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: hepatocellular tumor. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the liver, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful for diagnosis and treatment of hepatocellular cancer because of its abundant expression in this tissue.

FEATURES OF PROTEIN ENCODED BY GENE NO: 101

This gene is expressed primarily in Corpus Colosum, fetal lung and infant brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects of the Corpus Colosum or defects of the fetal lung. Similarly, polypeptides and antibodies directed to

these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the Corpus Colosum and brain in general, and fetal lung, expression of this gene at significantly higher or lower levels may be routinely detected

5 in certain tissues and cell types (e.g., lung, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the

10 disorder.

The tissue distribution indicates that the protein product of this clone is useful for diagnosis and treatment of defects of the Corpus Colosum and brain in general, and defects of fetal lung.

15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 102**

This gene is expressed primarily in T cells and stromal cells, and to a lesser extent in adrenal gland.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a

20 biological sample and for diagnosis of diseases and conditions: defects of T cell immunity and stromal cell development. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at

25 significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, stromal cells, and adrenal gland, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily

30 fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful for diagnosis and treatment of defects of T cell immunity and stromal cell development because of its abundant expression in these tissues.

35 **FEATURES OF PROTEIN ENCODED BY GENE NO: 103**

This gene is expressed primarily in infant brain and placenta.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects of the brain and nervous system. Similarly, polypeptides and antibodies directed to these polypeptides
5 are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous system, especially brain, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and placenta, cancerous and
10 wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful
15 for detecting defects of the brain, especially in young children.

FEATURES OF PROTEIN ENCODED BY GENE NO: 105

This gene is expressed primarily in human osteoclastoma and to a lesser extent in human pancreas tumor.

20 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer particularly osteoclastoma and pancreatic tumor. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing
25 immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly in transformed tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone and pancreas, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or
30 another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful for diagnosis and treatment of some types of tumors, particularly pancreatic cancer and
35 osteoclastoma.

FEATURES OF PROTEIN ENCODED BY GENE NO: 106

This gene is expressed primarily in fetal liver/spleen, and to a lesser extent in activated T-Cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, spleen, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis or treatment of immune disorders.

20 FEATURES OF PROTEIN ENCODED BY GENE NO: 107

This gene is expressed primarily in human embryo and to a lesser extent in spleen and chronic lymphocytic leukemia.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: leukemia. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune or hemopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., embryonic tissue, spleen, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful for the diagnosis and treatment of leukemia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 108

This gene is expressed primarily in placenta, and to a lesser extent in early stage human brain and in lung.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: fetal developmental abnormalities. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s)
10 or cell type(s). For a number of disorders of the above tissues or cells, particularly in fetal and amniotic tissue, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., placenta, brain and other tissue of the nervous system, and lung, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another
15 tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this is useful for production of growth factor(s) associated with fetal development. Preferred
20 polypeptides comprise the full-length polypeptide shown in the sequence listing, truncated however, at the amino terminus and beginning with QTIE.

FEATURES OF PROTEIN ENCODED BY GENE NO: 109

This gene is expressed primarily in fetal spleen, and to a lesser extent in B-Cell
25 lymphoma and T-Cell lymphoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: lymphoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing
30 immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., spleen and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal
35 fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful for the treatment and diagnosis of human lymphomas.

FEATURES OF PROTEIN ENCODED BY GENE NO: 110

5 The translation product of this gene shares sequence homology with sarcoma amplified sequence (SAS), a tetraspan receptor which is thought to be important in malignant fibrous histiocyoma and liposarcoma.

This gene is expressed primarily in human osteoclastoma, and to a lesser extent in pineal gland and infant brain.

10 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: malignant fibrous histiocyoma and liposarcoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification
15 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone, pineal gland, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal
20 fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to sarcoma amplified sequence (SAS) indicate that the protein product of this clone is useful for treatment of, osteosarcoma,
25 malignant fibrous histiocyoma and liposarcoma and related cancers, particularly sarcomas.

FEATURES OF PROTEIN ENCODED BY GENE NO: 111

30 The translation product of this gene shares sequence homology with 6.8K proteolipid protein, mitochondrial - bovine.

This gene is expressed primarily in Wilm's tumor and to a lesser extent in cerebellum and placenta.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
35 biological sample and for diagnosis of diseases and conditions: Wilm's tumor. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell

type(s). For a number of disorders of the above tissues or cells, particularly of the immune or renal systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and placenta, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to 6.8K proteolipid protein indicate that the protein product of this clone is useful for diagnostic and therapeutics associated with tumors, particularly Wilm's tumor disease.

FEATURES OF PROTEIN ENCODED BY GENE NO: 112

This gene is expressed primarily in embryonic tissue and to a lesser extent in osteoblasts, endothelial cells, macrophages (GM-CSF treated), and bone marrow.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., embryonic tissue, bone, endothelial cells, blood cells and bone marrow, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment or diagnosis of immune disorders. Preferred polypeptides encoded by this gene comprise the following amino acid sequence: MITDVQLAIFANMLGVSLFLLVLYHYVAVNNPKKQE (SEQ ID NO: 636).

FEATURES OF PROTEIN ENCODED BY GENE NO: 113

This gene is expressed primarily in hepatocellular tumor, and to a lesser extent in fetal liver/spleen.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumors, particularly hepatocellular tumors. Similarly, polypeptides and antibodies directed to these

5 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hepatic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, and spleen, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma,

10 urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful

15 for diagnosis and treatment of tumors, particularly hepatocellular tumors.

FEATURES OF PROTEIN ENCODED BY GENE NO: 114

The translation product of this gene exhibits a very high degree of sequence identity with the human Pig8 gene which is thought to be important in p53 mediated

20 apoptosis. The sequence of this gene has since been published by Polyak and colleagues (Nature 389, 300-306 (1997)). In addition, the predicted translation product of this contig exhibits very high sequence homology with a murine gene denoted as EI24 which is also thought to be important in p53 mediated apoptosis.

This gene is expressed primarily in infant brain and activated T-cells and to a

25 lesser extent in bone marrow, fetal liver, and prostate.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, and tissue damage by radiation and anti-cancer drugs. Similarly,

30 polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the

35 nervous system, blood cells, bone marrow, liver, and prostate, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder,

relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to human Pig8 and murine EI24 genes indicate that polynucleotides and polypeptides corresponding to this gene are useful for preventing apoptosis in patients being treated with anti-oncogenic drugs such as etoposide, hydroperoxycyclophosphamide, and X-irradiation, since this protein product is upregulated in cells undergoing such treatment where p53 was overexpressed. It may also be useful in the treatment of hematopoietic disorders and in boosting numbers of hematopoietic stem cells by interfering with the apoptosis of progenitor cells. The mature polypeptide is predicted to comprise the following amino acid sequence:

EEMADSVKTFLQDLARGIKDSIWGICTISKLDARIQQKREEQRRRRASSVLAQRRRAQSIERKQES
 EPRIVSRIEQCCAWNGGVFWFSLLLFYRVFIPVLQSVTARIIGDPSLHGDVWSWLEFFLTSIFSA
 LWVLPLFVLSKVVNAIWFQDIADLAFEVSGRKPHFPSPSVSKIIADMLFNLLLQALFIQGMFVSL
 FPIHLVGQLVSLHMSLLYSLYCFEYRWFNKGIEMHQRLSNIERNWPYYFGFGLPLAFLTAMQ
 SSYIISGCLFSILFPLFIISANEAKTPGKAYLFQLRLFSLVVFLSNRLFHKTVYQLQSALSSSTSAEK
 FPSHPSPAKLKATAGH (SEQ ID NO: 637). Accordingly, polypeptides comprising the foregoing amino acid sequence are provided as are polynucleotides encoded such polypeptides.

20 FEATURES OF PROTEIN ENCODED BY GENE NO: 115

This gene is expressed primarily in stromal cells and to a lesser extent in multiple sclerosis.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: affecting the nervous system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., stromal cells and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of multiple sclerosis and other autoimmune diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 116

This gene is expressed primarily in the gall bladder

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions: gall stones or infection
of the digestive system . Similarly, polypeptides and antibodies directed to these
polypeptides are useful in providing immunological probes for differential identification
of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells,
10 particularly of the digestive system or renal system, expression of this gene at
significantly higher or lower levels may be routinely detected in certain tissues and cell
types (e.g., gall bladder and tissue of the digestive system, and cancerous and wounded
tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or
another tissue or cell sample taken from an individual having such a disorder, relative to
15 the standard gene expression level, i.e., the expression level in healthy tissue or bodily
fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
corresponding to this gene are useful for possible prevention of digestive disorders
where there may be a lack of digestive enzymes produced or in the detection and
20 possible prevention of gall stones.

FEATURES OF PROTEIN ENCODED BY GENE NO: 117

The translation product of this gene shares sequence homology with dystrophin
gene which is thought to be important in building and maintenance of muscles.

25 This gene is expressed primarily in placenta and to a lesser extent in fetal brain
and fetal liver, and spleen.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions: muscular dystrophy,
30 Duchenne and Becker's muscular dystrophies. Similarly, polypeptides and antibodies
directed to these polypeptides are useful in providing immunological probes for
differential identification of the tissue(s) or cell type(s). For a number of disorders of
the above tissues or cells, particularly of the skeletal muscle system, expression of this
gene at significantly higher or lower levels may be routinely detected in certain tissues
and cell types (e.g., placenta, brain and other tissue of the nervous system, muscle,
35 liver, and spleen, and cancerous and wounded tissues) or bodily fluids (e.g., serum,
plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from

an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

5 The tissue distribution and homology to the dystrophin gene indicate that polynucleotides and polypeptides corresponding to this gene are useful for diseases related the degenerative myopathies that are characterized by the weakness and atrophy of muscles without neural degradation; such as Duchenne and Becker's muscular dystrophies.

10 **FEATURES OF PROTEIN ENCODED BY GENE NO: 118**

This gene is expressed primarily in olfactory tissue and to a lesser extent in cartilage.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
15 biological sample and for diagnosis of diseases and conditions: connective tissue diseases; chondrosarcoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the connective tissue, expression of this gene at significantly higher or
20 lower levels may be routinely detected in certain tissues and cell types (e.g., olfactory tissue and cartilage, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the
25 disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for tumors of connective tissues, osteoarthritis and the treatment and diagnosis of chondrosarcoma.

30 **FEATURES OF PROTEIN ENCODED BY GENE NO: 119**

This gene is expressed primarily in Activated Neutrophils and to a lesser extent in fetal spleen, and CD34 positive cells from cord blood.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
35 biological sample and for diagnosis of diseases and conditions: allergies, defects in hematopoiesis and inflammation. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential

identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system and hematopoiesis system the, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and spleen, and cancerous and
5 wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
10 corresponding to this gene are useful for reducing the allergic effects felt by allergy suffers by neutralizing the activity of the immune system, especially since neutrophils are abundant in persons suffering from allergies and other inflammatory conditions.

FEATURES OF PROTEIN ENCODED BY GENE NO: 120

15 The translation product of this gene shares sequence homology with poly A binding protein II which is thought to be important in RNA binding for transcription of RNA to DNA

This gene is expressed primarily in colon and to a lesser extent in brain and immune system.

20 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: colon cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a
25 number of disorders of the above tissues or cells, particularly of the immune and digestive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., colon, tissue and cells of the immune system, and brain or other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal
30 fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to poly A binding protein II indicate that polynucleotides and polypeptides corresponding to this gene are useful for detection
35 and treatment of colon cancer and other disorders of the digestive system..

FEATURES OF PROTEIN ENCODED BY GENE NO: 121

The translation product of this gene shares sequence homology with thymidine diphosphoglucose 4.6 dehydrase which is thought to be important in the metabolism of sugar.

- 5 This gene is expressed primarily in fetal liver and spleen and to a lesser extent in infant brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: diabetes. Similarly,
10 polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the endocrine system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, spleen, and brain and other tissue of the
15 nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- 20 The tissue distribution and homology to thymidine diphosphoglucose 4.6 dehydrase indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment of persons with diabetes since it appears that this protein is needed in the metabolism of sugar in to its more basic components.

25 **FEATURES OF PROTEIN ENCODED BY GENE NO: 122**

- The translation product of this gene shares sequence homology with ceruloplasmin which is thought to be important in the metabolism and transport of iron and copper. Ceruloplasmin also contains domains with homology to clotting factors V and VIII. Defects in the circulating levels of ceruloplasmin (aceruloplasminemia) have
30 been associated with certain disease conditions such as Wilson disease, and the accompanying hepatolenticular degeneration.

This gene is expressed primarily in brain and retina and to a lesser extent in endothelial cells.

- Therefore, polynucleotides and polypeptides of the invention are useful as
35 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: diseases marked by defects in iron metabolism; aceruloplasminemia not characterized by defects in the

known ceruloplasmin gene locus; nonclassical Wilson disease; movement disorders; and tumors derived from a brain tissue origin. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain, retina, and nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, retinal tissue, and endothelial cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to ceruloplasmin indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment of patients with aceruloplasminemia, or other defects in iron and/or copper metabolism. Mutations in this locus could also be diagnostic for patients currently experiencing or predicted to experience aceruloplasminemia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 123

This gene is expressed primarily in brain and B cell lymphoma and to a lesser extent in fetal liver and spleen.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: B cell lymphoma; tumors and diseases of the brain and/or spleen; hematopoietic defects. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain and hematopoietic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, blood cells, liver, and spleen, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of disorders in neuronal,

hematopoietic, and immune systems. It could potentially be useful for neurodegenerative disorders and neuronal and/or hematopoietic cell survival or proliferation.

5 **FEATURES OF PROTEIN ENCODED BY GENE NO: 124**

This gene is expressed primarily in osteoclastoma, dermatofibrosarcoma, and B cell lymphoma and to a lesser extent in endothelial cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer in particular osteoclastoma, dermatofibrosarcoma, and B cell lymphoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the bone, immune, and circulatory system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone, epidermis, blood cells, and endothelial cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of cancers and lymphoma; osteoporosis; and the control of cell proliferation and/or differentiation.

25 **FEATURES OF PROTEIN ENCODED BY GENE NO: 125**

This gene is expressed primarily in immune tissues and hematopoietic cells, particularly in activated T cells and neutrophils, spleen, and fetal liver, and to a lesser extent in infant adrenal gland.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects in T cell activation; hematopoietic disorders; tumors of a hematopoietic and/or adrenal gland origin. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic and/or endocrine systems, expression of this gene at significantly higher

or lower levels may be routinely detected in certain tissues and cell types (e.g., cells and tissues of the immune system, hematopoietic cells, blood cells, liver, and adrenal gland, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual
5 having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for immune and/or hematopoietic disorders;
10 diseases related to proliferation and/or differentiation of hematopoietic cells; defects in T cell and neutrophil activation and responsiveness; and endocrine and/or metabolic disorders, particularly of early childhood.

FEATURES OF PROTEIN ENCODED BY GENE NO: 126

15 This gene is expressed primarily in placenta and endothelial cells and to a lesser extent in melanocytes and embryonic tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumors of an endothelial
20 cell origin; angiogenesis associated with tumor development and metastasis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the vascular system and developing embryo, expression of this gene at significantly higher or lower levels
25 may be routinely detected in certain tissues and cell types (e.g., placenta, endothelial cells, melanocytes, and embryonic tissues, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily
30 fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of developmental disorders; inhibition of angiogenesis; and vascular patterning.

35 FEATURES OF PROTEIN ENCODED BY GENE NO: 127

This gene is expressed primarily in endothelial cells and hematopoietic tissues, including spleen, tonsils, leukocytes, and both B- and T-cell lymphomas.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumors of an endothelial cell and/or hematopoietic origin; leukemias and lymphomas. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and vascular systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., endothelial cells, hematopoietic cells, spleen, tonsils, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the manipulation of angiogenesis; the differentiation and morphogenesis of endothelial cells; the proliferation and/or differentiation of hematopoietic cells; and the commitment of hematopoietic cells to distinct cell lineages.

20

FEATURES OF PROTEIN ENCODED BY GENE NO: 128

This gene is expressed primarily in kidney medulla and to a lesser extent in spleen from chronic myelogenous leukemia patients, prostate cancer, and some other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumors of a kidney origin; chronic myelogenous leukemia; prostate cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the kidney and spleen, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., kidney, spleen, and prostate, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of kidney disorders and cancer, particularly chronic myelogenous leukemia and prostate cancer. It may also be useful for the enhancement of kidney tubule regeneration in the treatment of acute renal failure.

FEATURES OF PROTEIN ENCODED BY GENE NO: 129

This gene is expressed primarily in adult and infant brain and to a lesser extent in mesenchymal or fibroblast cells, as well as tissues with a mesenchymal origin.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumors of a brain and/or mesenchymal origin; neurodegenerative disorders; cancer; fibrosis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain and of mesenchymal cells and tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis of tumors of a brain and/or mesenchymal origin; neurodegenerative disorders; cancer; and fibrosis, based upon the expression of this gene within those tissues. Fibrosis is considered as mesenchymal cells and fibroblasts are the primary cellular targets involved in this pathological condition.

FEATURES OF PROTEIN ENCODED BY GENE NO: 130

This gene is expressed primarily in hepatocellular cancer and to a lesser extent in fetal tissues as well as testes tumor.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: liver cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing

immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the digestive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, fetal tissue, and testes and other

5 reproductive tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

10 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of liver cancer.

FEATURES OF PROTEIN ENCODED BY GENE NO: 131

This gene is expressed only in infant early brain.

15 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: development and diseases of the nervous system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification
20 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain and nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another
25 tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating diseases of the brain in children and in
30 treating nervous system disorders such as Alzheimer's disease, schizophrenia, dementia, depression, etc.

FEATURES OF PROTEIN ENCODED BY GENE NO: 132

This gene is expressed primarily in brain and to a lesser extent in glioblastoma.

35 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: Alzheimer's disease,

schizophrenia, depression, mania, and dementia. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain and nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating brain disorders such as Alzheimer's disease, schizophrenia, depression, mania, and dementia.

15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 133**

The translation product of this gene shares sequence homology with ribitol dehydrogenase of bacteria which is thought to be important in metabolism of sugars.

This gene is expressed primarily in macrophage and to a lesser extent in T-cell lymphoma and lung.

20 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tissue destruction in inflammation. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells and lung, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

30 The tissue distribution and homology to ribitol dehydrogenase indicate that polynucleotides and polypeptides corresponding to this gene are useful for altering macrophage metabolism in diseases such as inflammation where macrophages are causing excess tissue destruction.

FEATURES OF PROTEIN ENCODED BY GENE NO: 134

This gene is expressed primarily in pancreatic tumor and to a lesser extent in synovial sarcoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the endocrine and connective tissue systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., pancreas, and synovial tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating and diagnosing various cancers.

20 FEATURES OF PROTEIN ENCODED BY GENE NO: 135

This gene is expressed primarily in T cell lines such as Raji and to a lesser extent in infant brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immune system disorders and inflammation. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating and diagnosing inflammatory diseases

such as rheumatoid arthritis, sepsis, inflammatory bowel disease, and psoriasis, as well as neutropenia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 136

5 The translation product of this gene shares high sequence homology with SAR1 subfamily of GTP-binding proteins which is thought to be important in vesicular transport in mammalian cells.

 This gene is expressed primarily in serum-stimulated smooth muscle cells and to a lesser extent in a T-cell lymphoma.

10 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: diseases affecting vesicular transport. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification
15 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the muscular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and smooth muscle, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample
20 taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

 The tissue distribution and homology to GTP-binding proteins indicate that polynucleotides and polypeptides corresponding to this gene are useful for gene therapy
25 in treating the large number of diseases involved in defective vesicular transport within cells..

FEATURES OF PROTEIN ENCODED BY GENE NO: 137

 The translation product of this gene shares sequence homology with a protein
30 found in *C. elegans* cosmid F25B5.

 This gene is expressed primarily in a fetal tissues and to a lesser extent in melanocytes.

 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
35 biological sample and for diagnosis of diseases and conditions: abnormal fetal development, especially of the pulmonary system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes

for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the fetal pulmonary system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., fetal tissue, pulmonary tissue, and melanocytes, and
5 cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
10 corresponding to this gene are useful for treatment and diagnosis of diseases affecting the pulmonary system, such as emphysema.

FEATURES OF PROTEIN ENCODED BY GENE NO: 138

This gene is expressed primarily in gall bladder and to a lesser extent in smooth
15 muscle.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: digestive system disease and gall bladder problems. Similarly, polypeptides and antibodies directed to these
20 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the digestive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., gall bladder and tissue of the digestive system, and smooth muscle, and cancerous and
25 wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
30 corresponding to this gene are useful for treating diseases of the digestive system.

FEATURES OF PROTEIN ENCODED BY GENE NO: 139

This gene is expressed primarily in placenta and to a lesser extent in brain.

Therefore, polynucleotides and polypeptides of the invention are useful as
35 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: abnormal fetal development. Similarly, polypeptides and antibodies directed to these polypeptides are

useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of developing tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., placenta, and brain and other
5 tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

10 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating and diagnosing abnormal fetal development.

FEATURES OF PROTEIN ENCODED BY GENE NO: 140

15 This gene is expressed primarily in smooth muscle and to a lesser extent in ovary, prostate cancer, and activated monocytes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: hypertension and
20 atherosclerosis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the circulatory system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., smooth
25 muscle, ovary and other reproductive tissue, prostate, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

30 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating diseases of the circulatory system, such as hypertension, atherosclerosis, etc.

FEATURES OF PROTEIN ENCODED BY GENE NO: 141

35 This gene is expressed primarily in fetal spleen and to a lesser extent in placenta and bone marrow.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: anemia and other diseases affecting blood cells. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the circulatory and pulmonary systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., spleen, placenta, bone marrow, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the generation of red and white blood cells and for the diagnosis of disease of these cells.

FEATURES OF PROTEIN ENCODED BY GENE NO: 142

The predicted translation product of this contig is a human homolog of the murine tetracycline/sugar transporter molecule recently reported by Matsuo and colleagues (Biochem. Biophys. Res. Commun. 238 (1), 126-129 (1997)).

This gene is expressed primarily in synovium and to a lesser extent in endothelial cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: rheumatoid arthritis and inflammation. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and lymphatic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., synovial tissue, and endothelial cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of inflammatory diseases, such as rheumatoid arthritis, leukemia, neutropenia, inflammatory bowel disease, psoriasis, sepsis, and the like.

5

FEATURES OF PROTEIN ENCODED BY GENE NO: 143

This gene is expressed primarily in placenta and to a lesser extent in melanocyte, fetal liver and spleen, and bone marrow.

Therefore, polynucleotides and polypeptides of the invention are useful as
10 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: abnormal early development. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, lower levels
15 may be routinely detected in certain tissues and cell types (e.g., placenta, melanocytes, liver, spleen, and bone marrow, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an
20 individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of abnormal early development phenomena and diseases.

25 FEATURES OF PROTEIN ENCODED BY GENE NO: 144

This gene is expressed primarily in fetal liver and spleen.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: anemia and neutropenia.
30 Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and blood systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver and spleen,
35 and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the

expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful in hematopoiesis and bone marrow regeneration as it is most abundant in fetal tissues responsible for the generation of hematopoietic cells.

FEATURES OF PROTEIN ENCODED BY GENE NO: 145

The translation product of this gene shares sequence homology with protein tyrosine phosphatase which is thought to be important in transducing signal to activate cells such as T cell, B cell and other cell types.

This gene is expressed primarily in T cells and tissues in early stages of development and to a lesser extent in cancers.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immuno-related diseases and cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., embryonic and fetal tissue, undifferentiated cells, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to the protein tyrosine phosphatase family indicate that polynucleotides and polypeptides corresponding to this gene are useful for modulating the immune system.

FEATURES OF PROTEIN ENCODED BY GENE NO: 146

This gene is expressed primarily in T cell and to a lesser extent in B cell, macrophages and tumor tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immuno-disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in

providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for regulating the immune system therefore can be used in treating diseases such as autoimmune diseases and cancers.

FEATURES OF PROTEIN ENCODED BY GENE NO: 147

This gene is expressed primarily in placenta and to a lesser extent in endothelial cells, testis tumor, ovarian cancer, uterine cancer.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., placenta, endothelial cells, testis and ovary and other reproductive tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of cancers.

FEATURES OF PROTEIN ENCODED BY GENE NO: 148

This sequence has significant homology to mouse torsin A. Recently, another group cloned the human Torsin A gene. (See, Accession No. 2358279; see also Nature Genet. 17, 40-48 (1997).)

This gene is expressed primarily in osteoclastoma, T-cell, and placenta and to a lesser extent in fetal lung, fetal liver, fetal brain, adult brain and tumor tissues

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: disease conditions in hematopoiesis and cancers. Similarly, polypeptides and antibodies directed to these
- 5 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoiesis system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, bone, placenta, lung, liver, and brain and other tissues of the nervous system,
- 10 and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.
- 15 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating blood related diseases such as deficiencies in red blood cell, white blood cell, platelet and other hematopoiesis cells.

FEATURES OF PROTEIN ENCODED BY GENE NO: 149

- 20 This gene is expressed primarily in T cell, prostate and prostate cancer, endothelial cells and to a lesser extent in monocyte, dendritic cell, bone marrow, salivary gland, colon cancer, stomach cancer, pancreatic tumor, uterine cancer, fetal spleen and osteoclastoma.
- Therefore, polynucleotides and polypeptides of the invention are useful as
- 25 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immuno-related diseases and cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells,
- 30 particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, prostate, endothelial cells, dendritic cells, bone marrow, salivary gland, colon, stomach, pancreas, uterus, spleen and bone, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another
- 35 tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of cancers.

FEATURES OF PROTEIN ENCODED BY GENE NO: 150

5 This gene was recently cloned by another group, calling it eIF3-p66. (See
Accession No. 2351378.) This gene plays a role in RNA binding and macromolecular
assembly, and therefore, any mutations in this gene would likely result in a diseased
phenotype. Preferred polypeptide fragments comprise the amino acid sequence:
MAKFMTPVIQDNPSGWGPCAVPEQFRDMPYQPFSGDRLGKVADWTGATYQDKRYTNKYSS
10 QFGGGSQYAYFHEEDESFLVDTARTQKTAYQRNRMFAQRNLRRDKDRRNLQFNLQILP
KSAKQKERERIRLQKKFQKQFQVGRQKWDQKSQKPRDSSVEVRSDWEVKEEMDFPQLMKMRY
LEVSEPQDIECCGALEYDYKAFDRITRSEKPLRXXKRIFHTVTTTDDPVIRKLAKTQGNVFATD
AILATLMSCTRSVYSWDIVVQVRVGSKLFFDKRDNSDFDLLTVSETANEPPQDEGNSFNSPRNL
AMEATYINHNFSQQCLRMGKERYNFPNPNPFVEDDMDKNEIASVAYRYSKGLGDDIDLIVRC
15 EHDGVMGTANGEVSFINIKTLNEWDSRHCNGVDWRQKLDSSQRGAVIATELKNNYSYKLARWTC
CALLAGSEYLKLGYSRYHVKDSSRHVILGTQQFKPNEFASQINLSVENAWGILRCVIDICMKL
EEGKYLLKDPNKQVIRVYSLPDGTFSS (SEQ ID NO: 638), as well as N-terminal and C-
terminal deletions of this polypeptide fragment.

20 This gene is expressed primarily in T cell, bone marrow, embryo and
endothelial cells and to a lesser extent in testis tumor and endometrial tumor.

 Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions: immune diseases and
tumors. Similarly, polypeptides and antibodies directed to these polypeptides are useful
25 in providing immunological probes for differential identification of the tissue(s) or cell
type(s). For a number of disorders of the above tissues or cells, particularly of the
immune system and reproductive system, expression of this gene at significantly higher
or lower levels may be routinely detected in certain tissues and cell types (e.g.,
cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial
30 fluid or spinal fluid) or another tissue or cell sample taken from an individual having
such a disorder, relative to the standard gene expression level; i.e., the expression level
in healthy tissue or bodily fluid from an individual not having the disorder.

 The tissue distribution indicates that polynucleotides and polypeptides
corresponding to this gene are useful for immune disorders and cancers.

FEATURES OF PROTEIN ENCODED BY GENE NO: 151

This gene is expressed primarily in testis and to a lesser extent in T cell, spinal cord, placenta, neutrophil and monocyte.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: male reproductive and endocrine disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive, immune and endocrine systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., testis and other reproductive tissue, blood cells, tissue of the nervous system, and placenta, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for regulating immune and reproductive functions.

FEATURES OF PROTEIN ENCODED BY GENE NO: 152

The translation product of this gene shares sequence homology with tyrosyl-tRNA synthetase which is thought to be important in cell growth.

This gene is expressed primarily in brain, liver, keratinocytes, tonsils, and heart.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer autoimmune diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain, liver, keratinocytes, tonsils, heart expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissues of the nervous system, liver, keratinocytes, tonsils and heart, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard

gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to tyrosyl-tRNA synthetase indicate that polynucleotides and polypeptides corresponding to this gene are useful for modulating
5 cell growth.

FEATURES OF PROTEIN ENCODED BY GENE NO: 153

This gene is homologous to the *Drosophila* transcriptional regulator dre4. (See Accession No. 2511745.) Dre4 is a gene required for steroidogenesis in *Drosophila*
10 melanogaster and encodes a developmentally expressed homologue of the yeast transcriptional regulator CDC68. Preferred polypeptide fragments comprise the amino acid sequence: KKRHTDVQFYTEVGEITDGLGKHQMHDRDDLYAEQMEREMRHKLKTAFTKN
FIEKVEALTKEELEFEVPPFDLGFNGAPYRSTCLLQPTSSALVNATEWPPFVVTLDEVELIHFXR
VQFHLKNFDMVIVYKDYSKKVTMINAIPVASLDPIKEWLNCDLKYTEGVQSLNWTKIMKTIVD
15 DPEGFFEQGGWSFL (SEQ ID NO: 639), as well as N-terminal and C-terminal deletions of this fragments. Also preferred are polynucleotide fragments encoding this polypeptide fragment.

This gene is expressed primarily in fetal liver, spleen, placenta, lung, T cell, thyroid, testes.

20 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: brain tumor, heart and liver diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s)
25 or cell type(s). For a number of disorders of the above tissues or cells, particularly of the fetal liver, spleen, placenta, lung, T cell, thyroid, testes expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, spleen, placenta, lung, blood cells, thyroid, and testes and other reproductive tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum,
30 plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

35 FEATURES OF PROTEIN ENCODED BY GENE NO: 154

This gene is expressed primarily in brain and to a lesser extent in fetal heart, testis, spleen, lung.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: heart, liver and spleen diseases, immunological diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain, fetal heart, testis, spleen, lung expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, heart, testes and other reproductive tissue, spleen, and lung, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 155

Activation of T cells through the T cell antigen receptor (TCR) results in the rapid tyrosine phosphorylation of a number of cellular proteins, one of the earliest being a 100 kDa protein. This gene is the human equivalent of murine valosin containing protein (VCP). VCP is a member of a family of ATP binding, homo-oligomeric proteins, and the mammalian homolog of *Saccharomyces cerevisiae* cdc48p, a protein essential to the completion of mitosis in yeast. Both endogenous and expressed murine VCP are tyrosine phosphorylated in response to T cell activation. Thus we have identified a novel component of the TCR mediated tyrosine kinase activation pathway that may provide a link between TCR activation and cell cycle control.

25

This gene is expressed primarily in brain, liver, spleen, placenta.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer immunological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain, liver, spleen, placenta expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, liver, spleen, and placenta, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from

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an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

5 The tissue distribution and homology to VCR indicate that polynucleotides and polypeptides corresponding to this gene are useful for treating cancer.

FEATURES OF PROTEIN ENCODED BY GENE NO: 156

The translation product of this gene shares sequence homology with rat growth response protein which is thought to be important in cell growth. A group recently
10 cloned the human homolog of this gene, calling it insulin induced protein 1. (See Accession No. 2358269, see also, Genomics 43 (3), 278-284 (1997).) Preferred polypeptide fragments comprise the amino acid sequence: RSGLGLGITIAFLATLITQF LVYNGVYQYTSPDFLYIRSWLPCIFFSGGVTVGNIGRQLAMGVPEKPHSD (SEQ ID NO: 640), as well as N-terminal and C-terminal deletions of this polypeptide fragment. Also
15 preferred are polynucleotide fragments encoding these polypeptide fragments.

This gene is expressed primarily in brain, liver, placenta, heart, spleen, lymphoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
20 biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer immunological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain, liver, placenta, heart, spleen.
25 expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, liver, placenta, heart, spleen, and lymphoid tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the
30 standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to growth-response protein indicate that polynucleotides and polypeptides corresponding to this gene are useful for modulating cell growth.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 157

This gene is expressed primarily in Glioblastoma, endometrial tumor, lymphoma and pancreas tumor.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: Glioblastoma, Endometrial tumor, lymphoma and pancreas tumor. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., endometrium, lymphoid tissue, pancreas, and tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

FEATURES OF PROTEIN ENCODED BY GENE NO: 158

The translation product of this gene shares sequence homology with IGE receptor which is thought to be important in allergy and asthma.

This gene is expressed primarily in T cell, and fetal liver.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: allergy and asthma and other immunological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and liver, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to IgE receptor indicate that polynucleotides and polypeptides corresponding to this gene are useful for allergy and asthma.

5 **FEATURES OF PROTEIN ENCODED BY GENE NO: 159**

The translation product of this gene shares sequence homology with immunoglobulin heavy chain which is thought to be important in immune response to the antigen.

10 This gene is expressed primarily in activated neutrophil and to a lesser extent in activated T cell, monocyte and heart.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: infection, inflammation and cancer. Similarly, polypeptides and antibodies directed to these polypeptides are
15 useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and heart, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial
20 fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to immunoglobulin heavy chain variable region indicate that polynucleotides and polypeptides corresponding to this gene are
25 useful for making the ligand to block specific antigen which cause certain disease.

FEATURES OF PROTEIN ENCODED BY GENE NO: 160

The translation product of this gene shares sequence homology with mouse X inactive specific transcript protein which is thought to be important in X chromosome
30 inactivation.

This gene is expressed primarily in HSA172 cell and to a lesser extent in normal ovary tissue, ovarian cancer, frontal cortex and brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
35 biological sample and for diagnosis of diseases and conditions: ovarian tumor, schizophrenia and other neurological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for

differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and neural system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., ovary and other reproductive tissue, and brain and other
5 tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

10 The tissue distribution and homology to X inactive specific transcript protein indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of reproductive system tumors and CNS tumors.

FEATURES OF PROTEIN ENCODED BY GENE NO: 161

15 This gene is expressed primarily in adipose cell and to a lesser extent in liver and prostate.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: obesity and liver
20 disorder. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the adipose cell, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., adipose cells, liver, and
25 prostate, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

30 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of obesity and liver disorder.

FEATURES OF PROTEIN ENCODED BY GENE NO: 162

35 The translation product of this gene shares sequence homology with yeast ubiquitin activating enzyme homolog which is thought to be important in protein posttraslation processing.

This gene is expressed primarily in stromal cell and to a lesser extent in retina, H. Atrophic Endometrium, colon carcinoma and myeloid progenitor cell.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects of stromal cell development, neuronal growth disorders and tumors. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and neural system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., retinal cells, endometrium, colon, and bone marrow, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to ubiquitin-activating enzyme homolog indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis or treatment of some type of tumors, fucosidosis and neuronal growth disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 163

This gene is expressed primarily in primary breast cancer and hemangiopericytoma and to a lesser extent in adult brain and cerebellum.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: breast cancer, leukemia and cerebellum disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system and neural system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., mammary tissue, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis or treatment of various tumors and disease involved in neural system.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 164

The translation product of this gene shares sequence homology with proline rich proteins. Recently, another group has also cloned this gene, calling it CD84 leukocyte antigen, a new member of the Ig superfamily. (See Accession No. U82988, see also, Blood 90 (6), 2398-2405 (1997).)

10 This gene is expressed primarily in Weizmann olfactory tissue and osteoclastoma and to a lesser extent in anergic T-cell.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: osteoporosis and immune
15 disease. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., olfactory tissue, bone, and
20 blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

25 The tissue distribution and homology to the Ig superfamily indicate that the protein product of this clone is useful for treatment of osteoporosis, autoimmune disease, and other immune disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 165

30 This gene is expressed primarily in atrophic endometrium and colon cancer and to a lesser extent in some fetal tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumors. Similarly,
35 polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system,

expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., endometrium, colon, and fetal tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having
 5 such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of tumors, specifically endometrium and colon tumors.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 166

This gene is expressed primarily in human primary breast cancer and to a lesser extent in activated monocyte. Although the predicted signal sequence is identified in Table 1, other upstream sequences are also relevant. Preferred polypeptide fragments comprise
 15 the amino acid sequence: VTQPKHLSASMGGSEIPFSFYYPWELAXXPXVRISWRRGHFHG QSFYSTRPPSIHKDYVNRLFLNWTEGQESGFLRISNLRKEDQSVYFCRVELDTRRSG (SEQ ID NO: 641), as well as N-terminal and C-terminal deletions. Also preferred are polynucleotide fragments encoding these polypeptide fragments.

Therefore, polynucleotides and polypeptides of the invention are useful as
 20 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: breast cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system,
 25 expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., mammary tissue, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in
 30 healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis of breast cancer.

FEATURES OF PROTEIN ENCODED BY GENE NO: 167

35 This gene is expressed primarily in fetal tissues and to a lesser extent in adult lung. This gene has also been mapped to chromosomal location 9q34, and thus, can be used as a marker for linkage analysis for chromosome 9.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the embryo tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., fetal tissues, and lung, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

FEATURES OF PROTEIN ENCODED BY GENE NO: 168

The translation product of this gene shares sequence homology with Ig Heavy Chain which is thought to be important in immune response.

This gene is expressed primarily in prostate cancer tissue specifically

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: prostate cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the prostate, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., prostate, tissue and cells of the immune system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

FEATURES OF PROTEIN ENCODED BY GENE NO: 169

The translation product of this gene shares sequence homology with cytosolic acyl coenzyme-A hydrolase, which is thought to be important in neuron-specific fatty acid metabolism. The gene represented by this contig has since been published by Hajra and colleagues (GenBank Accession No. U91316).

This gene is expressed primarily in human pituitary gland and to a lesser extent in colorectal cancer tissue. This gene has also been observed in the LNCAP cell line.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: hyperlipidemias of familial and/or idiopathic origins. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly blood, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., pituitary and colon, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to rat cytosolic acyl coenzyme-A hydrolase indicate that polynucleotides and polypeptides corresponding to this gene are useful for the detection or treatment of hyperlipidemia disease states by virtue of the ability of specific drugs to activate the enzyme.

FEATURES OF PROTEIN ENCODED BY GENE NO: 170

The translation product of this gene shares sequence homology with a *Caenorhabditis elegans* gene which is thought to be important in organism development.

This gene is expressed primarily in human synovial sarcoma tissue, bone marrow, and to a lesser extent in human brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, of bone, specifically synovial sarcoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the bone, connective tissues and possibly immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., synovial tissue, bone marrow, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another

tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- 5 The tissue distribution and homology to *Caenorhabditis elegans* indicate that polynucleotides and polypeptides corresponding to this gene are useful as a diagnostic and/or therapeutic modality directed at the detection and/or treatment of connective tissue sarcomas or other related bone diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 171

- 10 The translation product of this gene shares sequence homology with beta1-6GlcNAc transferase which is thought to be important in the transfer and metabolism of beta1-6, N-acetylglucosamine. This gene product has previously been shown to suppress melanoma lung metastasis in both syngeneic and nude mice, decreased invasiveness into the matrigel, and inhibition of cell attachment to collagen and laminin
15 without affecting cell growth.

This gene is expressed primarily in human testes and prostate tissues, and to a lesser extent in kidney, medulla, and pancreas.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
20 biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer particularly melanoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at
25 significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., testes and other reproductive tissue, prostate, kidney, pancreas, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard
30 gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- The tissue distribution and homology to beta1-6GlcNAc transferase indicate that the protein product of this clone is useful for the development of diagnostic and/or therapeutic modalities directed at the detection and/or treatment of cancer, the metastasis
35 of malignant tissue or cells. Defects in this potentially secreted enzyme may play a role in metastasis.

FEATURES OF PROTEIN ENCODED BY GENE NO: 172

This gene is expressed primarily in fetal spleen and liver.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions: immune disorders,
Wilm's tumor disease, hepatic disorders, and hematopoietic disorders. Similarly,
polypeptides and antibodies directed to these polypeptides are useful in providing
immunological probes for differential identification of the tissue(s) or cell type(s). For a
10 number of disorders of the above tissues or cells, particularly of the hematopoiesis and
immune systems, expression of this gene at significantly higher or lower levels may be
routinely detected in certain tissues and cell types (e.g., spleen and liver, and cancerous
and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or
spinal fluid) or another tissue or cell sample taken from an individual having such a
15 disorder, relative to the standard gene expression level, i.e., the expression level in
healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
corresponding to this gene are useful for the treatment and identification of fetal defects
along with correcting diseases that affect hematopoiesis and the immune system.

20

FEATURES OF PROTEIN ENCODED BY GENE NO: 173

The translation product of this gene shares sequence homology with ret II
oncogene which is thought to be important in Hirschsprung disease and many types of
cancers.

25 This gene is expressed in multiple tissues including the lymphatic system, brain,
and thyroid.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for identification of the tissue(s) or cell type(s) present in a biological sample
and for diagnosis of diseases and conditions: Hirschsprung disease and multiple
30 cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful
in providing immunological probes for identification of the tissue(s) or cell type(s). For
a number of disorders of the above tissues or cells, particularly of the immune and
central nervous system, expression of this gene at significantly higher or lower levels
may be routinely detected in certain tissues and cell types (e.g., lymphoid tissue,
35 thyroid, and brain and other tissue of the nervous system, and cancerous and wounded
tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or
another tissue or cell sample taken from an individual having such a disorder, relative to

the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to ret II oncogene indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of various cancers. It would also be useful for the diagnosis and treatment of Hirschsprung disease. Preferred polypeptides of the invention comprise the amino acid sequence: MEAQVNEAESAREQLQLHDQIAGQKASKQELETelerlkQEFHYIEEDLY RTKNTLQSRIKDRDEEIQKLRNQLTNKTLSSSQSELENRLHQLTETLIQKQTMLESLSSTEKNSL VFQLERLEQQMNSASGSSSSNGSSINMSGIDNGEGTRLRNVPVLFNDTETNLAGMYGKVRKAAS
10 SIDQFSIRLGIFLRRYPiARVFVIIYMALLHLWVMIVLLTYTPem HHDQPYGK (SEQ ID NO: 642).

FEATURES OF PROTEIN ENCODED BY GENE NO: 174

The translation product of this gene shares sequence homology with testis enhanced gene transcript which is thought to be important in regulation of human development.

This gene is expressed primarily in infant brain and to a lesser extent in a variety of other tissues and cell types, including the prostate, testes, monocytes, macrophages, dendritic cells, keratinocytes, and adipocytes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neurological, developmental, immune and inflammation disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, prostate, testes and other reproductive tissue, blood cells, keratinocytes, and adipocytes, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to testis enhanced gene transcript indicate that the protein product of this clone is useful for diagnosis and treatment of disorders involving the developing brain and the immune system.

FEATURES OF PROTEIN ENCODED BY GENE NO: 175

This gene is expressed primarily in prostate and to a lesser extent in various other tissues, including placenta.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancers, especially of the prostate. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for
10 differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the prostate, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., prostate and placenta, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell
15 sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful for diagnosis and treatment of prostate disorders and cancer. It may also be useful for
20 the diagnosis and treatment of endocrine disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 176

The translation product of this gene shares sequence homology with
25 *Sacchomyces cerevisiae* YNT20 gene which is thought to be important in mitochondrial function.

This gene is expressed at a particularly high level in muscle tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases related to such tissues and cell types
30 including: muscle wasting diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the neuromuscular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell
35 types (e.g., muscle and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,

the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to the YNT20 gene indicate that this protein is useful for treatment and detection of neuromuscular diseases caused by loss of mitochondrial function. For example this gene or its protein product could be used in replacement therapy for such diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 177

This gene is expressed primarily in the brain and to a lesser extent in kidney, placenta, smooth muscle, heart and lung.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neuromuscular diseases, degenerative diseases of the central nervous system, and heart disease. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the neuromuscular system, central nervous system, and heart, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, kidney, placenta, muscle, heart and lung, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

This gene or its protein product could also be used for replacement therapy for the above mentioned diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 178

The translation product of this gene shares sequence homology with caldesmon which is thought to be important in the cellular response to changes in glucose levels.

This gene is expressed primarily in multiple tissues including brain and retina.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: central nervous system disorders and retinopathy. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for identification of the tissue(s) or cell

type(s). For a number of disorders of the above tissues or cells, particularly of the CNS disorders and retinopathy, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and retinal tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to caldesmon indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment of retinopathies.

FEATURES OF PROTEIN ENCODED BY GENE NO: 179

The translation product of this gene shares sequence homology with mouse fibrosin protein which is thought to be important in regulation of fibrinogenesis in certain chronic inflammatory diseases.

This gene is expressed primarily in amniotic cells and breast tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of breast cancer and abnormal embryo development. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., amniotic cells, and mammary tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to fibrosin indicate that the protein product of this clone is useful for treatment of breast cancer. This gene or its protein product could be used in replacement therapy for breast cancer. In addition the protein product of this gene is useful in the treatment of chronic inflammatory diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 180

This gene is expressed several infant tissues including brain and liver and various adult tissues including brain, lung, liver, testes, and prostate.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, brain cancer, lung cancer, liver cancer and cancers of the reproductive system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, hepatic system, and reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, lung, liver, testes and other reproductive tissue, and prostate, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution of this gene product indicates that the protein product of this clone is involved in growth regulation and could be used as a growth factor or growth blocker in a variety of settings including treatment of cancers.

20 FEATURES OF PROTEIN ENCODED BY GENE NO: 181

This gene is expressed primarily in activated monocytes and to a lesser extent in melanocytes and dendritic cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of immune system diseases and cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, melanocytes, and dendritic cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone could be involved in growth regulation and could be used as a growth factor or growth blocker in a variety of settings including treatment of cancers.

FEATURES OF PROTEIN ENCODED BY GENE NO: 182

This gene is expressed primarily in placenta and several tumors of various tissue origin and to a lesser extent in normal tissues including liver, lung, brain, and skin,

- 5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of cancers of all kinds. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders
10 of the above tissues or cells, particularly of the central nervous system, respiratory system and skin, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, lung, brain and other tissues of the nervous system, and skin, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or
15 cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- The high expression of this gene in multiple tumors indicates that the protein product of the clone may be involved in cell growth control and therefore would be
20 useful for treatment of certain cancers. Likewise molecules developed to block the activity of the protein product of this clone could be used to block its potential role in tumor growth promotion.

FEATURES OF PROTEIN ENCODED BY GENE NO: 183

- 25 The translation product of this gene shares sequence homology with the mouse Ndr1 gene which is thought to be important in cancer progression.

This gene is expressed multiple cell types and tissues including brain, lung, kidney, bone marrow, liver, and spleen.

- Therefore, polynucleotides and polypeptides of the invention are useful as
30 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of all types of cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous, immune, and endocrine
35 systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, lung, kidney, bone marrow, liver and spleen, and cancerous and wounded

tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

5 The tissue distribution and homology to Ndr1 gene, which is thought to be involved in cancer progression, indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment of certain cancers. Likewise molecules developed to block the activity of the protein product of this clone could be used to block its potential role in tumor growth promotion.

10

FEATURES OF PROTEIN ENCODED BY GENE NO: 184

This gene is expressed primarily in early stage human brain and liver and to a lesser extent in several other fetal tissues.

15 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: brain and liver cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the
20 central nervous system and immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, liver, and fetal tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder,
25 relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The expression of this gene in embryonic tissues indicates that the protein could be involved in growth regulation and could be used as a growth factor or growth blocker in a variety of settings including treatment of cancers.

30

FEATURES OF PROTEIN ENCODED BY GENE NO: 185

This gene is expressed primarily in infant and embryonic brain.

35 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of degenerative nervous system disorders and brain cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell

type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., embryonic tissue, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The expression of this gene in embryonic tissues indicates that the protein could be involved in growth regulation and could be used as a growth factor or growth blocker in a variety of settings including treatment of cancers.

FEATURES OF PROTEIN ENCODED BY GENE NO: 186

This gene is expressed primarily in multiple tissues including placenta, fetal lung, fetal liver, and brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of all types of cancers including liver, brain and lung. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, pulmonary system, and hepatic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., placenta, lung, liver, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The expression of this gene in embryonic tissues indicates that the protein could be involved in growth regulation and could be used as a growth factor or growth blocker in a variety of settings including treatment of cancers.

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
1	HTTEZ21	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	11	582	1	582	177	177	313	1	18	19	22
1	HTTEZ21	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	197	1020	296	830	442	442	499	1	18	19	22
2	HBGBW52	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	12	465	1	465	81	81	314	1	30	31	128
2	HBGBW52	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	198	524	229	343		196	500	1	20	21	33
3	HCUFM41	97897 02/26/97 209043 05/15/97	ZAP Express	13	474	1	474	1	1	315	1	24	25	28
3	HCUFM41	97897 02/26/97 209043 05/15/97	ZAP Express	199	332	1	319	35	35	501	1	24	25	28

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
4	HCUFQ22	97897 02/26/97 209043 05/15/97	ZAP Express	14	314	1	298	122	122	316	1	34	35	64
5	HCUFV01	97897 02/26/97 209043 05/15/97	ZAP Express	15	613	1	613	30	30	317	1	18	19	21
6	HCUGA50	97897 02/26/97 209043 05/15/97	ZAP Express	16	356	1	356	239	239	318	1	22	23	39
7	HCUIM14	97897 02/26/97 209043 05/15/97	ZAP Express	17	414	185	414	278	278	319	1	26	27	33
8	HLDOU93	97897 02/26/97 209043 05/15/97	pCMVSPORT 3.0	18	469	1	469	77	77	320	1	44	45	88
9	HEIAX07	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	19	550	1	550	129	129	321	1	21	22	23

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
9	HEIAX07	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	200	376	9	376		1	502	1	8	9	15
10	HSAXR76	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	20	741	55	741	190	190	322	1			27
11	HNGJJ68	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	21	991	1	991	62	62	323	1	30	31	64
11	HNGJJ68	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	201	1192	253	1137		409	503	1			19
12	HCFAW04	97897 02/26/97 209043 05/15/97	pSport1	22	653	1	653	64	64	324	1	30	31	196
12	HCFAW04	97897 02/26/97 209043 05/15/97	pSport1	202	589	1	513	109	109	504	1			29

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
13	HLMAV65	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	23	1486	596	1418	102	102	325	1	54	55	252
13	HLMAV65	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	203	847	1	839	87	87	505	1	30	31	75
13	HLMAV65	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	204	852	75	850		690	506	1			10
13	HTXEF04	209235 09/04/97	Uni-ZAP XR	205	1354	54	1354	100	100	507	1	33	34	207
14	HPMFD84	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	24	2323	1017	2059	1242	1242	326	1	21	22	68
14	HPMFD84	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	206	1378	113	1226	303	303	508	1	25	26	36
15	HE6DB26	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	25	683	1	683	304	304	327	1	30	31	84

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
15	HE6DB26	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	207	1166	281	884	567	567	509	1	18	19	19
16	HHFFL33	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	26	2036	14	1959	214	214	328	1	20	21	36
17	HODBD33	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	27	717	1	717	70	70	329	1	30	31	63
17	HODBD33	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	208	697	2	697	33	33	510	1	31	32	32
18	HMDAE90	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	28	495	1	495	39	39	330	1	24	25	35
19	HOUAW01	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	29	556	1	556	116	116	331	1	19	20	23

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
20	HBJAE44	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	30	434	1	434	78	78	332	1	35	36	40
21	HCFME41	97897 02/26/97 209043 05/15/97	pSport1	31	715	1	715	87	87	333	1	30	31	111
21	HCFME41	97897 02/26/97 209043 05/15/97	pSport1	209	932	274	932	387	387	511	1	27	28	28
22	HOGCO71	97897 02/26/97 209043 05/15/97	pCMVSPORT 2.0	32	486	1	486	137	137	334	1	21	22	106
23	HOSEX08	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	33	725	1	725	436	436	335	1	30	31	50
23	HOSEX08	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	210	661	1	647	81	81	512	1	25	26	26

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
24	HSKNJ72	97897 02/26/97 209043 05/15/97	pBluescript	34	437	1	437	85	85	336	1	30	31	48
25	HEBEB69	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	35	943	1	943	196	196	337	1	30	31	41
25	HEBEB69	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	211	592	1	534	72	72	513	1	24	25	33
26	HE6EH18	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	36	604	1	604	375	375	338	1	20	21	76
26	HE6EH18	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	212	938	1	509		17	514	1	30	31	47
27	HSAUZ47	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	37	349	1	349		201	339	1	20	21	31

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
28	HSSDM73	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	38	672	1	672	22	22	340	1	38	39	42
29	HBMVK68	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	39	1908	135	1908	309	309	341	1	20	21	26
30	HMKDC66	97898 02/26/97 209044 05/15/97	pSport1	40	458	93	458	147	147	342	1	24	25	26
31	HMKCU94	97898 02/26/97 209044 05/15/97	pSport1	41	1153	500	1153	427	427	343	1	30	31	157
31	HMKCU94	97898 02/26/97 209044 05/15/97	pSport1	213	1079	502	896		739	515	1	23	24	43
32	HRDEW41	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	42	1983	1092	1983	27	27	344	1	11	12	520

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
32	HRDEW41	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	214	3791	2757	3357		2030	516	1			3
33	HTOJN06	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	43	1406	1	695		19	345	1	19	20	39
34	HBGDA21	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	44	1391	851	1153	74	74	346	1	30	31	234
34	HBGDA21	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	215	1334	822	1036		638	517	1	18	19	174
35	HFGAK75	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	45	1569	768	1569	14	14	347	1	19	20	169
35	HFGAK75	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	216	1511	770	1404	844	844	518	1	32	33	43

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
36	HHPBD40	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	46	1924	1	1681	62	62	348	1	19	20	43
37	HOVCL83	97898 02/26/97 209044 05/15/97	pSport1	47	475	252	396	141	141	349	1	37	38	78
38	HBCAY62	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	48	346	1	346	61	61	350	1	19	20	24
39	HBICM48	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	49	1366	882	1300	177	177	351	1	30	31	274
39	HBICM48	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	217	642	192	581		448	519	1			13
40	HLTCL35	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	50	1405	110	1404	61	61	352	1	30	31	47

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
40	HLTCL35	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	218	1241	1	1241	172	172	520	1	21	22	30
41	HLHCK50	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	51	504	207	485	222	222	353	1			3
42	HRSAN45	97899 02/26/97 209045 05/15/97	ZAP Express	52	777	1	214	113	113	354	1	24	25	52
43	HSNBB14	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	53	602	1	419	41	41	355	1	59	60	132
43	HSNBB14	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	219	1080	186	686	399	399	521	1	26	27	47
44	HMA BL38	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	54	1749	222	1749	166	166	356	1	30	31	204

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
44	HMA38	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	220	1258	149	1190	254	254	522	1	18	19	26
45	HSKDK47	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	55	1896	596	1614	650	650	357	1	33	34	47
46	HOSFH03	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	56	1753	555	1753	414	414	358	1	18	19	73
46	HOSFH03	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	221	1693	554	1693		526	523	1	25	26	58
47	HOGAV75	97899 02/26/97 209045 05/15/97	pCMVSPORT 2.0	57	1220	690	1024	128	128	359	1	30	31	102
47	HOGAV75	97899 02/26/97 209045 05/15/97	pCMVSPORT 2.0	222	1196	712	1163		1097	524	1			19

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
48	HFCAl74	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	58	1049	362	1049	335	335	360	1	33	34	48
49	HAGBI17	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	59	1776	854	1737	189	189	361	1	30	31	179
49	HAGBI17	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	223	1791	979	1791	1164	1164	525	1	18	19	40
50	HLFBC91	97899 02/26/97 209045 05/15/97	pBluescript SK-	60	443	1	443	164	164	362	1	21	22	25
51	HPRCA31	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	61	2888	1909	2888	90	90	363	1	30	31	224
51	HPRCA31	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	224	2517	1597	2517	1953	1953	526	1	18	19	57

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of Secreted Portion
52	HPRCE95	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	62	1851	1568	1736	139	139	364	1	30	31	349
52	HPRCE95	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	225	2424	299	2309		530	527	1	17	18	21
53	HHTLC66	97899 02/26/97 209045 05/15/97	ZAP Express	63	3542	883	3492	964	964	365	1	25	26	467
54	HMADJ02	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	64	883	237	883	229	229	366	1	30	31	152
54	HMADJ02	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	226	1080	242	1033	436	436	528	1	24	25	39
55	HPRCU93	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	65	1541	1	1541	236	236	367	1	30	31	373

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of AA of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
55	HPRCU93	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	227	1336	4	1336	946	946	529	1	25	26	128
56	HSAXS65	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	66	732	41	698	163	163	368	1	18	19	83
56	HSAXS65	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	228	2043	1133	1756	1262	1262	530	1	20	21	82
57	HKTAG35	209011 04/28/97	Uni-ZAP XR	67	629	1	629	264	264	369	1			21
57	HMEFX42	97899 02/26/97 209045 05/15/97	Lambda ZAP II	229	540	25	536	227	227	531	1			20
58	HHFHN61	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	68	1751	375	1751	95	95	370	1	19	20	227
59	HCWEF90	97899 02/26/97 209045 05/15/97	ZAP Express	69	508	1	508	22	22	371	1	30	31	79

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
59	HCWEF90	97899 02/26/97 209045 05/15/97	ZAP Express	230	448	9	448		1	532	1	22	23	75
60	HHGCM20	97899 02/26/97 209045 05/15/97	Lambda ZAP II	70	245	1	245	93	93	372	1	1	2	51
61	HFRAU10	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	71	361	1	361	1	1	373	1	30	31	61
61	HFRAU10	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	231	407	1	407	210	210	533	1	17	18	60
62	HATDT67	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	72	713	8	713	169	169	374	1	30	31	40
62	HATDT67	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	232	830	190	580	329	329	534	1	28	29	39

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
63	HOUBG93	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	73	862	1	862	67	67	375	1	30	31	44
63	HOUBG93	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	233	932	138	905	287	287	535	1			2
64	HMWEX24	97900 02/26/97 209046 05/15/97	Uni-Zap XR	74	4602	4162	4525	730	730	376	1	30	31	203
64	HMWEX24	97900 02/26/97 209046 05/15/97	Uni-Zap XR	234	2786	2406	2739	2577	2577	536	1	22	23	36
65	HSGBA84	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	75	1255	1	1195	112	112	377	1	28	29	29
66	HTOCD52	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	76	475	1	475	13	13	378	1	30	31	136

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
66	HTOCD52	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	235	458	1	458	26	26	537	1			14
67	HTGCP16	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	77	465	25	299	74	74	379	1	33	34	41
68	HKIXR69	97900 02/26/97 209046 05/15/97	pBluescript	78	1907	1627	1730	26	26	380	1	30	31	468
68	HKIXR69	97900 02/26/97 209046 05/15/97	pBluescript	236	591	1	444	251	251	538	1			18
69	HETG109	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	79	1168	136	1168	267	267	381	1	20	21	29
70	HOBNC61	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	80	1285	132	1285	292	292	382	1	27	28	29

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
71	HFFAH94	97900 02/26/97 209046 05/15/97	Lambda ZAP II	81	1290	768 1054	701	701	383	1	21	22	138
72	HBIAB95	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	82	684	1 684	119	119	384	1	30	31	74
73	HSQEL25	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	83	2024	1609 1953	200	200	385	1	30	31	521
73	HSQEL25	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	237	1286	391 959	1204	1204	539	1	9	10	11
74	HEBEG68	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	84	931	14 537	85	85	386	1	25	26	137
75	HBIAB39	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	85	825	59 802	66	66	387	1	30	31	186

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	5' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
75	HBIAB39	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	238	734	1	734	1	1	540	1	37	38	108
75	HBIAB39	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	239	809	80	794		294	541	1	15	16	106
76	HTXDU73	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	86	1238	36	918	17	17	388	1			1
77	HOEAS24	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	87	1460	9	1458	166	166	389	1	53	54	299
77	HOEAS24	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	240	2201	841	2080	507	507	542	1	43	44	136
77	HOEAS24	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	241	1661	311	1520	390	390	543	1	35	36	424

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
78	HTEIY30	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	88	1395	567	1395	639	639	390	1	36	37	49
79	HSKNE46	97900 02/26/97 209046 05/15/97	pBluescript	89	1186	352	1186	540	540	391	1	49	50	61
79	HSKNE46	97900 02/26/97 209046 05/15/97	pBluescript	242	1146	329	1146	564	564	544	1	21	22	39
80	HPMFL27	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	90	1821	1203	1614	1503	1503	392	1	30	31	79
81	HMWDN32	97900 02/26/97 209046 05/15/97	Uni-Zap XR	91	862	253	862	359	359	393	1	32	33	36
82	HPRAX55	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	92	696	349	696	98	98	394	1	30	31	180

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
82	HPRAX55	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	243	1350	265	1230	348	348	545	1	32	33	58
83	HHFFW36	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	93	1886	1	1759	197	197	395	1			21
84	HE2PL77	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	94	1774	742	1772	785	785	396	1	21	22	60
85	HSDFV29	209076 05/22/97	Uni-ZAP XR	95	2503	1	1648	206	206	397	1	32	33	152
85	HCQAV53	97901 02/26/97 209047 05/15/97	Lambda ZAP II	244	1529	72	911	191	191	546	1	20	21	33
86	HTPEG42	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	96	2801	418	2801	234	234	398	1	30	31	480
86	HTPEG42	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	245	1537	1	1537	125	125	547	1	21	22	367

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
87	HLHDR57	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	97	1631	916	1631	1	1	399	1	1	2	423
88	HAUAV32	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	98	504	26	504	197	197	400	1	23	24	78
88	HAUAV32	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	246	506	1	499	183	183	548	1	32	33	77
89	HNEBI60	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	99	1416	145	1416	456	456	401	1	18	19	74
89	HNEBI60	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	247	1348	84	1348	363	363	549	1	21	22	47
90	HSHCJ16	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	100	2847	1	2847		2	402	1			20

Gene No.	cDNA Clone ID	ATCC Deposit *No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	5' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
91	HTSEL31	97901 02/26/97 209047 05/15/97	pBluescript	101	1394	608	1346	602	602	403	1	23	24	87
92	HAUBL57	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	102	794	1	794	518	518	404	1	30	31	92
92	HAUBL57	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	248	1766	42	1766	356	356	550	1	30	31	168
92	HAUBL57	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	249	2664	47	1708		147	551	1	18	19	124
93	HODAS59	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	103	1544	898	1531	975	975	405	1			21
94	HE6CT48	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	104	871	106	871	248	248	406	1	34	35	174

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
94	HE6CT48	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	250	865	97	865	258	258	552	1	19	20	177
95	HMDAA61	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	105	404	1	404	16	16	407	1	21	22	64
95	HMDAA61	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	251	2082	852	2074	829	829	553	1	22	23	72
96	HAQBK61	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	106	1542	506	1542	122	122	408	1	51	52	280
96	HAQBK61	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	252	1482	508	1482		633	554	1	15	16	45
96	HCUHB01	209215 08/21/97	ZAP Express	253	834	1	834	82	82	555	1	40	41	251
97	HAQBF73	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	107	2327	1528	2327	465	465	409	1	30	31	284

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
97	HAQBF73	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	254	1508	885	1508		988	556	1			19
98	HAQBT94	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	108	1062	157	1062	172	172	410	1	28	29	187
99	HETHE07	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	109	2539	275	2501	903	903	411	1	30	31	237
99	HETHE07	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	255	2514	592	2431	176	176	557	1	30	31	217
99	HETHE07	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	256	2357	465	2288		1151	558	1	12	13	82
100	HLQAB52	97901 02/26/97 209047 05/15/97	Lambda ZAP II	110	1751	969	1751	4	4	412	1	46	47	192

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
100	HLQAB52	97901 02/26/97 209047 05/15/97	Lambda ZAP II	257	689	218	655	314	314	559	1	18	19	95
100	HEONN58	209119 06/12/97	pSport1	258	2377	5	2377	25	25	560	1	28	29	54
101	HCRAM28	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	111	1117	1	1117		1	413	1	19	20	21
101	HIBEK16	209627 02/12/98	Other	259	1193	69	1135	242	242	561	1	24	25	108
102	HE2BG03	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	112	1313	128	1313	271	271	414	1	30	31	51
102	HE2BG03	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	260	1262	26	1262	35	35	562	1	35	36	50
103	HEBDJ82	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	113	1654	553	1654	709	709	415	1			32

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
104	HCUBC79	97901 02/26/97 209047 05/15/97	ZAP Express	114	1171	540	1171	337	337	416	1	30	31	163
104	HCUBC79	97901 02/26/97 209047 05/15/97	ZAP Express	261	1179	626	1161	335	335	563	1	30	31	253
104	HCUBC79	97901 02/26/97 209047 05/15/97	ZAP Express	262	1162	629	1131	942	942	564	1			18
105	HSVAF07	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	115	842	373	800	100	100	417	1	65	66	174
105	HSVAF07	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	263	735	290	735			565	1			
105	HSVAF07	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	264	783	416	783		413	566	1	33	34	73

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
106	HT3AM65	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	116	1640	187	1470	581	581	418	1	30	31	50
106	HT3AM65	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	265	1638	301	1405	119	119	567	1	30	31	263
106	HT3AM65	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	266	1455	148	1188	438	438	568	1	24	25	70
107	HE6DK18	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	117	952	418	906	499	499	419	1	28	29	120
108	HEBEK93	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	118	1256	21	1079	301	301	420	1	30	31	159
108	HEBEK93	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	267	1086	25	1050	227	227	569	1	23	24	34

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
109	HJPCM10	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	119	1143	171	1051	175	175	421	1	50	51	154
109	HJPCM10	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	268	1003	21	1003	115	115	570	1	34	35	104
109	HJPCM10	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	269	1234	174	1015	232	232	571	1	27	28	132
110	HSXBL78	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	120	1782	1	1720	138	138	422	1	32	33	204
111	HOEAW81	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	121	610	18	609	50	50	423	1	30	31	67
111	HOEAW81	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	270	574	1	566	337	337	572	1	27	28	32

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
112	HOEAP41	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	122	526	185	375	143	143	424	1	21	22	25
113	HEAAR60	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	123	2081	1179	1976	48	48	425	1	30	31	299
113	HEAAR60	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	271	1731	889	1626	886	886	573	1	18	19	28
114	HTXGS75	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	124	1717	764	1640	76	76	426	1			13
115	HOVBA03	97902 02/26/97 209048 05/15/97	pSportl	125	804	1	804	145	145	427	1	15	16	198
115	HOVBA03	97902 02/26/97 209048 05/15/97	pSportl	272	1320	77	637	280	280	574	1	22	23	40

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
116	HGBGK76	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	126	431	1	431	73	73	428	1	38	39	47
116	HGBGK76	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	273	515	1	515	43	43	575	1	20	21	30
117	HBMUW78	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	127	3752	3465	3752	748	748	429	1	30	31	370
117	HBMUW78	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	274	2995	2738	2995	2777	2777	576	1	18	19	29
118	HASAS24	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	128	1144	669	1144	896	896	430	1			30
119	HSIDN55	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	129	1830	1234	1830	1265	1265	431	1			24

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
120	HGBGZ64	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	130	1864	1505	1741	1578	1578	432	1	37	38	53
121	H6EBJ64	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	131	2041	1	1214	46	46	433	1	35	36	176
121	H6EBJ64	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	275	1990	8	1128	71	71	577	1	16	17	92
122	HOECP43	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	132	2012	853	1986	1127	1127	434	1	22	23	77
123	H2CBV31	97902 02/26/97 209048 05/15/97	pBluescript SK-	133	1669	670	1632	962	962	435	1	25	26	32
124	HPCAD23	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	134	1565	281	1565	274	274	436	1	25	26	30

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
125	HSPAG15	97902 02/26/97 209048 05/15/97	pSport1	135	2007	1101	2007	1124	1124	437	1	39	40	69
126	HELGH31	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	136	1291	1	1180	107	107	438	1			19
127	HUSHH48	97902 02/26/97 209048 05/15/97	Lambda ZAP II	137	1906	1	1906	184	184	439	1	30	31	43
127	HUSHH48	97902 02/26/97 209048 05/15/97	Lambda ZAP II	276	2436	572	2436	726	726	578	1	30	31	42
128	HLAU95	97902 02/26/97 209048 05/15/97	pSport1	138	1935	1044	1794	1183	1183	440	1	18	19	33
129	HHSCV65	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	139	1446	572	1347	585	585	441	1	25	26	53

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
130	HTTAD57	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	140	1109	639	1109	676	676	442	1	24	25	64
131	HEBGA37	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	141	497	9	497	95	95	443	1			34
132	HEBFU93	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	142	269	1	269	1	1	444	1	30	31	89
132	HEBFU93	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	277	782	408	781		571	579	1	31	32	70
133	HSGSC60	97902 02/26/97 209048 05/15/97	Lambda ZAP II	143	1269	55	1262	55	55	445	1	25	26	350
134	HPMGD24	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	144	1944	97	1871	306	306	446	1	16	17	49

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
135	HPTVC60	97902 02/26/97 209048 05/15/97	pBluescript	145	1021	526	1021	74	74	447	1	30	31	278
135	HPTVC60	97902 02/26/97 209048 05/15/97	pBluescript	278	961	524	961	545	545	580	1	23	24	110
136	HSKNE18	97902 02/26/97 209048 05/15/97	pBluescript	146	1285	5	1285	116	116	448	1	30	31	199
136	HSKNE18	97902 02/26/97 209048 05/15/97	pBluescript	279	1228	9	1228	324	324	581	1	26	27	30
137	HMWIF35	97902 02/26/97 209048 05/15/97	Uni-Zap XR	147	1386	169	1272	165	165	449	1	30	31	258
137	HMWIF35	97902 02/26/97 209048 05/15/97	Uni-Zap XR	280	1327	169	1208	160	160	582	1	23	24	71

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	5' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
138	HMWGI25	97902 02/26/97 209048 05/15/97	Uni-Zap XR	148	2098	721	2044	784	784	450	1	18	19	87
139	HSKGF03	97902 02/26/97 209048 05/15/97	pBluescript	149	1847	1689	1847	241	241	451	1	33	34	315
139	HSKGF03	97902 02/26/97 209048 05/15/97	pBluescript	281	799	1	799		243	583	1	12	13	47
140	HMSKE75	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	150	1569	113	1517	417	417	452	1	21	22	52
141	HCMSH30	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	151	1540	538	1540	48	48	453	1	30	31	383
141	HCMSH30	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	282	2196	270	2196	294	294	584	1	32	33	39

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
142	HTWCB92	97902 02/26/97 209048 05/15/97	pSport1	152	1719	690	1575	6	6	454	1	52	53	186
143	HBMDM46	97902 02/26/97 209048 05/15/97	pBluescript	153	863	1	863	195	195	455	1	26	27	163
143	HBMDM46	97902 02/26/97 209048 05/15/97	pBluescript	283	1185	277	1166	621	621	585	1			19
144	HFAMG13	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	154	1101	1	512	40	40	456	1	21	22	46
145	HFXHL79	97903 02/26/97 209049 05/15/97	Lambda ZAP II	155	2031	669	2031	411	411	457	1	23	24	105
145	HFXHL79	97903 02/26/97 209049 05/15/97	Lambda ZAP II	284	1634	615	1485	878	878	586	1	20	21	23

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID: NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
146	HSNAK17	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	156	1981	1458	1809	1592	1592	458	1	23	24	70
146	HSNAK17	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	285	1795	1458	1749	1562	1562	587	1	33	34	69
147	HCFBC03	97903 02/26/97 209049 05/15/97	pSport1	157	915	45	912	22	22	459	1	22	23	155
147	HCFBC03	97903 02/26/97 209049 05/15/97	pSport1	286	858	46	858	224	224	588	1	30	31	77
147	HSJAP03	209139 07/03/97	Uni-ZAP XR	287	915	1	915	22	22	589	1	22	23	155
148	HSKGO26	97903 02/26/97 209049 05/15/97	pBluescript	158	2117	51	1422	32	32	460	1	23	24	332
149	HCQAV96	97903 02/26/97 209049 05/15/97	Lambda ZAP II	159	2395	1509	2382	1440	1440	461	1			5

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
150	HSHCC16	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	160	2120	1223	2108	1416	1416	462	1			14
151	HTLEF62	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	161	900	482	900	46	46	463	1	30	31	285
151	HTLEF62	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	288	1517	783	1517	1062	1062	590	1			24
152	HTLAD94	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	162	1003	1	1003	288	288	464	1	30	31	80
152	HTLAD94	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	289	3865	217	1195	281	281	591	1	16	17	38
153	HTSFQ12	97903 02/26/97 209049 05/15/97	pBluescript	163	2196	1607	2180	1611	1611	465	1	30	31	47

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
154	HE6FL83	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	164	1945	271	1840	299	299	466	1	63	64	96
154	HE6FL83	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	290	1910	279	1818	355	355	592	1	39	40	69
155	HTXFJ55	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	165	2933	489	2871	258	258	467	1	30	31	399
155	HTXFJ55	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	291	3276	486	2838		525	593	1	45	46	308
156	HUPCI76	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	166	2243	343	2221		341	468	1			1
157	HLTED27	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	167	1816	1130	1816	284	284	469	1	31	32	273

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
157	HLTED27	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	292	1695	1098	1548	1306	1306	594	1			22
158	HMKBA64	97903 02/26/97 209049 05/15/97	pSport1	168	945	1	787	208	208	470	1	18	19	192
159	HNFIP24	97903 02/26/97 209049 05/15/97	pBluescript	169	902	46	816	19	19	471	1	26	27	234
160	HCELB21	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	170	1883	798	1869	1001	1001	472	1	45	46	105
160	HCELB21	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	293	1501	438	1501	510	510	595	1			24
161	HAWBA28	97903 02/26/97 209049 05/15/97	pBluescript SK-	171	2100	1642	2100	1722	1722	473	1	23	24	32

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	5' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
162	HSAAS44	97903 02/26/97 209049 05/15/97	pBluescript SK-	172	1930	187	1930	65	65	474	1	30	31	571
162	HSAAS44	97903 02/26/97 209049 05/15/97	pBluescript SK-	294	2683	183	2683	431	431	596	1			24
163	HAFAL73	97903 02/26/97 209049 05/15/97	pBluescript SK-	173	1509	962	1451	122	122	475	1	30	31	312
163	HAFAL73	97903 02/26/97 209049 05/15/97	pBluescript SK-	295	1454	961	1420	976	976	597	1			1
164	HSAWF26	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	174	3173	2197	2972	51	51	476	1	21	22	329
164	HSAWF26	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	296	828	52	828	305	305	598	1			8

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
165	HEAAL31	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	175	991	374	970	60	60	477	1	24	25	178
165	HEAAL31	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	297	2416	1387	2413	1473	1473	599	1	18	19	25
166	HFKFX55	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	176	1290	499	1290		688	478	1	25	26	52
167	H2LAO11	97903 02/26/97 209049 05/15/97	pBluescript SK-	177	2290	1	2290	173	173	479	1	22	23	62
168	HPFDZ95	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	178	549	1	549	11	11	480	1	21	22	27
168	HPFDZ95	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	298	545	1	545	17	17	600	1	21	22	27

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
169	HPTTU11	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	179	1509	294	1352	92	92	481	1	30	31	339
169	HPTTU11	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	299	1530	385	1530	562	562	601	1	23	24	61
170	HCFAE79	97904 02/26/97 209050 05/15/97	pSport1	180	1316	985	1250	995	995	482	1	26	27	32
171	HTEDI34	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	181	777	1	777	51	51	483	1	30	31	48
171	HTEDI34	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	300	997	244	997	300	300	602	1	23	24	29
172	HODCW06	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	182	791	1	791	14	14	484	1	29	30	38

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
173	HFTAR26	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	183	1405	346	1405	575	575	485	1	20	21	61
174	H2MBF44	97904 02/26/97 209050 05/15/97	pBluescript SK-	184	1596	75	1596	131	131	486	1	24	25	346
174	H2MBF44	97904 02/26/97 209050 05/15/97	pBluescript SK-	301	2345	75	2345	233	233	603	1	56	57	69
175	HE8BI92	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	185	2293	355	2288	67	67	487	1	30	31	237
175	HE8BI92	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	302	2369	2	1946		60	604	1	9	10	24
176	HFTBR48	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	186	1212	462	1180	257	257	488	1	30	31	200

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of AA ORF
176	HFTBR48	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	303	1181	424	1149	663	663	605	1	23	24	35
177	HE9CM64	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	187	1605	770	1534	166	166	489	1	30	31	351
177	HE9CM64	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	304	1537	719	1515		787	606	1	43	44	130
178	HATAV51	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	188	1516	960	1516	8	8	490	1	30	31	265
178	HATAV51	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	305	1493	1	1261	54	54	607	1	18	19	23
179	HAQAF27	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	189	681	287	681		401	491	1			25

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	5' NT of Clone Seq.	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
180	HCEEK08	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	190	1014	703	1014	360	492	1	30	31	159
180	HCEEK08	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	306	577	1	577	175	608	1			6
181	HAFUI8	97904 02/26/97 209050 05/15/97	pBluescript SK-	191	2779	2207	2630	1153	493	1	30	31	279
181	HAFUI8	97904 02/26/97 209050 05/15/97	pBluescript SK-	307	2860	163	2860	21	609	1	30	31	232
181	HAFUI8	97904 02/26/97 209050 05/15/97	pBluescript SK-	308	876	275	876	302	610	1	32	33	34
182	HETBY74	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	192	1923	30	1923	45	494	1	33	34	193

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
183	HTOAF35	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	193	2346	1160	2286	178	178	495	1	30	31	205
183	HTOAF35	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	309	2025	840	2025	971	971	611	1	18	19	21
184	HCRBX32	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	194	3054	2004	3054	434	434	496	1	11	12	147
184	HCRBX32	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	310	3026	1966	3026	2131	2131	612	1			9
185	HEBGB80	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	195	907	152	907	297	297	497	1	30	31	64
185	HEBGB80	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	311	712	67	712	107	107	613	1	18	19	29

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
186	HFAMH74	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	196	1290	84	809	225	225	498	1	30	31	94
186	HFAMH74	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	312	1289	785	1289	927	927	614	1	28	29	30

Table 1 summarizes the information corresponding to each "Gene No." described above. The nucleotide sequence identified as "NT SEQ ID NO:X" was assembled from partially homologous ("overlapping") sequences obtained from the "cDNA clone ID" identified in Table 1 and, in some cases, from additional related DNA clones. The overlapping sequences were assembled into a single contiguous sequence of high redundancy (usually three to five overlapping sequences at each nucleotide position), resulting in a final sequence identified as SEQ ID NO:X.

The cDNA Clone ID was deposited on the date and given the corresponding deposit number listed in "ATCC Deposit No:Z and Date." Some of the deposits contain multiple different clones corresponding to the same gene. "Vector" refers to the type of vector contained in the cDNA Clone ID.

"Total NT Seq." refers to the total number of nucleotides in the contig identified by "Gene No." The deposited clone may contain all or most of these sequences, reflected by the nucleotide position indicated as "5' NT of Clone Seq." and the "3' NT of Clone Seq." of SEQ ID NO:X. The nucleotide position of SEQ ID NO:X of the putative start codon (methionine) is identified as "5' NT of Start Codon." Similarly, the nucleotide position of SEQ ID NO:X of the predicted signal sequence is identified as "5' NT of First AA of Signal Pep."

The translated amino acid sequence, beginning with the methionine, is identified as "AA SEQ ID NO:Y," although other reading frames can also be easily translated using known molecular biology techniques. The polypeptides produced by these alternative open reading frames are specifically contemplated by the present invention.

The first and last amino acid position of SEQ ID NO:Y of the predicted signal peptide is identified as "First AA of Sig Pep" and "Last AA of Sig Pep." The predicted first amino acid position of SEQ ID NO:Y of the secreted portion is identified as "Predicted First AA of Secreted Portion." Finally, the amino acid position of SEQ ID NO:Y of the last amino acid in the open reading frame is identified as "Last AA of ORF."

SEQ ID NO:X and the translated SEQ ID NO:Y are sufficiently accurate and otherwise suitable for a variety of uses well known in the art and described further below. For instance, SEQ ID NO:X is useful for designing nucleic acid hybridization probes that will detect nucleic acid sequences contained in SEQ ID NO:X or the cDNA contained in the deposited clone. These probes will also hybridize to nucleic acid molecules in biological samples, thereby enabling a variety of forensic and diagnostic methods of the invention. Similarly, polypeptides identified from SEQ ID NO:Y may be used to generate antibodies which bind specifically to the secreted proteins encoded by the cDNA clones identified in Table 1.

Nevertheless, DNA sequences generated by sequencing reactions can contain sequencing errors. The errors exist as misidentified nucleotides, or as insertions or deletions of nucleotides in the generated DNA sequence. The erroneously inserted or deleted nucleotides cause frame shifts in the reading frames of the predicted amino acid sequence. In these cases, the predicted amino acid sequence diverges from the actual amino acid sequence, even though the generated DNA sequence may be greater than 99.9% identical to the actual DNA sequence (for example, one base insertion or deletion in an open reading frame of over 1000 bases).

Accordingly, for those applications requiring precision in the nucleotide sequence or the amino acid sequence, the present invention provides not only the generated nucleotide sequence identified as SEQ ID NO:X and the predicted translated amino acid sequence identified as SEQ ID NO:Y, but also a sample of plasmid DNA containing a human cDNA of the invention deposited with the ATCC, as set forth in Table 1. The nucleotide sequence of each deposited clone can readily be determined by sequencing the deposited clone in accordance with known methods. The predicted amino acid sequence can then be verified from such deposits. Moreover, the amino acid sequence of the protein encoded by a particular clone can also be directly determined by peptide sequencing or by expressing the protein in a suitable host cell containing the deposited human cDNA, collecting the protein, and determining its sequence.

The present invention also relates to the genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, or the deposited clone. The corresponding gene can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include preparing probes or primers from the disclosed sequence and identifying or amplifying the corresponding gene from appropriate sources of genomic material.

Also provided in the present invention are species homologs. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source for the desired homologue.

The polypeptides of the invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.

The polypeptides may be in the form of the secreted protein, including the mature form, or may be a part of a larger protein, such as a fusion protein (see below).

It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which aid in purification, such as multiple histidine residues, or an additional sequence for stability during recombinant production.

- 5 The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of a polypeptide, including the secreted polypeptide, can be substantially purified by the one-step method described in Smith and Johnson, *Gene* 67:31-40 (1988). Polypeptides of the invention also can be purified from natural or recombinant sources
- 10 using antibodies of the invention raised against the secreted protein in methods which are well known in the art.

Signal Sequences

- 15 Methods for predicting whether a protein has a signal sequence, as well as the cleavage point for that sequence, are available. For instance, the method of McGeoch, *Virus Res.* 3:271-286 (1985), uses the information from a short N-terminal charged region and a subsequent uncharged region of the complete (uncleaved) protein. The method of von Heinje, *Nucleic Acids Res.* 14:4683-4690 (1986) uses the information from the residues surrounding the cleavage site, typically residues -13 to +2, where +1
- 20 indicates the amino terminus of the secreted protein. The accuracy of predicting the cleavage points of known mammalian secretory proteins for each of these methods is in the range of 75-80%. (von Heinje, *supra*.) However, the two methods do not always produce the same predicted cleavage point(s) for a given protein.

- 25 In the present case, the deduced amino acid sequence of the secreted polypeptide was analyzed by a computer program called SignalP (Henrik Nielsen et al., *Protein Engineering* 10:1-6 (1997)), which predicts the cellular location of a protein based on the amino acid sequence. As part of this computational prediction of localization, the methods of McGeoch and von Heinje are incorporated. The analysis of the amino acid sequences of the secreted proteins described herein by this program provided the results
- 30 shown in Table 1.

- As one of ordinary skill would appreciate, however, cleavage sites sometimes vary from organism to organism and cannot be predicted with absolute certainty. Accordingly, the present invention provides secreted polypeptides having a sequence shown in SEQ ID NO:Y which have an N-terminus beginning within 5 residues (i.e., +
- 35 or - 5 residues) of the predicted cleavage point. Similarly, it is also recognized that in some cases, cleavage of the signal sequence from a secreted protein is not entirely

uniform, resulting in more than one secreted species. These polypeptides, and the polynucleotides encoding such polypeptides, are contemplated by the present invention.

Moreover, the signal sequence identified by the above analysis may not necessarily predict the naturally occurring signal sequence. For example, the naturally occurring signal sequence may be further upstream from the predicted signal sequence. However, it is likely that the predicted signal sequence will be capable of directing the secreted protein to the ER. These polypeptides, and the polynucleotides encoding such polypeptides, are contemplated by the present invention.

10 **Polynucleotide and Polypeptide Variants**

"Variant" refers to a polynucleotide or polypeptide differing from the polynucleotide or polypeptide of the present invention, but retaining essential properties thereof. Generally, variants are overall closely similar, and, in many regions, identical to the polynucleotide or polypeptide of the present invention.

15 "Identity" per se has an art-recognized meaning and can be calculated using published techniques. (See, e.g.: (COMPUTATIONAL MOLECULAR BIOLOGY, Lesk, A.M., ed., Oxford University Press, New York, (1988); BIOCOMPUTING: INFORMATICS AND GENOME PROJECTS, Smith, D.W., ed., Academic Press, New York, (1993); COMPUTER ANALYSIS OF SEQUENCE DATA, PART I, Griffin, A.M., and Griffin, H.G., eds., Humana Press, New Jersey, (1994);
20 SEQUENCE ANALYSIS IN MOLECULAR BIOLOGY, von Heinje, G., Academic Press, (1987); and SEQUENCE ANALYSIS PRIMER, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, (1991).) While there exists a number of methods to measure identity between two polynucleotide or polypeptide sequences, the term "identity" is well known to skilled artisans. (Carillo, H., and Lipton, D., SIAM J
25 Applied Math 48:1073 (1988).) Methods commonly employed to determine identity or similarity between two sequences include, but are not limited to, those disclosed in "Guide to Huge Computers," Martin J. Bishop, ed., Academic Press, San Diego, (1994), and Carillo, H., and Lipton, D., SIAM J Applied Math 48:1073 (1988).
30 Methods for aligning polynucleotides or polypeptides are codified in computer programs, including the GCG program package (Devereux, J., et al., Nucleic Acids Research (1984) 12(1):387 (1984)), BLASTP, BLASTN, FASTA (Atschul, S.F. et al., J. Molec. Biol. 215:403 (1990), Bestfit program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park,
35 575 Science Drive, Madison, WI 53711 (using the local homology algorithm of Smith and Waterman, Advances in Applied Mathematics 2:482-489 (1981).)

When using any of the sequence alignment programs to determine whether a particular sequence is, for instance, 95% identical to a reference sequence, the parameters are set so that the percentage of identity is calculated over the full length of the reference polynucleotide and that gaps in identity of up to 5% of the total number of nucleotides in the reference polynucleotide are allowed.

A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. 6:237-245 (1990).) The term "sequence" includes nucleotide and amino acid sequences. In a sequence alignment the query and subject sequences are either both nucleotide sequences or both amino acid sequences. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB search of a DNA sequence to calculate percent identity are: Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30, Randomization Group Length=0, and Cutoff Score=1, Gap Penalty=5, Gap Size Penalty 0.05, and Window Size=500 or query sequence length in nucleotide bases, whichever is shorter. Preferred parameters employed to calculate percent identity and similarity of an amino acid alignment are: Matrix=PAM 150, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Gap Penalty=5, Gap Size Penalty=0.05, and Window Size=500 or query sequence length in amino acid residues, whichever is shorter.

As an illustration, a polynucleotide having a nucleotide sequence of at least 95% "identity" to a sequence contained in SEQ ID NO:X or the cDNA contained in the deposited clone, means that the polynucleotide is identical to a sequence contained in SEQ ID NO:X or the cDNA except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the total length (not just within a given 100 nucleotide stretch). In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to SEQ ID NO:X or the deposited clone, up to 5% of the nucleotides in the sequence contained in SEQ ID NO:X or the cDNA can be deleted, inserted, or substituted with other nucleotides. These changes may occur anywhere throughout the polynucleotide.

Further embodiments of the present invention include polynucleotides having at least 85% identity, more preferably at least 90% identity, and most preferably at least 95%, 96%, 97%, 98% or 99% identity to a sequence contained in SEQ ID NO:X or the cDNA contained in the deposited clone. Of course, due to the degeneracy of the genetic code, one of ordinary skill in the art will immediately recognize that a large number of the polynucleotides having at least 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity

will encode a polypeptide identical to an amino acid sequence contained in SEQ ID NO:Y or the expressed protein produced by the deposited clone.

Similarly, by a polypeptide having an amino acid sequence having at least, for example, 95% "identity" to a reference polypeptide, is intended that the amino acid
5 sequence of the polypeptide is identical to the reference polypeptide except that the polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the total length of the reference polypeptide. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a reference amino acid sequence, up to 5% of the amino acid residues in the reference sequence may be
10 deleted or substituted with another amino acid, or a number of amino acids up to 5% of the total amino acid residues in the reference sequence may be inserted into the reference sequence. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the
15 reference sequence or in one or more contiguous groups within the reference sequence.

Further embodiments of the present invention include polypeptides having at least 80% identity, more preferably at least 85% identity, more preferably at least 90% identity, and most preferably at least 95%, 96%, 97%, 98% or 99% identity to an amino acid sequence contained in SEQ ID NO:Y or the expressed protein produced by
20 the deposited clone. Preferably, the above polypeptides should exhibit at least one biological activity of the protein.

In a preferred embodiment, polypeptides of the present invention include polypeptides having at least 90% similarity, more preferably at least 95% similarity, and still more preferably at least 96%, 97%, 98%, or 99% similarity to an amino acid
25 sequence contained in SEQ ID NO:Y or the expressed protein produced by the deposited clone.

The variants may contain alterations in the coding regions, non-coding regions, or both. Especially preferred are polynucleotide variants containing alterations which produce silent substitutions, additions, or deletions, but do not alter the properties or
30 activities of the encoded polypeptide. Nucleotide variants produced by silent substitutions due to the degeneracy of the genetic code are preferred. Moreover, variants in which 5-10, 1-5, or 1-2 amino acids are substituted, deleted, or added in any combination are also preferred. Polynucleotide variants can be produced for a variety of reasons, e.g., to optimize codon expression for a particular host (change codons in
35 the human mRNA to those preferred by a bacterial host such as E. coli).

Naturally occurring variants are called "allelic variants," and refer to one of several alternate forms of a gene occupying a given locus on a chromosome of an

organism. (Genes II, Lewin, B., ed., John Wiley & Sons, New York (1985).) These allelic variants can vary at either the polynucleotide and/or polypeptide level.

Alternatively, non-naturally occurring variants may be produced by mutagenesis techniques or by direct synthesis.

- 5 Using known methods of protein engineering and recombinant DNA technology, variants may be generated to improve or alter the characteristics of the polypeptides of the present invention. For instance, one or more amino acids can be deleted from the N-terminus or C-terminus of the secreted protein without substantial loss of biological function. The authors of Ron et al., J. Biol. Chem. 268: 2984-2988
10 (1993), reported variant KGF proteins having heparin binding activity even after deleting 3, 8, or 27 amino-terminal amino acid residues. Similarly, Interferon gamma exhibited up to ten times higher activity after deleting 8-10 amino acid residues from the carboxy terminus of this protein. (Dobeli et al., J. Biotechnology 7:199-216 (1988).)

- Moreover, ample evidence demonstrates that variants often retain a biological
15 activity similar to that of the naturally occurring protein. For example, Gayle and coworkers (J. Biol. Chem 268:22105-22111 (1993)) conducted extensive mutational analysis of human cytokine IL-1a. They used random mutagenesis to generate over 3,500 individual IL-1a mutants that averaged 2.5 amino acid changes per variant over the entire length of the molecule. Multiple mutations were examined at every possible
20 amino acid position. The investigators found that "[m]ost of the molecule could be altered with little effect on either [binding or biological activity]." (See, Abstract.) In fact, only 23 unique amino acid sequences, out of more than 3,500 nucleotide sequences examined, produced a protein that significantly differed in activity from wild-type.

- 25 Furthermore, even if deleting one or more amino acids from the N-terminus or C-terminus of a polypeptide results in modification or loss of one or more biological functions, other biological activities may still be retained. For example, the ability of a deletion variant to induce and/or to bind antibodies which recognize the secreted form will likely be retained when less than the majority of the residues of the secreted form are removed from the N-terminus or C-terminus. Whether a particular polypeptide
30 lacking N- or C-terminal residues of a protein retains such immunogenic activities can readily be determined by routine methods described herein and otherwise known in the art.

- Thus, the invention further includes polypeptide variants which show
35 substantial biological activity. Such variants include deletions, insertions, inversions, repeats, and substitutions selected according to general rules known in the art so as have little effect on activity. For example, guidance concerning how to make

phenotypically silent amino acid substitutions is provided in Bowie, J. U. et al., Science 247:1306-1310 (1990), wherein the authors indicate that there are two main strategies for studying the tolerance of an amino acid sequence to change.

5 The first strategy exploits the tolerance of amino acid substitutions by natural selection during the process of evolution. By comparing amino acid sequences in different species, conserved amino acids can be identified. These conserved amino acids are likely important for protein function. In contrast, the amino acid positions where substitutions have been tolerated by natural selection indicates that these positions are not critical for protein function. Thus, positions tolerating amino acid
10 substitution could be modified while still maintaining biological activity of the protein.

The second strategy uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene to identify regions critical for protein function. For example, site directed mutagenesis or alanine-scanning mutagenesis (introduction of single alanine mutations at every residue in the molecule) can be used. (Cunningham
15 and Wells, Science 244:1081-1085 (1989).) The resulting mutant molecules can then be tested for biological activity.

As the authors state, these two strategies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The authors further indicate which amino acid changes are likely to be permissive at certain amino acid positions in the
20 protein. For example, most buried (within the tertiary structure of the protein) amino acid residues require nonpolar side chains, whereas few features of surface side chains are generally conserved. Moreover, tolerated conservative amino acid substitutions involve replacement of the aliphatic or hydrophobic amino acids Ala, Val, Leu and Ile; replacement of the hydroxyl residues Ser and Thr; replacement of the acidic residues
25 Asp and Glu; replacement of the amide residues Asn and Gln, replacement of the basic residues Lys, Arg, and His; replacement of the aromatic residues Phe, Tyr, and Trp, and replacement of the small-sized amino acids Ala, Ser, Thr, Met, and Gly.

Besides conservative amino acid substitution, variants of the present invention include (i) substitutions with one or more of the non-conserved amino acid residues,
30 where the substituted amino acid residues may or may not be one encoded by the genetic code, or (ii) substitution with one or more of amino acid residues having a substituent group, or (iii) fusion of the mature polypeptide with another compound, such as a compound to increase the stability and/or solubility of the polypeptide (for example, polyethylene glycol), or (iv) fusion of the polypeptide with additional amino
35 acids, such as an IgG Fc fusion region peptide, or leader or secretory sequence, or a sequence facilitating purification. Such variant polypeptides are deemed to be within the scope of those skilled in the art from the teachings herein.

For example, polypeptide variants containing amino acid substitutions of charged amino acids with other charged or neutral amino acids may produce proteins with improved characteristics, such as less aggregation. Aggregation of pharmaceutical formulations both reduces activity and increases clearance due to the aggregate's immunogenic activity. (Pinckard et al., Clin. Exp. Immunol. 2:331-340 (1967); Robbins et al., Diabetes 36: 838-845 (1987); Cleland et al., Crit. Rev. Therapeutic Drug Carrier Systems 10:307-377 (1993).)

Polynucleotide and Polypeptide Fragments

10 In the present invention, a "polynucleotide fragment" refers to a short polynucleotide having a nucleic acid sequence contained in the deposited clone or shown in SEQ ID NO:X. The short nucleotide fragments are preferably at least about 15 nt, and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt in length. A fragment "at least 20 nt in
15 length," for example, is intended to include 20 or more contiguous bases from the cDNA sequence contained in the deposited clone or the nucleotide sequence shown in SEQ ID NO:X. These nucleotide fragments are useful as diagnostic probes and primers as discussed herein. Of course, larger fragments (e.g., 50, 150, 500, 600, 2000 nucleotides) are preferred.

20 Moreover, representative examples of polynucleotide fragments of the invention, include, for example, fragments having a sequence from about nucleotide number 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-400, 401-450, 451-500, 501-550, 551-600, 651-700, and 701 to the end of SEQ ID NO:X or the cDNA contained in the deposited clone. In this context "about" includes the particularly
25 recited ranges, larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Preferably, these fragments encode a polypeptide which has biological activity.

In the present invention, a "polypeptide fragment" refers to a short amino acid sequence contained in SEQ ID NO:Y or encoded by the cDNA contained in the
30 deposited clone. Protein fragments may be "free-standing," or comprised within a larger polypeptide of which the fragment forms a part or region, most preferably as a single continuous region. Representative examples of polypeptide fragments of the invention, include, for example, fragments from about amino acid number 1-20, 21-40, 41-60, 61-80, 81-100, 102-120, 121-140, 141-160, and 161 to the end of the coding
35 region. Moreover, polypeptide fragments can be about 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, or 150 amino acids in length. In this context "about"

includes the particularly recited ranges, larger or smaller by several (5, 4, 3, 2, or 1) amino acids, at either extreme or at both extremes.

Preferred polypeptide fragments include the secreted protein as well as the mature form. Further preferred polypeptide fragments include the secreted protein or the mature form having a continuous series of deleted residues from the amino or the carboxy terminus, or both. For example, any number of amino acids, ranging from 1-60, can be deleted from the amino terminus of either the secreted polypeptide or the mature form. Similarly, any number of amino acids, ranging from 1-30, can be deleted from the carboxy terminus of the secreted protein or mature form. Furthermore, any combination of the above amino and carboxy terminus deletions are preferred. Similarly, polynucleotide fragments encoding these polypeptide fragments are also preferred.

Also preferred are polypeptide and polynucleotide fragments characterized by structural or functional domains, such as fragments that comprise alpha-helix and alpha-helix forming regions, beta-sheet and beta-sheet-forming regions, turn and turn-forming regions, coil and coil-forming regions, hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta amphipathic regions, flexible regions, surface-forming regions, substrate binding region, and high antigenic index regions. Polypeptide fragments of SEQ ID NO:Y falling within conserved domains are specifically contemplated by the present invention. Moreover, polynucleotide fragments encoding these domains are also contemplated.

Other preferred fragments are biologically active fragments. Biologically active fragments are those exhibiting activity similar, but not necessarily identical, to an activity of the polypeptide of the present invention. The biological activity of the fragments may include an improved desired activity, or a decreased undesirable activity.

Epitopes & Antibodies

In the present invention, "epitopes" refer to polypeptide fragments having antigenic or immunogenic activity in an animal, especially in a human. A preferred embodiment of the present invention relates to a polypeptide fragment comprising an epitope, as well as the polynucleotide encoding this fragment. A region of a protein molecule to which an antibody can bind is defined as an "antigenic epitope." In contrast, an "immunogenic epitope" is defined as a part of a protein that elicits an antibody response. (See, for instance, Geysen et al., Proc. Natl. Acad. Sci. USA 81:3998-4002 (1983).)

Fragments which function as epitopes may be produced by any conventional means. (See, e.g., Houghten, R. A., Proc. Natl. Acad. Sci. USA 82:5131-5135 (1985) further described in U.S. Patent No. 4,631,211.)

In the present invention, antigenic epitopes preferably contain a sequence of at least seven, more preferably at least nine, and most preferably between about 15 to about 30 amino acids. Antigenic epitopes are useful to raise antibodies, including monoclonal antibodies, that specifically bind the epitope. (See, for instance, Wilson et al., Cell 37:767-778 (1984); Sutcliffe, J. G. et al., Science 219:660-666 (1983).)

Similarly, immunogenic epitopes can be used to induce antibodies according to methods well known in the art. (See, for instance, Sutcliffe et al., supra; Wilson et al., supra; Chow, M. et al., Proc. Natl. Acad. Sci. USA 82:910-914; and Bittle, F. J. et al., J. Gen. Virol. 66:2347-2354 (1985).) A preferred immunogenic epitope includes the secreted protein. The immunogenic epitopes may be presented together with a carrier protein, such as an albumin, to an animal system (such as rabbit or mouse) or, if it is long enough (at least about 25 amino acids), without a carrier. However, immunogenic epitopes comprising as few as 8 to 10 amino acids have been shown to be sufficient to raise antibodies capable of binding to, at the very least, linear epitopes in a denatured polypeptide (e.g., in Western blotting.)

As used herein, the term "antibody" (Ab) or "monoclonal antibody" (Mab) is meant to include intact molecules as well as antibody fragments (such as, for example, Fab and F(ab')₂ fragments) which are capable of specifically binding to protein. Fab and F(ab')₂ fragments lack the Fc fragment of intact antibody, clear more rapidly from the circulation, and may have less non-specific tissue binding than an intact antibody. (Wahl et al., J. Nucl. Med. 24:316-325 (1983).) Thus, these fragments are preferred, as well as the products of a FAB or other immunoglobulin expression library. Moreover, antibodies of the present invention include chimeric, single chain, and humanized antibodies.

Fusion Proteins

Any polypeptide of the present invention can be used to generate fusion proteins. For example, the polypeptide of the present invention, when fused to a second protein, can be used as an antigenic tag. Antibodies raised against the polypeptide of the present invention can be used to indirectly detect the second protein by binding to the polypeptide. Moreover, because secreted proteins target cellular locations based on trafficking signals, the polypeptides of the present invention can be used as targeting molecules once fused to other proteins.

Examples of domains that can be fused to polypeptides of the present invention include not only heterologous signal sequences, but also other heterologous functional regions. The fusion does not necessarily need to be direct, but may occur through linker sequences.

5 Moreover, fusion proteins may also be engineered to improve characteristics of the polypeptide of the present invention. For instance, a region of additional amino acids, particularly charged amino acids, may be added to the N-terminus of the polypeptide to improve stability and persistence during purification from the host cell or subsequent handling and storage. Also, peptide moieties may be added to the
10 polypeptide to facilitate purification. Such regions may be removed prior to final preparation of the polypeptide. The addition of peptide moieties to facilitate handling of polypeptides are familiar and routine techniques in the art.

 Moreover, polypeptides of the present invention, including fragments, and specifically epitopes, can be combined with parts of the constant domain of
15 immunoglobulins (IgG), resulting in chimeric polypeptides. These fusion proteins facilitate purification and show an increased half-life in vivo. One reported example describes chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. (EP A 394,827; Traunecker et al., Nature 331:84-86
20 (1988).) Fusion proteins having disulfide-linked dimeric structures (due to the IgG) can also be more efficient in binding and neutralizing other molecules, than the monomeric secreted protein or protein fragment alone. (Fountoulakis et al., J. Biochem. 270:3958-3964 (1995).)

 Similarly, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion
25 proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, the Fc part in a fusion protein is beneficial in therapy and diagnosis, and thus can result in, for example, improved pharmacokinetic properties. (EP-A 0232 262.) Alternatively, deleting the Fc part after the fusion protein has been expressed, detected, and purified,
30 would be desired. For example, the Fc portion may hinder therapy and diagnosis if the fusion protein is used as an antigen for immunizations. In drug discovery, for example, human proteins, such as hIL-5, have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. (See, D. Bennett et al., J. Molecular Recognition 8:52-58 (1995); K. Johanson et al., J. Biol.
35 Chem. 270:9459-9471 (1995).)

 Moreover, the polypeptides of the present invention can be fused to marker sequences, such as a peptide which facilitates purification of the fused polypeptide. In

preferred embodiments, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311), among others, many of which are commercially available. As described in Gentz et al., Proc. Natl. Acad. Sci. USA 86:821-824 (1989), for
5 instance, hexa-histidine provides for convenient purification of the fusion protein. Another peptide tag useful for purification, the "HA" tag, corresponds to an epitope derived from the influenza hemagglutinin protein. (Wilson et al., Cell 37:767 (1984).)

Thus, any of these above fusions can be engineered using the polynucleotides or the polypeptides of the claimed invention.

10

Vectors, Host Cells, and Protein Production

The present invention also relates to vectors containing the polynucleotide of the present invention, host cells, and the production of polypeptides by recombinant techniques. The vector may be, for example, a phage, plasmid, viral, or retroviral
15 vector. Retroviral vectors may be replication competent or replication defective. In the latter case, viral propagation generally will occur only in complementing host cells.

The polynucleotides may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid. If the vector is
20 a virus, it may be packaged in vitro using an appropriate packaging cell line and then transduced into host cells.

The polynucleotide insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the E. coli lac, trp, phoA and tac promoters, the SV40 early and late promoters and promoters of retroviral LTRs, to
25 name a few. Other suitable promoters will be known to the skilled artisan. The expression constructs will further contain sites for transcription initiation, termination, and, in the transcribed region, a ribosome binding site for translation. The coding portion of the transcripts expressed by the constructs will preferably include a translation initiating codon at the beginning and a termination codon (UAA, UGA or
30 UAG) appropriately positioned at the end of the polypeptide to be translated.

As indicated, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase, G418 or neomycin resistance for eukaryotic cell culture and tetracycline, kanamycin or ampicillin resistance genes for culturing in E. coli and other bacteria. Representative examples of
35 appropriate hosts include, but are not limited to, bacterial cells, such as E. coli, Streptomyces and Salmonella typhimurium cells; fungal cells, such as yeast cells; insect cells such as Drosophila S2 and Spodoptera Sf9 cells; animal cells such as CHO, COS,

293, and Bowes melanoma cells; and plant cells. Appropriate culture mediums and conditions for the above-described host cells are known in the art.

Among vectors preferred for use in bacteria include pQE70, pQE60 and pQE-9, available from QIAGEN, Inc.; pBluescript vectors, Phagescript vectors, pNH8A, 5 pNH16a, pNH18A, pNH46A, available from Stratagene Cloning Systems, Inc.; and ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 available from Pharmacia Biotech, Inc. Among preferred eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; and pSVK3, pBPV, pMSG and pSVL available from Pharmacia. Other suitable vectors will be readily apparent to the skilled artisan.

10 Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection, or other methods. Such methods are described in many standard laboratory manuals, such as Davis et al., Basic Methods In Molecular Biology (1986). It is specifically contemplated that the polypeptides of the 15 present invention may in fact be expressed by a host cell lacking a recombinant vector.

A polypeptide of this invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, 20 phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography ("HPLC") is employed for purification.

Polypeptides of the present invention, and preferably the secreted form, can also be recovered from: products purified from natural sources, including bodily fluids, 25 tissues and cells, whether directly isolated or cultured; products of chemical synthetic procedures; and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, higher plant, insect, and mammalian cells. Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be 30 non-glycosylated. In addition, polypeptides of the invention may also include an initial modified methionine residue, in some cases as a result of host-mediated processes. Thus, it is well known in the art that the N-terminal methionine encoded by the translation initiation codon generally is removed with high efficiency from any protein after translation in all eukaryotic cells. While the N-terminal methionine on most 35 proteins also is efficiently removed in most prokaryotes, for some proteins, this prokaryotic removal process is inefficient, depending on the nature of the amino acid to which the N-terminal methionine is covalently linked.

Uses of the Polynucleotides

Each of the polynucleotides identified herein can be used in numerous ways as reagents. The following description should be considered exemplary and utilizes
5 known techniques.

The polynucleotides of the present invention are useful for chromosome identification. There exists an ongoing need to identify new chromosome markers, since few chromosome marking reagents, based on actual sequence data (repeat polymorphisms), are presently available. Each polynucleotide of the present invention
10 can be used as a chromosome marker.

Briefly, sequences can be mapped to chromosomes by preparing PCR primers (preferably 15-25 bp) from the sequences shown in SEQ ID NO:X. Primers can be selected using computer analysis so that primers do not span more than one predicted exon in the genomic DNA. These primers are then used for PCR screening of somatic
15 cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to the SEQ ID NO:X will yield an amplified fragment.

Similarly, somatic hybrids provide a rapid method of PCR mapping the polynucleotides to particular chromosomes. Three or more clones can be assigned per day using a single thermal cycler. Moreover, sublocalization of the polynucleotides can
20 be achieved with panels of specific chromosome fragments. Other gene mapping strategies that can be used include in situ hybridization, prescreening with labeled flow-sorted chromosomes, and preselection by hybridization to construct chromosome specific-cDNA libraries.

Precise chromosomal location of the polynucleotides can also be achieved using
25 fluorescence in situ hybridization (FISH) of a metaphase chromosomal spread. This technique uses polynucleotides as short as 500 or 600 bases; however, polynucleotides 2,000-4,000 bp are preferred. For a review of this technique, see Verma et al., "Human Chromosomes: a Manual of Basic Techniques," Pergamon Press, New York (1988).

For chromosome mapping, the polynucleotides can be used individually (to
30 mark a single chromosome or a single site on that chromosome) or in panels (for marking multiple sites and/or multiple chromosomes). Preferred polynucleotides correspond to the noncoding regions of the cDNAs because the coding sequences are more likely conserved within gene families, thus increasing the chance of cross
35 hybridization during chromosomal mapping.

Once a polynucleotide has been mapped to a precise chromosomal location, the physical position of the polynucleotide can be used in linkage analysis. Linkage

analysis establishes coinheritance between a chromosomal location and presentation of a particular disease. (Disease mapping data are found, for example, in V. McKusick, Mendelian Inheritance in Man (available on line through Johns Hopkins University Welch Medical Library) .) Assuming 1 megabase mapping resolution and one gene per
5 20 kb, a cDNA precisely localized to a chromosomal region associated with the disease could be one of 50-500 potential causative genes.

Thus, once coinheritance is established, differences in the polynucleotide and the corresponding gene between affected and unaffected individuals can be examined. First, visible structural alterations in the chromosomes, such as deletions or
10 translocations, are examined in chromosome spreads or by PCR. If no structural alterations exist, the presence of point mutations are ascertained. Mutations observed in some or all affected individuals, but not in normal individuals, indicates that the mutation may cause the disease. However, complete sequencing of the polypeptide and the corresponding gene from several normal individuals is required to distinguish the
15 mutation from a polymorphism. If a new polymorphism is identified, this polymorphic polypeptide can be used for further linkage analysis.

Furthermore, increased or decreased expression of the gene in affected individuals as compared to unaffected individuals can be assessed using polynucleotides of the present invention. Any of these alterations (altered expression,
20 chromosomal rearrangement, or mutation) can be used as a diagnostic or prognostic marker.

In addition to the foregoing, a polynucleotide can be used to control gene expression through triple helix formation or antisense DNA or RNA. Both methods rely on binding of the polynucleotide to DNA or RNA. For these techniques, preferred
25 polynucleotides are usually 20 to 40 bases in length and complementary to either the region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxy-nucleotides as Antisense Inhibitors of Gene Expression, CRC
30 Press, Boca Raton, FL (1988).) Triple helix formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques are effective in model systems, and the information disclosed herein can be used to design antisense or triple helix polynucleotides in an effort to treat disease.

35 Polynucleotides of the present invention are also useful in gene therapy. One goal of gene therapy is to insert a normal gene into an organism having a defective gene, in an effort to correct the genetic defect. The polynucleotides disclosed in the

present invention offer a means of targeting such genetic defects in a highly accurate manner. Another goal is to insert a new gene that was not present in the host genome, thereby producing a new trait in the host cell.

The polynucleotides are also useful for identifying individuals from minute
5 biological samples. The United States military, for example, is considering the use of restriction fragment length polymorphism (RFLP) for identification of its personnel. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identifying personnel. This method does not suffer from the current limitations of "Dog Tags"
10 which can be lost, switched, or stolen, making positive identification difficult. The polynucleotides of the present invention can be used as additional DNA markers for RFLP.

The polynucleotides of the present invention can also be used as an alternative to RFLP, by determining the actual base-by-base DNA sequence of selected portions of an
15 individual's genome. These sequences can be used to prepare PCR primers for amplifying and isolating such selected DNA, which can then be sequenced. Using this technique, individuals can be identified because each individual will have a unique set of DNA sequences. Once an unique ID database is established for an individual, positive identification of that individual, living or dead, can be made from extremely
20 small tissue samples.

Forensic biology also benefits from using DNA-based identification techniques as disclosed herein. DNA sequences taken from very small biological samples such as tissues, e.g., hair or skin, or body fluids, e.g., blood, saliva, semen, etc., can be amplified using PCR. In one prior art technique, gene sequences amplified from
25 polymorphic loci, such as DQa class II HLA gene, are used in forensic biology to identify individuals. (Erich, H., PCR Technology, Freeman and Co. (1992).) Once these specific polymorphic loci are amplified, they are digested with one or more restriction enzymes, yielding an identifying set of bands on a Southern blot probed with DNA corresponding to the DQa class II HLA gene. Similarly, polynucleotides of the
30 present invention can be used as polymorphic markers for forensic purposes.

There is also a need for reagents capable of identifying the source of a particular tissue. Such need arises, for example, in forensics when presented with tissue of unknown origin. Appropriate reagents can comprise, for example, DNA probes or primers specific to particular tissue prepared from the sequences of the present
35 invention. Panels of such reagents can identify tissue by species and/or by organ type. In a similar fashion, these reagents can be used to screen tissue cultures for contamination.

In the very least, the polynucleotides of the present invention can be used as molecular weight markers on Southern gels, as diagnostic probes for the presence of a specific mRNA in a particular cell type, as a probe to "subtract-out" known sequences in the process of discovering novel polynucleotides, for selecting and making oligomers
5 for attachment to a "gene chip" or other support, to raise anti-DNA antibodies using DNA immunization techniques, and as an antigen to elicit an immune response.

Uses of the Polypeptides

Each of the polypeptides identified herein can be used in numerous ways. The
10 following description should be considered exemplary and utilizes known techniques.

A polypeptide of the present invention can be used to assay protein levels in a biological sample using antibody-based techniques. For example, protein expression in tissues can be studied with classical immunohistological methods. (Jalkanen, M., et al., J. Cell. Biol. 101:976-985 (1985); Jalkanen, M., et al., J. Cell . Biol. 105:3087-
15 3096 (1987).) Other antibody-based methods useful for detecting protein gene expression include immunoassays, such as the enzyme linked immunosorbent assay (ELISA) and the radioimmunoassay (RIA). Suitable antibody assay labels are known in the art and include enzyme labels, such as, glucose oxidase, and radioisotopes, such as iodine (125I, 121I), carbon (14C), sulfur (35S), tritium (3H), indium (112In), and
20 technetium (99mTc), and fluorescent labels, such as fluorescein and rhodamine, and biotin.

In addition to assaying secreted protein levels in a biological sample, proteins can also be detected in vivo by imaging. Antibody labels or markers for in vivo imaging of protein include those detectable by X-radiography, NMR or ESR. For X-
25 radiography, suitable labels include radioisotopes such as barium or cesium, which emit detectable radiation but are not overtly harmful to the subject. Suitable markers for NMR and ESR include those with a detectable characteristic spin, such as deuterium, which may be incorporated into the antibody by labeling of nutrients for the relevant hybridoma.

A protein-specific antibody or antibody fragment which has been labeled with an appropriate detectable imaging moiety, such as a radioisotope (for example, 131I, 112In, 99mTc), a radio-opaque substance, or a material detectable by nuclear magnetic resonance, is introduced (for example, parenterally, subcutaneously, or
30 intraperitoneally) into the mammal. It will be understood in the art that the size of the subject and the imaging system used will determine the quantity of imaging moiety needed to produce diagnostic images. In the case of a radioisotope moiety, for a human
35 subject, the quantity of radioactivity injected will normally range from about 5 to 20

millicuries of ^{99m}Tc. The labeled antibody or antibody fragment will then preferentially accumulate at the location of cells which contain the specific protein. In vivo tumor imaging is described in S.W. Burchiel et al., "Immunopharmacokinetics of Radiolabeled Antibodies and Their Fragments." (Chapter 13 in Tumor Imaging: The Radiochemical Detection of Cancer, S.W. Burchiel and B. A. Rhodes, eds., Masson Publishing Inc. (1982).)

Thus, the invention provides a diagnostic method of a disorder, which involves (a) assaying the expression of a polypeptide of the present invention in cells or body fluid of an individual; (b) comparing the level of gene expression with a standard gene expression level, whereby an increase or decrease in the assayed polypeptide gene expression level compared to the standard expression level is indicative of a disorder.

Moreover, polypeptides of the present invention can be used to treat disease. For example, patients can be administered a polypeptide of the present invention in an effort to replace absent or decreased levels of the polypeptide (e.g., insulin), to supplement absent or decreased levels of a different polypeptide (e.g., hemoglobin S for hemoglobin B), to inhibit the activity of a polypeptide (e.g., an oncogene), to activate the activity of a polypeptide (e.g., by binding to a receptor), to reduce the activity of a membrane bound receptor by competing with it for free ligand (e.g., soluble TNF receptors used in reducing inflammation), or to bring about a desired response (e.g., blood vessel growth).

Similarly, antibodies directed to a polypeptide of the present invention can also be used to treat disease. For example, administration of an antibody directed to a polypeptide of the present invention can bind and reduce overproduction of the polypeptide. Similarly, administration of an antibody can activate the polypeptide, such as by binding to a polypeptide bound to a membrane (receptor).

At the very least, the polypeptides of the present invention could be used as molecular weight markers on SDS-PAGE gels or on molecular sieve gel filtration columns using methods well known to those of skill in the art. Polypeptides can also be used to raise antibodies, which in turn are used to measure protein expression from a recombinant cell, as a way of assessing transformation of the host cell. Moreover, the polypeptides of the present invention can be used to test the following biological activities.

Biological Activities

The polynucleotides and polypeptides of the present invention can be used in assays to test for one or more biological activities. If these polynucleotides and polypeptides do exhibit activity in a particular assay, it is likely that these molecules

may be involved in the diseases associated with the biological activity. Thus, the polynucleotides and polypeptides could be used to treat the associated disease.

Immune Activity

5 A polypeptide or polynucleotide of the present invention may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilization (chemotaxis) of immune cells. Immune cells develop through a process called hematopoiesis, producing myeloid (platelets, red blood cells, neutrophils, and macrophages) and lymphoid (B and T lymphocytes) cells
10 from pluripotent stem cells. The etiology of these immune deficiencies or disorders may be genetic, somatic, such as cancer or some autoimmune disorders, acquired (e.g., by chemotherapy or toxins), or infectious. Moreover, a polynucleotide or polypeptide of the present invention can be used as a marker or detector of a particular immune system disease or disorder.

15 A polynucleotide or polypeptide of the present invention may be useful in treating or detecting deficiencies or disorders of hematopoietic cells. A polypeptide or polynucleotide of the present invention could be used to increase differentiation and proliferation of hematopoietic cells, including the pluripotent stem cells, in an effort to treat those disorders associated with a decrease in certain (or many) types hematopoietic
20 cells. Examples of immunologic deficiency syndromes include, but are not limited to: blood protein disorders (e.g. agammaglobulinemia, dysgammaglobulinemia), ataxia telangiectasia, common variable immunodeficiency, Digeorge Syndrome, HIV infection, HTLV-BLV infection, leukocyte adhesion deficiency syndrome, lymphopenia, phagocyte bactericidal dysfunction, severe combined immunodeficiency
25 (SCIDs), Wiskott-Aldrich Disorder, anemia, thrombocytopenia, or hemoglobinuria.

Moreover, a polypeptide or polynucleotide of the present invention could also be used to modulate hemostatic (the stopping of bleeding) or thrombolytic activity (clot formation). For example, by increasing hemostatic or thrombolytic activity, a polynucleotide or polypeptide of the present invention could be used to treat blood
30 coagulation disorders (e.g., afibrinogenemia, factor deficiencies), blood platelet disorders (e.g. thrombocytopenia), or wounds resulting from trauma, surgery, or other causes. Alternatively, a polynucleotide or polypeptide of the present invention that can decrease hemostatic or thrombolytic activity could be used to inhibit or dissolve clotting. These molecules could be important in the treatment of heart attacks
35 (infarction), strokes, or scarring.

A polynucleotide or polypeptide of the present invention may also be useful in treating or detecting autoimmune disorders. Many autoimmune disorders result from

inappropriate recognition of self as foreign material by immune cells. This inappropriate recognition results in an immune response leading to the destruction of the host tissue. Therefore, the administration of a polypeptide or polynucleotide of the present invention that inhibits an immune response, particularly the proliferation,
5 differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing autoimmune disorders.

Examples of autoimmune disorders that can be treated or detected by the present invention include, but are not limited to: Addison's Disease, hemolytic anemia, antiphospholipid syndrome, rheumatoid arthritis, dermatitis, allergic encephalomyelitis,
10 glomerulonephritis, Goodpasture's Syndrome, Graves' Disease, Multiple Sclerosis, Myasthenia Gravis, Neuritis, Ophthalmia, Bullous Pemphigoid, Pemphigus, Polyendocrinopathies, Purpura, Reiter's Disease, Stiff-Man Syndrome, Autoimmune Thyroiditis, Systemic Lupus Erythematosus, Autoimmune Pulmonary Inflammation, Guillain-Barre Syndrome, insulin dependent diabetes mellitus, and autoimmune
15 inflammatory eye disease.

Similarly, allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems, may also be treated by a polypeptide or polynucleotide of the present invention. Moreover, these molecules can be used to treat anaphylaxis, hypersensitivity to an antigenic molecule, or blood group incompatibility.

20 A polynucleotide or polypeptide of the present invention may also be used to treat and/or prevent organ rejection or graft-versus-host disease (GVHD). Organ rejection occurs by host immune cell destruction of the transplanted tissue through an immune response. Similarly, an immune response is also involved in GVHD, but, in this case, the foreign transplanted immune cells destroy the host tissues. The
25 administration of a polypeptide or polynucleotide of the present invention that inhibits an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing organ rejection or GVHD.

Similarly, a polypeptide or polynucleotide of the present invention may also be used to modulate inflammation. For example, the polypeptide or polynucleotide may
30 inhibit the proliferation and differentiation of cells involved in an inflammatory response. These molecules can be used to treat inflammatory conditions, both chronic and acute conditions, including inflammation associated with infection (e.g., septic shock, sepsis, or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute
35 rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, Crohn's disease, or resulting from over production of cytokines (e.g., TNF or IL-1.)

Hyperproliferative Disorders

A polypeptide or polynucleotide can be used to treat or detect hyperproliferative disorders, including neoplasms. A polypeptide or polynucleotide of the present invention may inhibit the proliferation of the disorder through direct or indirect interactions. Alternatively, a polypeptide or polynucleotide of the present invention may proliferate other cells which can inhibit the hyperproliferative disorder.

For example, by increasing an immune response, particularly increasing antigenic qualities of the hyperproliferative disorder or by proliferating, differentiating, or mobilizing T-cells, hyperproliferative disorders can be treated. This immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, decreasing an immune response may also be a method of treating hyperproliferative disorders, such as a chemotherapeutic agent.

Examples of hyperproliferative disorders that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but are not limited to neoplasms located in the: abdomen, bone, breast, digestive system, liver, pancreas, peritoneum, endocrine glands (adrenal, parathyroid, pituitary, testicles, ovary, thymus, thyroid), eye, head and neck, nervous (central and peripheral), lymphatic system, pelvic, skin, soft tissue, spleen, thoracic, and urogenital.

Similarly, other hyperproliferative disorders can also be treated or detected by a polynucleotide or polypeptide of the present invention. Examples of such hyperproliferative disorders include, but are not limited to: hypergammaglobulinemia, lymphoproliferative disorders, paraproteinemias, purpura, sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other hyperproliferative disease, besides neoplasia, located in an organ system listed above.

Infectious Disease

A polypeptide or polynucleotide of the present invention can be used to treat or detect infectious agents. For example, by increasing the immune response, particularly increasing the proliferation and differentiation of B and/or T cells, infectious diseases may be treated. The immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, the polypeptide or polynucleotide of the present invention may also directly inhibit the infectious agent, without necessarily eliciting an immune response.

- Viruses are one example of an infectious agent that can cause disease or symptoms that can be treated or detected by a polynucleotide or polypeptide of the present invention. Examples of viruses, include, but are not limited to the following DNA and RNA viral families: Arbovirus, Adenoviridae, Arenaviridae, Arterivirus,
- 5 Bimaviridae, Bunyaviridae, Caliciviridae, Circoviridae, Coronaviridae, Flaviviridae, Hepadnaviridae (Hepatitis), Herpesviridae (such as, Cytomegalovirus, Herpes Simplex, Herpes Zoster), Mononegavirus (e.g., Paramyxoviridae, Morbillivirus, Rhabdoviridae), Orthomyxoviridae (e.g., Influenza), Papovaviridae, Parvoviridae, Picornaviridae, Poxviridae (such as Smallpox or Vaccinia), Reoviridae (e.g.,
- 10 Rotavirus), Retroviridae (HTLV-I, HTLV-II, Lentivirus), and Togaviridae (e.g., Rubivirus). Viruses falling within these families can cause a variety of diseases or symptoms, including, but not limited to: arthritis, bronchiolitis, encephalitis, eye infections (e.g., conjunctivitis, keratitis), chronic fatigue syndrome, hepatitis (A, B, C, E, Chronic Active, Delta), meningitis, opportunistic infections (e.g., AIDS),
- 15 pneumonia, Burkitt's Lymphoma, chickenpox, hemorrhagic fever, Measles, Mumps, Parainfluenza, Rabies, the common cold, Polio, leukemia, Rubella, sexually transmitted diseases, skin diseases (e.g., Kaposi's, warts), and viremia. A polypeptide or polynucleotide of the present invention can be used to treat or detect any of these symptoms or diseases.
- 20 Similarly, bacterial or fungal agents that can cause disease or symptoms and that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but not limited to, the following Gram-Negative and Gram-positive bacterial families and fungi: Actinomycetales (e.g., Corynebacterium, Mycobacterium, Norcardia), Aspergillosis, Bacillaceae (e.g., Anthrax, Clostridium), Bacteroidaceae,
- 25 Blastomycosis, Bordetella, Borrelia, Brucellosis, Candidiasis, Campylobacter, Coccidioidomycosis, Cryptococcosis, Dermatocycoses, Enterobacteriaceae (Klebsiella, Salmonella, Serratia, Yersinia), Erysipelothrix, Helicobacter, Legionellosis, Leptospirosis, Listeria, Mycoplasmatales, Neisseriaceae (e.g., Acinetobacter, Gonorrhea, Meningococcal), Pasteurellaceae Infections (e.g., Actinobacillus,
- 30 Haemophilus, Pasteurella), Pseudomonas, Rickettsiaceae, Chlamydiaceae, Syphilis, and Staphylococcal. These bacterial or fungal families can cause the following diseases or symptoms, including, but not limited to: bacteremia, endocarditis, eye infections (conjunctivitis, tuberculosis, uveitis), gingivitis, opportunistic infections (e.g., AIDS related infections), paronychia, prosthesis-related infections, Reiter's Disease,
- 35 respiratory tract infections, such as Whooping Cough or Empyema, sepsis, Lyme Disease, Cat-Scratch Disease, Dysentery, Paratyphoid Fever, food poisoning, Typhoid, pneumonia, Gonorrhea, meningitis, Chlamydia, Syphilis, Diphtheria,

Leprosy, Paratuberculosis, Tuberculosis, Lupus, Botulism, gangrene, tetanus, impetigo, Rheumatic Fever, Scarlet Fever, sexually transmitted diseases, skin diseases (e.g., cellulitis, dermatocycoses), toxemia, urinary tract infections, wound infections. A polypeptide or polynucleotide of the present invention can be used to treat or detect
5 any of these symptoms or diseases.

Moreover, parasitic agents causing disease or symptoms that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but not limited to, the following families: Amebiasis, Babesiosis, Coccidiosis, Cryptosporidiosis, Dientamoebiasis, Dourine, Ectoparasitic, Giardiasis, Helminthiasis,
10 Leishmaniasis, Theileriasis, Toxoplasmosis, Trypanosomiasis, and Trichomonas. These parasites can cause a variety of diseases or symptoms, including, but not limited to: Scabies, Trombiculiasis, eye infections, intestinal disease (e.g., dysentery, giardiasis), liver disease, lung disease, opportunistic infections (e.g., AIDS related), Malaria, pregnancy complications, and toxoplasmosis. A polypeptide or polynucleotide
15 of the present invention can be used to treat or detect any of these symptoms or diseases.

Preferably, treatment using a polypeptide or polynucleotide of the present invention could either be by administering an effective amount of a polypeptide to the patient, or by removing cells from the patient, supplying the cells with a polynucleotide
20 of the present invention, and returning the engineered cells to the patient (ex vivo therapy). Moreover, the polypeptide or polynucleotide of the present invention can be used as an antigen in a vaccine to raise an immune response against infectious disease.

Regeneration

25 A polynucleotide or polypeptide of the present invention can be used to differentiate, proliferate, and attract cells, leading to the regeneration of tissues. (See, Science 276:59-87 (1997).) The regeneration of tissues could be used to repair, replace, or protect tissue damaged by congenital defects, trauma (wounds, burns, incisions, or ulcers), age, disease (e.g. osteoporosis, osteoarthritis, periodontal
30 disease, liver failure), surgery, including cosmetic plastic surgery, fibrosis, reperfusion injury, or systemic cytokine damage.

Tissues that could be regenerated using the present invention include organs (e.g., pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac), vascular (including vascular endothelium), nervous, hematopoietic, and
35 skeletal (bone, cartilage, tendon, and ligament) tissue. Preferably, regeneration occurs without or decreased scarring. Regeneration also may include angiogenesis.

Moreover, a polynucleotide or polypeptide of the present invention may increase regeneration of tissues difficult to heal. For example, increased tendon/ligament regeneration would quicken recovery time after damage. A polynucleotide or polypeptide of the present invention could also be used prophylactically in an effort to avoid damage. Specific diseases that could be treated include of tendinitis, carpal tunnel syndrome, and other tendon or ligament defects. A further example of tissue regeneration of non-healing wounds includes pressure ulcers, ulcers associated with vascular insufficiency, surgical, and traumatic wounds.

Similarly, nerve and brain tissue could also be regenerated by using a polynucleotide or polypeptide of the present invention to proliferate and differentiate nerve cells. Diseases that could be treated using this method include central and peripheral nervous system diseases, neuropathies, or mechanical and traumatic disorders (e.g., spinal cord disorders, head trauma, cerebrovascular disease, and stroke). Specifically, diseases associated with peripheral nerve injuries, peripheral neuropathy (e.g., resulting from chemotherapy or other medical therapies), localized neuropathies, and central nervous system diseases (e.g., Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome), could all be treated using the polynucleotide or polypeptide of the present invention.

Chemotaxis

A polynucleotide or polypeptide of the present invention may have chemotaxis activity. A chemotactic molecule attracts or mobilizes cells (e.g., monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells) to a particular site in the body, such as inflammation, infection, or site of hyperproliferation. The mobilized cells can then fight off and/or heal the particular trauma or abnormality.

A polynucleotide or polypeptide of the present invention may increase chemotactic activity of particular cells. These chemotactic molecules can then be used to treat inflammation, infection, hyperproliferative disorders, or any immune system disorder by increasing the number of cells targeted to a particular location in the body. For example, chemotactic molecules can be used to treat wounds and other trauma to tissues by attracting immune cells to the injured location. Chemotactic molecules of the present invention can also attract fibroblasts, which can be used to treat wounds.

It is also contemplated that a polynucleotide or polypeptide of the present invention may inhibit chemotactic activity. These molecules could also be used to treat

disorders. Thus, a polynucleotide or polypeptide of the present invention could be used as an inhibitor of chemotaxis.

Binding Activity

5 A polypeptide of the present invention may be used to screen for molecules that bind to the polypeptide or for molecules to which the polypeptide binds. The binding of the polypeptide and the molecule may activate (agonist), increase, inhibit (antagonist), or decrease activity of the polypeptide or the molecule bound. Examples of such molecules include antibodies, oligonucleotides, proteins (e.g., receptors), or
10 small molecules.

Preferably, the molecule is closely related to the natural ligand of the polypeptide, e.g., a fragment of the ligand, or a natural substrate, a ligand, a structural or functional mimetic. (See, Coligan et al., Current Protocols in Immunology 1(2):Chapter 5 (1991).) Similarly, the molecule can be closely related to the natural
15 receptor to which the polypeptide binds, or at least, a fragment of the receptor capable of being bound by the polypeptide (e.g., active site). In either case, the molecule can be rationally designed using known techniques.

Preferably, the screening for these molecules involves producing appropriate cells which express the polypeptide, either as a secreted protein or on the cell
20 membrane. Preferred cells include cells from mammals, yeast, *Drosophila*, or *E. coli*. Cells expressing the polypeptide (or cell membrane containing the expressed polypeptide) are then preferably contacted with a test compound potentially containing the molecule to observe binding, stimulation, or inhibition of activity of either the polypeptide or the molecule.

25 The assay may simply test binding of a candidate compound to the polypeptide, wherein binding is detected by a label, or in an assay involving competition with a labeled competitor. Further, the assay may test whether the candidate compound results in a signal generated by binding to the polypeptide.

Alternatively, the assay can be carried out using cell-free preparations,
30 polypeptide/molecule affixed to a solid support, chemical libraries, or natural product mixtures. The assay may also simply comprise the steps of mixing a candidate compound with a solution containing a polypeptide, measuring polypeptide/molecule activity or binding, and comparing the polypeptide/molecule activity or binding to a standard.

35 Preferably, an ELISA assay can measure polypeptide level or activity in a sample (e.g., biological sample) using a monoclonal or polyclonal antibody. The

antibody can measure polypeptide level or activity by either binding, directly or indirectly, to the polypeptide or by competing with the polypeptide for a substrate.

All of these above assays can be used as diagnostic or prognostic markers. The molecules discovered using these assays can be used to treat disease or to bring about a particular result in a patient (e.g., blood vessel growth) by activating or inhibiting the polypeptide/molecule. Moreover, the assays can discover agents which may inhibit or enhance the production of the polypeptide from suitably manipulated cells or tissues.

Therefore, the invention includes a method of identifying compounds which bind to a polypeptide of the invention comprising the steps of: (a) incubating a candidate binding compound with a polypeptide of the invention; and (b) determining if binding has occurred. Moreover, the invention includes a method of identifying agonists/antagonists comprising the steps of: (a) incubating a candidate compound with a polypeptide of the invention, (b) assaying a biological activity, and (b) determining if a biological activity of the polypeptide has been altered.

Other Activities

A polypeptide or polynucleotide of the present invention may also increase or decrease the differentiation or proliferation of embryonic stem cells, besides, as discussed above, hematopoietic lineage.

A polypeptide or polynucleotide of the present invention may also be used to modulate mammalian characteristics, such as body height, weight, hair color, eye color, skin, percentage of adipose tissue, pigmentation, size, and shape (e.g., cosmetic surgery). Similarly, a polypeptide or polynucleotide of the present invention may be used to modulate mammalian metabolism affecting catabolism, anabolism, processing, utilization, and storage of energy.

A polypeptide or polynucleotide of the present invention may be used to change a mammal's mental state or physical state by influencing biorhythms, cardiac rhythms, depression (including depressive disorders), tendency for violence, tolerance for pain, reproductive capabilities (preferably by Activin or Inhibin-like activity), hormonal or endocrine levels, appetite, libido, memory, stress, or other cognitive qualities.

A polypeptide or polynucleotide of the present invention may also be used as a food additive or preservative, such as to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components.

Other Preferred Embodiments

Other preferred embodiments of the claimed invention include an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 50 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1.

Also preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the Clone Sequence and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Also preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the Start Codon and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Similarly preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the First Amino Acid of the Signal Peptide and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 150 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X.

Further preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 500 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X.

A further preferred embodiment is a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the nucleotide sequence of SEQ ID NO:X beginning with the nucleotide at about the position of the 5' Nucleotide of the First Amino Acid of the Signal Peptide and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the complete nucleotide sequence of SEQ ID NO:X.

Also preferred is an isolated nucleic acid molecule which hybridizes under stringent hybridization conditions to a nucleic acid molecule, wherein said nucleic acid molecule which hybridizes does not hybridize under stringent hybridization conditions to a nucleic acid molecule having a nucleotide sequence consisting of only A residues or of only T residues.

Also preferred is a composition of matter comprising a DNA molecule which comprises a human cDNA clone identified by a cDNA Clone Identifier in Table 1, which DNA molecule is contained in the material deposited with the American Type Culture Collection and given the ATCC Deposit Number shown in Table 1 for said cDNA Clone Identifier.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in the nucleotide sequence of a human cDNA clone identified by a cDNA Clone Identifier in Table 1, which DNA molecule is contained in the deposit given the ATCC Deposit Number shown in Table 1.

Also preferred is an isolated nucleic acid molecule, wherein said sequence of at least 50 contiguous nucleotides is included in the nucleotide sequence of the complete open reading frame sequence encoded by said human cDNA clone.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 150 contiguous nucleotides in the nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 500 contiguous nucleotides in the nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the complete nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is a method for detecting in a biological sample a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1; which method comprises a step of comparing a nucleotide sequence of at least one nucleic acid molecule in said sample with a sequence selected from said group and determining

whether the sequence of said nucleic acid molecule in said sample is at least 95% identical to said selected sequence.

Also preferred is the above method wherein said step of comparing sequences comprises determining the extent of nucleic acid hybridization between nucleic acid molecules in said sample and a nucleic acid molecule comprising said sequence selected from said group. Similarly, also preferred is the above method wherein said step of comparing sequences is performed by comparing the nucleotide sequence determined from a nucleic acid molecule in said sample with said sequence selected from said group. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

A further preferred embodiment is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting nucleic acid molecules in said sample, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

The method for identifying the species, tissue or cell type of a biological sample can comprise a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a gene encoding a secreted protein identified in Table 1, which method comprises a step of detecting in a biological sample obtained from said subject nucleic acid molecules, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

The method for diagnosing a pathological condition can comprise a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

Also preferred is a composition of matter comprising isolated nucleic acid molecules wherein the nucleotide sequences of said nucleic acid molecules comprise a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence
5 selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

10 Also preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1.

Also preferred is a polypeptide, wherein said sequence of contiguous amino acids is included in the amino acid sequence of SEQ ID NO:Y in the range of positions
15 beginning with the residue at about the position of the First Amino Acid of the Secreted Portion and ending with the residue at about the Last Amino Acid of the Open Reading Frame as set forth for SEQ ID NO:Y in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the
20 amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence
25 at least 95% identical to the complete amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the
30 ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is a polypeptide wherein said sequence of contiguous amino acids is included in the amino acid sequence of a secreted portion of the secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in
35 Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the

amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at
5 least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at
10 least 95% identical to the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is an isolated antibody which binds specifically to a
15 polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in
20 the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is a method for detecting in a biological sample a polypeptide comprising an amino acid sequence which is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1;
25 and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1; which method comprises a step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group and determining
30 whether the sequence of said polypeptide molecule in said sample is at least 90% identical to said sequence of at least 10 contiguous amino acids.

Also preferred is the above method wherein said step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group comprises determining the extent of specific binding of
35 polypeptides in said sample to an antibody which binds specifically to a polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an

amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

5 Also preferred is the above method wherein said step of comparing sequences is performed by comparing the amino acid sequence determined from a polypeptide molecule in said sample with said sequence selected from said group.

Also preferred is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting polypeptide molecules in
10 said sample, if any, comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded
15 by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is the above method for identifying the species, tissue or cell type of a biological sample, which method comprises a step of detecting polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid
20 sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the above group.

Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a gene encoding a secreted protein identified in Table 1, which method comprises a step of detecting in a biological sample
25 obtained from said subject polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid
30 sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

In any of these methods, the step of detecting said polypeptide molecules includes using an antibody.

35 Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a nucleotide sequence encoding a polypeptide wherein said polypeptide comprises an amino acid sequence that is at least

90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated nucleic acid molecule, wherein said nucleotide sequence encoding a polypeptide has been optimized for expression of said polypeptide in a prokaryotic host.

Also preferred is an isolated nucleic acid molecule, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is a method of making a recombinant vector comprising inserting any of the above isolated nucleic acid molecule into a vector. Also preferred is the recombinant vector produced by this method. Also preferred is a method of making a recombinant host cell comprising introducing the vector into a host cell, as well as the recombinant host cell produced by this method.

Also preferred is a method of making an isolated polypeptide comprising culturing this recombinant host cell under conditions such that said polypeptide is expressed and recovering said polypeptide. Also preferred is this method of making an isolated polypeptide, wherein said recombinant host cell is a eukaryotic cell and said polypeptide is a secreted portion of a human secreted protein comprising an amino acid sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y beginning with the residue at the position of the First Amino Acid of the Secreted Portion of SEQ ID NO:Y wherein Y is an integer set forth in Table 1 and said position of the First Amino Acid of the Secreted Portion of SEQ ID NO:Y is defined in Table 1; and an amino acid sequence of a secreted portion of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1. The isolated polypeptide produced by this method is also preferred.

Also preferred is a method of treatment of an individual in need of an increased level of a secreted protein activity, which method comprises administering to such an individual a pharmaceutical composition comprising an amount of an isolated

polypeptide, polynucleotide, or antibody of the claimed invention effective to increase the level of said protein activity in said individual.

Having generally described the invention, the same will be more readily understood by reference to the following examples, which are provided by way of illustration and are not intended as limiting.

Examples

Example 1: Isolation of a Selected cDNA Clone From the Deposited Sample

Each cDNA clone in a cited ATCC deposit is contained in a plasmid vector. Table 1 identifies the vectors used to construct the cDNA library from which each clone was isolated. In many cases, the vector used to construct the library is a phage vector from which a plasmid has been excised. The table immediately below correlates the related plasmid for each phage vector used in constructing the cDNA library. For example, where a particular clone is identified in Table 1 as being isolated in the vector "Lambda Zap," the corresponding deposited clone is in "pBluescript."

	<u>Vector Used to Construct Library</u>	<u>Corresponding Deposited Plasmid</u>
	Lambda Zap	pBluescript (pBS)
	Uni-Zap XR	pBluescript (pBS)
20	Zap Express	pBK
	plafmid BA	plafmid BA
	pSport1	pSport1
	pCMVSPORT 2.0	pCMVSPORT 2.0
	pCMVSPORT 3.0	pCMVSPORT 3.0
25	pCR [®] 2.1	pCR [®] 2.1

Vectors Lambda Zap (U.S. Patent Nos. 5,128,256 and 5,286,636), Uni-Zap XR (U.S. Patent Nos. 5,128, 256 and 5,286,636), Zap Express (U.S. Patent Nos. 5,128,256 and 5,286,636), pBluescript (pBS) (Short, J. M. et al., Nucleic Acids Res. 16:7583-7600 (1988); Alting-Mees, M. A. and Short, J. M., Nucleic Acids Res. 17:9494 (1989)) and pBK (Alting-Mees, M. A. et al., Strategies 5:58-61 (1992)) are commercially available from Stratagene Cloning Systems, Inc., 11011 N. Torrey Pines Road, La Jolla, CA, 92037. pBS contains an ampicillin resistance gene and pBK contains a neomycin resistance gene. Both can be transformed into E. coli strain XL-1 Blue, also available from Stratagene. pBS comes in 4 forms SK+, SK-, KS+ and KS. The S and K refers to the orientation of the polylinker to the T7 and T3 primer sequences which flank the polylinker region ("S" is for SacI and "K" is for KpnI which are the first sites on each respective end of the linker). "+" or "-" refer to the orientation

of the f1 origin of replication ("ori"), such that in one orientation, single stranded rescue initiated from the f1 ori generates sense strand DNA and in the other, antisense.

Vectors pSport1, pCMVSPORT 2.0 and pCMVSPORT 3.0, were obtained from Life Technologies, Inc., P. O. Box 6009, Gaithersburg, MD 20897. All Sport vectors
5 contain an ampicillin resistance gene and may be transformed into E. coli strain DH10B, also available from Life Technologies. (See, for instance, Gruber, C. E., et al., Focus 15:59 (1993).) Vector lafmid BA (Bento Soares, Columbia University, NY) contains an ampicillin resistance gene and can be transformed into E. coli strain XL-1 Blue. Vector pCR[®]2.1, which is available from Invitrogen, 1600 Faraday Avenue,
10 Carlsbad, CA 92008, contains an ampicillin resistance gene and may be transformed into E. coli strain DH10B, available from Life Technologies. (See, for instance, Clark, J. M., Nuc. Acids Res. 16:9677-9686 (1988) and Mead, D. et al., Bio/Technology 9: (1991).) Preferably, a polynucleotide of the present invention does not comprise the phage vector sequences identified for the particular clone in Table 1, as well as the
15 corresponding plasmid vector sequences designated above.

The deposited material in the sample assigned the ATCC Deposit Number cited in Table 1 for any given cDNA clone also may contain one or more additional plasmids, each comprising a cDNA clone different from that given clone. Thus, deposits sharing the same ATCC Deposit Number contain at least a plasmid for each cDNA clone
20 identified in Table 1. Typically, each ATCC deposit sample cited in Table 1 comprises a mixture of approximately equal amounts (by weight) of about 50 plasmid DNAs, each containing a different cDNA clone; but such a deposit sample may include plasmids for more or less than 50 cDNA clones, up to about 500 cDNA clones.

Two approaches can be used to isolate a particular clone from the deposited
25 sample of plasmid DNAs cited for that clone in Table 1. First, a plasmid is directly isolated by screening the clones using a polynucleotide probe corresponding to SEQ ID NO:X.

Particularly, a specific polynucleotide with 30-40 nucleotides is synthesized using an Applied Biosystems DNA synthesizer according to the sequence reported.
30 The oligonucleotide is labeled, for instance, with ³²P-γ-ATP using T4 polynucleotide kinase and purified according to routine methods. (E.g., Maniatis et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring, NY (1982).) The plasmid mixture is transformed into a suitable host, as indicated above (such as XL-1 Blue (Stratagene)) using techniques known to those of skill in the art, such as
35 those provided by the vector supplier or in related publications or patents cited above. The transformants are plated on 1.5% agar plates (containing the appropriate selection

agent, e.g., ampicillin) to a density of about 150 transformants (colonies) per plate. These plates are screened using Nylon membranes according to routine methods for bacterial colony screening (e.g., Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd Edit., (1989), Cold Spring Harbor Laboratory Press, pages 1.93 to 1.104), or other techniques known to those of skill in the art.

Alternatively, two primers of 17-20 nucleotides derived from both ends of the SEQ ID NO:X (i.e., within the region of SEQ ID NO:X bounded by the 5' NT and the 3' NT of the clone defined in Table 1) are synthesized and used to amplify the desired cDNA using the deposited cDNA plasmid as a template. The polymerase chain reaction is carried out under routine conditions, for instance, in 25 µl of reaction mixture with 0.5 ug of the above cDNA template. A convenient reaction mixture is 1.5-5 mM MgCl₂, 0.01% (w/v) gelatin, 20 µM each of dATP, dCTP, dGTP, dTTP, 25 pmol of each primer and 0.25 Unit of Taq polymerase. Thirty five cycles of PCR (denaturation at 94°C for 1 min; annealing at 55°C for 1 min; elongation at 72°C for 1 min) are performed with a Perkin-Elmer Cetus automated thermal cycler. The amplified product is analyzed by agarose gel electrophoresis and the DNA band with expected molecular weight is excised and purified. The PCR product is verified to be the selected sequence by subcloning and sequencing the DNA product.

Several methods are available for the identification of the 5' or 3' non-coding portions of a gene which may not be present in the deposited clone. These methods include but are not limited to, filter probing, clone enrichment using specific probes, and protocols similar or identical to 5' and 3' "RACE" protocols which are well known in the art. For instance, a method similar to 5' RACE is available for generating the missing 5' end of a desired full-length transcript. (Fromont-Racine et al., *Nucleic Acids Res.* 21(7):1683-1684 (1993).)

Briefly, a specific RNA oligonucleotide is ligated to the 5' ends of a population of RNA presumably containing full-length gene RNA transcripts. A primer set containing a primer specific to the ligated RNA oligonucleotide and a primer specific to a known sequence of the gene of interest is used to PCR amplify the 5' portion of the desired full-length gene. This amplified product may then be sequenced and used to generate the full length gene.

This above method starts with total RNA isolated from the desired source, although poly-A⁺ RNA can be used. The RNA preparation can then be treated with phosphatase if necessary to eliminate 5' phosphate groups on degraded or damaged RNA which may interfere with the later RNA ligase step. The phosphatase should then be inactivated and the RNA treated with tobacco acid pyrophosphatase in order to

remove the cap structure present at the 5' ends of messenger RNAs. This reaction leaves a 5' phosphate group at the 5' end of the cap cleaved RNA which can then be ligated to an RNA oligonucleotide using T4 RNA ligase.

5 This modified RNA preparation is used as a template for first strand cDNA synthesis using a gene specific oligonucleotide. The first strand synthesis reaction is used as a template for PCR amplification of the desired 5' end using a primer specific to the ligated RNA oligonucleotide and a primer specific to the known sequence of the gene of interest. The resultant product is then sequenced and analyzed to confirm that the 5' end sequence belongs to the desired gene.

10

Example 2: Isolation of Genomic Clones Corresponding to a Polynucleotide

A human genomic P1 library (Genomic Systems, Inc.) is screened by PCR using primers selected for the cDNA sequence corresponding to SEQ ID NO:X.,
15 according to the method described in Example 1. (See also, Sambrook.)

Example 3: Tissue Distribution of Polypeptide

Tissue distribution of mRNA expression of polynucleotides of the present invention is determined using protocols for Northern blot analysis, described by,
20 among others, Sambrook et al. For example, a cDNA probe produced by the method described in Example 1 is labeled with P³² using the rediprime™ DNA labeling system (Amersham Life Science), according to manufacturer's instructions. After labeling, the probe is purified using CHROMA SPIN-100™ column (Clontech Laboratories, Inc.), according to manufacturer's protocol number PT1200-1. The purified labeled probe is
25 then used to examine various human tissues for mRNA expression.

Multiple Tissue Northern (MTN) blots containing various human tissues (H) or human immune system tissues (IM) (Clontech) are examined with the labeled probe using ExpressHyb™ hybridization solution (Clontech) according to manufacturer's protocol number PT1190-1. Following hybridization and washing, the blots are
30 mounted and exposed to film at -70°C overnight, and the films developed according to standard procedures.

Example 4: Chromosomal Mapping of the Polynucleotides

An oligonucleotide primer set is designed according to the sequence at the 5'
35 end of SEQ ID NO:X. This primer preferably spans about 100 nucleotides. This primer set is then used in a polymerase chain reaction under the following set of

conditions : 30 seconds, 95°C; 1 minute, 56°C; 1 minute, 70°C. This cycle is repeated 32 times followed by one 5 minute cycle at 70°C. Human, mouse, and hamster DNA is used as template in addition to a somatic cell hybrid panel containing individual chromosomes or chromosome fragments (Bios, Inc). The reactions is analyzed on either 8% polyacrylamide gels or 3.5 % agarose gels. Chromosome mapping is determined by the presence of an approximately 100 bp PCR fragment in the particular somatic cell hybrid.

Example 5: Bacterial Expression of a Polypeptide

10 A polynucleotide encoding a polypeptide of the present invention is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' ends of the DNA sequence, as outlined in Example 1, to synthesize insertion fragments. The primers used to amplify the cDNA insert should preferably contain restriction sites, such as BamHI and XbaI, at the 5' end of the primers in order to clone the amplified product into the expression vector. For example, BamHI and XbaI correspond to the restriction enzyme sites on the bacterial expression vector pQE-9. (Qiagen, Inc., Chatsworth, CA). This plasmid vector encodes antibiotic resistance (Amp^r), a bacterial origin of replication (ori), an IPTG-regulatable promoter/operator (P/O), a ribosome binding site (RBS), a 6-histidine tag (6-His), and restriction enzyme cloning sites.

20 The pQE-9 vector is digested with BamHI and XbaI and the amplified fragment is ligated into the pQE-9 vector maintaining the reading frame initiated at the bacterial RBS. The ligation mixture is then used to transform the E. coli strain M15/rep4 (Qiagen, Inc.) which contains multiple copies of the plasmid pREP4, which expresses the lacI repressor and also confers kanamycin resistance (Kan^r). Transformants are identified by their ability to grow on LB plates and ampicillin/kanamycin resistant colonies are selected. Plasmid DNA is isolated and confirmed by restriction analysis.

30 Clones containing the desired constructs are grown overnight (O/N) in liquid culture in LB media supplemented with both Amp (100 ug/ml) and Kan (25 ug/ml). The O/N culture is used to inoculate a large culture at a ratio of 1:100 to 1:250. The cells are grown to an optical density 600 (O.D.⁶⁰⁰) of between 0.4 and 0.6. IPTG (Isopropyl-B-D-thiogalacto pyranoside) is then added to a final concentration of 1 mM. IPTG induces by inactivating the lacI repressor, clearing the P/O leading to increased gene expression.

35 Cells are grown for an extra 3 to 4 hours. Cells are then harvested by centrifugation (20 mins at 6000Xg). The cell pellet is solubilized in the chaotropic

agent 6 Molar Guanidine HCl by stirring for 3-4 hours at 4°C. The cell debris is removed by centrifugation, and the supernatant containing the polypeptide is loaded onto a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (available from QIAGEN, Inc., *supra*). Proteins with a 6 x His tag bind to the Ni-NTA resin with high
5 affinity and can be purified in a simple one-step procedure (for details see: The QIAexpressionist (1995) QIAGEN, Inc., *supra*).

Briefly, the supernatant is loaded onto the column in 6 M guanidine-HCl, pH 8, the column is first washed with 10 volumes of 6 M guanidine-HCl, pH 8, then washed with 10 volumes of 6 M guanidine-HCl pH 6, and finally the polypeptide is eluted with
10 6 M guanidine-HCl, pH 5.

The purified protein is then renatured by dialyzing it against phosphate-buffered saline (PBS) or 50 mM Na-acetate, pH 6 buffer plus 200 mM NaCl. Alternatively, the protein can be successfully refolded while immobilized on the Ni-NTA column. The recommended conditions are as follows: renature using a linear 6M-1M urea gradient in
15 500 mM NaCl, 20% glycerol, 20 mM Tris/HCl pH 7.4, containing protease inhibitors. The renaturation should be performed over a period of 1.5 hours or more. After renaturation the proteins are eluted by the addition of 250 mM imidazole. Imidazole is removed by a final dialyzing step against PBS or 50 mM sodium acetate pH 6 buffer plus 200 mM NaCl. The purified protein is stored at 4°C or frozen at -80°C.

In addition to the above expression vector, the present invention further includes an expression vector comprising phage operator and promoter elements operatively linked to a polynucleotide of the present invention, called pHE4a. (ATCC Accession Number XXXXXX.) This vector contains: 1) a neomycinphosphotransferase gene as a selection marker, 2) an E. coli origin of replication, 3) a T5 phage promoter sequence,
25 4) two lac operator sequences, 5) a Shine-Delgarno sequence, and 6) the lactose operon repressor gene (*lacIq*). The origin of replication (*oriC*) is derived from pUC19 (LTI, Gaithersburg, MD). The promoter sequence and operator sequences are made synthetically.

DNA can be inserted into the pHEa by restricting the vector with NdeI and
30 XbaI, BamHI, XhoI, or Asp718, running the restricted product on a gel, and isolating the larger fragment (the stuffer fragment should be about 310 base pairs). The DNA insert is generated according to the PCR protocol described in Example 1, using PCR primers having restriction sites for NdeI (5' primer) and XbaI, BamHI, XhoI, or Asp718 (3' primer). The PCR insert is gel purified and restricted with compatible
35 enzymes. The insert and vector are ligated according to standard protocols.

The engineered vector could easily be substituted in the above protocol to express protein in a bacterial system.

Example 6: Purification of a Polypeptide from an Inclusion Body

- 5 The following alternative method can be used to purify a polypeptide expressed in *E. coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

 Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10°C and the cells harvested by continuous centrifugation at
10 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

15 The cells are then lysed by passing the solution through a microfluidizer (Microfluidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 xg for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

20 The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 xg centrifugation for 15 min., the pellet is discarded and the polypeptide containing supernatant is incubated at 4°C overnight to allow further GuHCl extraction.

 Following high speed centrifugation (30,000 xg) to remove insoluble particles,
25 the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4°C without mixing for 12 hours prior to further purification steps.

 To clarify the refolded polypeptide solution, a previously prepared tangential
30 filtration unit equipped with 0.16 µm membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same buffer, in a

stepwise manner. The absorbance at 280 nm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

Fractions containing the polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem
5 columns of strong anion (Poros HQ-50, Perseptive Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0
10 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant A_{280} monitoring of the effluent. Fractions containing the polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant polypeptide should exhibit greater than 95% purity after the above refolding and purification steps. No major contaminant bands should be observed from
15 Commassie blue stained 16% SDS-PAGE gel when 5 μ g of purified protein is loaded. The purified protein can also be tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

Example 7: Cloning and Expression of a Polypeptide in a Baculovirus Expression System

20

In this example, the plasmid shuttle vector pA2 is used to insert a polynucleotide into a baculovirus to express a polypeptide. This expression vector contains the strong polyhedrin promoter of the *Autographa californica* nuclear polyhedrosis virus (AcMNPV) followed by convenient restriction sites such as BamHI, Xba I and
25 Asp718. The polyadenylation site of the simian virus 40 ("SV40") is used for efficient polyadenylation. For easy selection of recombinant virus, the plasmid contains the beta-galactosidase gene from *E. coli* under control of a weak *Drosophila* promoter in the same orientation, followed by the polyadenylation signal of the polyhedrin gene. The inserted genes are flanked on both sides by viral sequences for cell-mediated
30 homologous recombination with wild-type viral DNA to generate a viable virus that express the cloned polynucleotide.

Many other baculovirus vectors can be used in place of the vector above, such as pAc373, pVL941, and pAcIM1, as one skilled in the art would readily appreciate, as long as the construct provides appropriately located signals for transcription,
35 translation, secretion and the like, including a signal peptide and an in-frame AUG as

required. Such vectors are described, for instance, in Luckow et al., *Virology* 170:31-39 (1989).

Specifically, the cDNA sequence contained in the deposited clone, including the AUG initiation codon and the naturally associated leader sequence identified in Table 1, is amplified using the PCR protocol described in Example 1. If the naturally occurring signal sequence is used to produce the secreted protein, the pA2 vector does not need a second signal peptide. Alternatively, the vector can be modified (pA2 GP) to include a baculovirus leader sequence, using the standard methods described in Summers et al., "A Manual of Methods for Baculovirus Vectors and Insect Cell Culture Procedures," Texas Agricultural Experimental Station Bulletin No. 1555 (1987).

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("GeneClean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

The plasmid is digested with the corresponding restriction enzymes and optionally, can be dephosphorylated using calf intestinal phosphatase, using routine procedures known in the art. The DNA is then isolated from a 1% agarose gel using a commercially available kit ("GeneClean" BIO 101 Inc., La Jolla, Ca.).

The fragment and the dephosphorylated plasmid are ligated together with T4 DNA ligase. *E. coli* HB101 or other suitable *E. coli* hosts such as XL-1 Blue (Stratagene Cloning Systems, La Jolla, CA) cells are transformed with the ligation mixture and spread on culture plates. Bacteria containing the plasmid are identified by digesting DNA from individual colonies and analyzing the digestion product by gel electrophoresis. The sequence of the cloned fragment is confirmed by DNA sequencing.

Five µg of a plasmid containing the polynucleotide is co-transfected with 1.0 µg of a commercially available linearized baculovirus DNA ("BaculoGold™ baculovirus DNA", Pharmingen, San Diego, CA), using the lipofection method described by Felgner et al., *Proc. Natl. Acad. Sci. USA* 84:7413-7417 (1987). One µg of BaculoGold™ virus DNA and 5 µg of the plasmid are mixed in a sterile well of a microtiter plate containing 50 µl of serum-free Grace's medium (Life Technologies Inc., Gaithersburg, MD). Afterwards, 10 µl Lipofectin plus 90 µl Grace's medium are added, mixed and incubated for 15 minutes at room temperature. Then the transfection mixture is added drop-wise to Sf9 insect cells (ATCC CRL 1711) seeded in a 35 mm tissue culture plate with 1 ml Grace's medium without serum. The plate is then incubated for 5 hours at 27° C. The transfection solution is then removed from the plate and 1 ml of Grace's insect medium supplemented with 10% fetal calf serum is added. Cultivation is then continued at 27° C for four days.

After four days the supernatant is collected and a plaque assay is performed, as described by Summers and Smith, *supra*. An agarose gel with "Blue Gal" (Life Technologies Inc., Gaithersburg) is used to allow easy identification and isolation of gal-expressing clones, which produce blue-stained plaques. (A detailed description of a "plaque assay" of this type can also be found in the user's guide for insect cell culture and baculovirology distributed by Life Technologies Inc., Gaithersburg, page 9-10.) After appropriate incubation, blue stained plaques are picked with the tip of a micropipettor (e.g., Eppendorf). The agar containing the recombinant viruses is then resuspended in a microcentrifuge tube containing 200 μ l of Grace's medium and the suspension containing the recombinant baculovirus is used to infect Sf9 cells seeded in 35 mm dishes. Four days later the supernatants of these culture dishes are harvested and then they are stored at 4° C.

To verify the expression of the polypeptide, Sf9 cells are grown in Grace's medium supplemented with 10% heat-inactivated FBS. The cells are infected with the recombinant baculovirus containing the polynucleotide at a multiplicity of infection ("MOI") of about 2. If radiolabeled proteins are desired, 6 hours later the medium is removed and is replaced with SF900 II medium minus methionine and cysteine (available from Life Technologies Inc., Rockville, MD). After 42 hours, 5 μ Ci of 35 S-methionine and 5 μ Ci 35 S-cysteine (available from Amersham) are added. The cells are further incubated for 16 hours and then are harvested by centrifugation. The proteins in the supernatant as well as the intracellular proteins are analyzed by SDS-PAGE followed by autoradiography (if radiolabeled).

Microsequencing of the amino acid sequence of the amino terminus of purified protein may be used to determine the amino terminal sequence of the produced protein.

25 **Example 8: Expression of a Polypeptide in Mammalian Cells**

The polypeptide of the present invention can be expressed in a mammalian cell. A typical mammalian expression vector contains a promoter element, which mediates the initiation of transcription of mRNA, a protein coding sequence, and signals required for the termination of transcription and polyadenylation of the transcript. Additional elements include enhancers, Kozak sequences and intervening sequences flanked by donor and acceptor sites for RNA splicing. Highly efficient transcription is achieved with the early and late promoters from SV40, the long terminal repeats (LTRs) from Retroviruses, e.g., RSV, HTLVI, HIVI and the early promoter of the cytomegalovirus (CMV). However, cellular elements can also be used (e.g., the human actin promoter).

35 Suitable expression vectors for use in practicing the present invention include, for example, vectors such as pSVL and pMSG (Pharmacia, Uppsala, Sweden),

pRSVcat (ATCC 37152), pSV2dhfr (ATCC 37146), pBC12MI (ATCC 67109), pCMVSPORT 2.0, and pCMVSPORT 3.0. Mammalian host cells that could be used include, human Hela, 293, H9 and Jurkat cells, mouse NIH3T3 and C127 cells, Cos 1, Cos 7 and CV1, quail QC1-3 cells, mouse L cells and Chinese hamster ovary (CHO) cells.

Alternatively, the polypeptide can be expressed in stable cell lines containing the polynucleotide integrated into a chromosome. The co-transfection with a selectable marker such as dhfr, gpt, neomycin, hygromycin allows the identification and isolation of the transfected cells.

The transfected gene can also be amplified to express large amounts of the encoded protein. The DHFR (dihydrofolate reductase) marker is useful in developing cell lines that carry several hundred or even several thousand copies of the gene of interest. (See, e.g., Alt, F. W., et al., J. Biol. Chem. 253:1357-1370 (1978); Hamlin, J. L. and Ma, C., Biochem. et Biophys. Acta, 1097:107-143 (1990); Page, M. J. and Sydenham, M. A., Biotechnology 9:64-68 (1991).) Another useful selection marker is the enzyme glutamine synthase (GS) (Murphy et al., Biochem J. 227:277-279 (1991); Bebbington et al., Bio/Technology 10:169-175 (1992). Using these markers, the mammalian cells are grown in selective medium and the cells with the highest resistance are selected. These cell lines contain the amplified gene(s) integrated into a chromosome. Chinese hamster ovary (CHO) and NSO cells are often used for the production of proteins.

Derivatives of the plasmid pSV2-dhfr (ATCC Accession No. 37146), the expression vectors pC4 (ATCC Accession No. 209646) and pC6 (ATCC Accession No. 209647) contain the strong promoter (LTR) of the Rous Sarcoma Virus (Cullen et al., Molecular and Cellular Biology, 438-447 (March, 1985)) plus a fragment of the CMV-enhancer (Boshart et al., Cell 41:521-530 (1985).) Multiple cloning sites, e.g., with the restriction enzyme cleavage sites BamHI, XbaI and Asp718, facilitate the cloning of the gene of interest. The vectors also contain the 3' intron, the polyadenylation and termination signal of the rat preproinsulin gene, and the mouse DHFR gene under control of the SV40 early promoter.

Specifically, the plasmid pC6, for example, is digested with appropriate restriction enzymes and then dephosphorylated using calf intestinal phosphatase by procedures known in the art. The vector is then isolated from a 1% agarose gel.

A polynucleotide of the present invention is amplified according to the protocol outlined in Example 1. If the naturally occurring signal sequence is used to produce the secreted protein, the vector does not need a second signal peptide. Alternatively, if the

naturally occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 96/34891.)

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("GeneClean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

The amplified fragment is then digested with the same restriction enzyme and purified on a 1% agarose gel. The isolated fragment and the dephosphorylated vector are then ligated with T4 DNA ligase. *E. coli* HB101 or XL-1 Blue cells are then transformed and bacteria are identified that contain the fragment inserted into plasmid pC6 using, for instance, restriction enzyme analysis.

Chinese hamster ovary cells lacking an active DHFR gene is used for transfection. Five μ g of the expression plasmid pC6 is cotransfected with 0.5 μ g of the plasmid pSVneo using lipofectin (Felgner et al., *supra*). The plasmid pSV2-neo contains a dominant selectable marker, the *neo* gene from Tn5 encoding an enzyme that confers resistance to a group of antibiotics including G418. The cells are seeded in alpha minus MEM supplemented with 1 mg/ml G418. After 2 days, the cells are trypsinized and seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus MEM supplemented with 10, 25, or 50 ng/ml of methotrexate plus 1 mg/ml G418. After about 10-14 days single clones are trypsinized and then seeded in 6-well petri dishes or 10 ml flasks using different concentrations of methotrexate (50 nM, 100 nM, 200 nM, 400 nM, 800 nM). Clones growing at the highest concentrations of methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1 μ M, 2 μ M, 5 μ M, 10 mM, 20 mM). The same procedure is repeated until clones are obtained which grow at a concentration of 100 - 200 μ M. Expression of the desired gene product is analyzed, for instance, by SDS-PAGE and Western blot or by reversed phase HPLC analysis.

Example 9: Protein Fusions

The polypeptides of the present invention are preferably fused to other proteins. These fusion proteins can be used for a variety of applications. For example, fusion of the present polypeptides to His-tag, HA-tag, protein A, IgG domains, and maltose binding protein facilitates purification. (See Example 5; see also EP A 394,827; Traunecker, et al., Nature 331:84-86 (1988).) Similarly, fusion to IgG-1, IgG-3, and albumin increases the halflife time in vivo. Nuclear localization signals fused to the polypeptides of the present invention can target the protein to a specific subcellular localization, while covalent heterodimer or homodimers can increase or decrease the activity of a fusion protein. Fusion proteins can also create chimeric molecules having

more than one function. Finally, fusion proteins can increase solubility and/or stability of the fused protein compared to the non-fused protein. All of the types of fusion proteins described above can be made by modifying the following protocol, which outlines the fusion of a polypeptide to an IgG molecule, or the protocol described in

5 Example 5.

Briefly, the human Fc portion of the IgG molecule can be PCR amplified, using primers that span the 5' and 3' ends of the sequence described below. These primers also should have convenient restriction enzyme sites that will facilitate cloning into an expression vector, preferably a mammalian expression vector.

10 For example, if pC4 (Accession No.209646) is used, the human Fc portion can be ligated into the BamHI cloning site. Note that the 3' BamHI site should be destroyed. Next, the vector containing the human Fc portion is re-restricted with BamHI, linearizing the vector, and a polynucleotide of the present invention, isolated by the PCR protocol described in Example 1, is ligated into this BamHI site. Note that
15 the polynucleotide is cloned without a stop codon, otherwise a fusion protein will not be produced.

If the naturally occurring signal sequence is used to produce the secreted protein, pC4 does not need a second signal peptide. Alternatively, if the naturally occurring signal sequence is not used, the vector can be modified to include a
20 heterologous signal sequence. (See, e.g., WO 96/34891.)

Human IgG Fc region:

```
GGGATCCGGAGCCCAAATCTTCTGACAAAACCTCACACATGCCCACCGTGCC
CAGCACCTGAATTCGAGGGTGCACCGTCAGTCTTCCTCTTCCCCCAAACCC
25 CAAGGACACCCCTCATGATCTCCCGGACTCCTGAGGTACATGCGTGGTGGT
GGACGTAAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACG
GCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAAC
AGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAACCCCC
30 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGT
GTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCT
GACCTGCCTGGTCAAAGGCTTCTATCCAAGCGACATCGCCGTGGAGTGGGA
GAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTGG
ACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCA
35 GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGC
ACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAGTGC
GACGGCCGCGACTCTAGAGGAT (SEQ ID NO:1)
```

Example 10: Production of an Antibody from a Polypeptide

The antibodies of the present invention can be prepared by a variety of methods. (See, Current Protocols, Chapter 2.) For example, cells expressing a polypeptide of the present invention is administered to an animal to induce the production of sera containing polyclonal antibodies. In a preferred method, a preparation of the secreted protein is prepared and purified to render it substantially free of natural contaminants. Such a preparation is then introduced into an animal in order to produce polyclonal antisera of greater specific activity.

In the most preferred method, the antibodies of the present invention are monoclonal antibodies (or protein binding fragments thereof). Such monoclonal antibodies can be prepared using hybridoma technology. (Köhler et al., Nature 256:495 (1975); Köhler et al., Eur. J. Immunol. 6:511 (1976); Köhler et al., Eur. J. Immunol. 6:292 (1976); Hammerling et al., in: Monoclonal Antibodies and T-Cell Hybridomas, Elsevier, N.Y., pp. 563-681 (1981).) In general, such procedures involve immunizing an animal (preferably a mouse) with polypeptide or, more preferably, with a secreted polypeptide-expressing cell. Such cells may be cultured in any suitable tissue culture medium; however, it is preferable to culture cells in Earle's modified Eagle's medium supplemented with 10% fetal bovine serum (inactivated at about 56°C), and supplemented with about 10 g/l of nonessential amino acids, about 1,000 U/ml of penicillin, and about 100 µg/ml of streptomycin.

The splenocytes of such mice are extracted and fused with a suitable myeloma cell line. Any suitable myeloma cell line may be employed in accordance with the present invention; however, it is preferable to employ the parent myeloma cell line (SP2O), available from the ATCC. After fusion, the resulting hybridoma cells are selectively maintained in HAT medium, and then cloned by limiting dilution as described by Wands et al. (Gastroenterology 80:225-232 (1981).) The hybridoma cells obtained through such a selection are then assayed to identify clones which secrete antibodies capable of binding the polypeptide.

Alternatively, additional antibodies capable of binding to the polypeptide can be produced in a two-step procedure using anti-idiotypic antibodies. Such a method makes use of the fact that antibodies are themselves antigens, and therefore, it is possible to obtain an antibody which binds to a second antibody. In accordance with this method, protein specific antibodies are used to immunize an animal, preferably a mouse. The splenocytes of such an animal are then used to produce hybridoma cells, and the hybridoma cells are screened to identify clones which produce an antibody

whose ability to bind to the protein-specific antibody can be blocked by the polypeptide. Such antibodies comprise anti-idiotypic antibodies to the protein-specific antibody and can be used to immunize an animal to induce formation of further protein-specific antibodies.

5 It will be appreciated that Fab and F(ab')₂ and other fragments of the antibodies of the present invention may be used according to the methods disclosed herein. Such fragments are typically produced by proteolytic cleavage, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')₂ fragments). Alternatively, secreted protein-binding fragments can be produced through the application of
10 recombinant DNA technology or through synthetic chemistry.

For in vivo use of antibodies in humans, it may be preferable to use "humanized" chimeric monoclonal antibodies. Such antibodies can be produced using genetic constructs derived from hybridoma cells producing the monoclonal antibodies described above. Methods for producing chimeric antibodies are known in the art.
15 (See, for review, Morrison, Science 229:1202 (1985); Oi et al., BioTechniques 4:214 (1986); Cabilly et al., U.S. Patent No. 4,816,567; Taniguchi et al., EP 171496; Morrison et al., EP 173494; Neuberger et al., WO 8601533; Robinson et al., WO 8702671; Boulianne et al., Nature 312:643 (1984); Neuberger et al., Nature 314:268 (1985).)

20

Example 11: Production Of Secreted Protein For High-Throughput Screening Assays

The following protocol produces a supernatant containing a polypeptide to be tested. This supernatant can then be used in the Screening Assays described in
25 Examples 13-20.

First, dilute Poly-D-Lysine (644 587 Boehringer-Mannheim) stock solution (1mg/ml in PBS) 1:20 in PBS (w/o calcium or magnesium 17-516F Biowhittaker) for a working solution of 50ug/ml. Add 200 ul of this solution to each well (24 well plates) and incubate at RT for 20 minutes. Be sure to distribute the solution over each well
30 (note: a 12-channel pipetter may be used with tips on every other channel). Aspirate off the Poly-D-Lysine solution and rinse with 1ml PBS (Phosphate Buffered Saline). The PBS should remain in the well until just prior to plating the cells and plates may be poly-lysine coated in advance for up to two weeks.

Plate 293T cells (do not carry cells past P+20) at 2×10^5 cells/well in .5ml
35 DMEM(Dulbecco's Modified Eagle Medium)(with 4.5 G/L glucose and L-glutamine (12-604F Biowhittaker))/10% heat inactivated FBS(14-503F Biowhittaker)/1x Penstrep(17-602E Biowhittaker). Let the cells grow overnight.

The next day, mix together in a sterile solution basin: 300 ul Lipofectamine (18324-012 Gibco/BRL) and 5ml Optimem I (31985070 Gibco/BRL)/96-well plate. With a small volume multi-channel pipetter, aliquot approximately 2ug of an expression vector containing a polynucleotide insert, produced by the methods described in Examples 8 or 9, into an appropriately labeled 96-well round bottom plate. With a multi-channel pipetter, add 50ul of the Lipofectamine/Optimem I mixture to each well. Pipette up and down gently to mix. Incubate at RT 15-45 minutes. After about 20 minutes, use a multi-channel pipetter to add 150ul Optimem I to each well. As a control, one plate of vector DNA lacking an insert should be transfected with each set of transfections.

Preferably, the transfection should be performed by tag-teaming the following tasks. By tag-teaming, hands on time is cut in half, and the cells do not spend too much time on PBS. First, person A aspirates off the media from four 24-well plates of cells, and then person B rinses each well with .5-1ml PBS. Person A then aspirates off PBS rinse, and person B, using a 12-channel pipetter with tips on every other channel, adds the 200ul of DNA/Lipofectamine/Optimem I complex to the odd wells first, then to the even wells, to each row on the 24-well plates. Incubate at 37°C for 6 hours.

While cells are incubating, prepare appropriate media, either 1%BSA in DMEM with 1x penstrep, or CHO-5 media (see below) with 2mm glutamine and 1x penstrep. (BSA (81-068-3 Bayer) 100gm dissolved in 1L DMEM for a 10% BSA stock solution). Filter the media and collect 50 ul for endotoxin assay in 15ml polystyrene conical.

The transfection reaction is terminated, preferably by tag-teaming, at the end of the incubation period. Person A aspirates off the transfection media, while person B adds 1.5ml appropriate media to each well. Incubate at 37°C for 45 or 72 hours depending on the media used: 1%BSA for 45 hours or CHO-5 for 72 hours.

On day four, using a 300ul multichannel pipetter, aliquot 600ul in one 1ml deep well plate and the remaining supernatant into a 2ml deep well. The supernatants from each well can then be used in the assays described in Examples 13-20.

It is specifically understood that when activity is obtained in any of the assays described below using a supernatant, the activity originates from either the polypeptide directly (e.g., as a secreted protein) or by the polypeptide inducing expression of other proteins, which are then secreted into the supernatant. Thus, the invention further provides a method of identifying the protein in the supernatant characterized by an activity in a particular assay.

HGS-CHO-5 medium formulation:**Inorganic Salts**

CaCl ₂ (anhyd)	116.6 mg/L
CuSO ₄ ·5H ₂ O	0.00130
Fe(NO ₃) ₃ ·9H ₂ O	0.050
FeSO ₄ ·7H ₂ O	0.417
KCl	311.80
MgCl ₂	28.64
MgSO ₄	48.84
NaCl	6995.50
NaHCO ₃	2400.0
NaH ₂ PO ₄ ·H ₂ O	62.50
Na ₂ HPO ₄	71.02
ZnSO ₄ ·7H ₂ O	.4320

5 Lipids

Arachidonic Acid	.002 mg/L
Cholesterol	1.022
DL-alpha-Tocopherol-Acetate	.070
Linoleic Acid	0.0520
Linolenic Acid	0.010
Myristic Acid	0.010
Oleic Acid	0.010
Palmitic Acid	0.010
Palmitic Acid	0.010
Pluronic F-68	100
Stearic Acid	0.010
Tween 80	2.20

Carbon Source

D-Glucose	4551 mg/L
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Amino Acids

L-Alanine	130.85 mg/ml
L-Arginine-HCL	147.50
L-Asparagine-H ₂ O	7.50
L-Aspartic Acid	6.65
L-Cystine-2HCL-H ₂ O	29.56
L-Cystine-2HCL	31.29
L-Glutamic Acid	7.35
L-Glutamine	365.0
Glycine	18.75
L-Histidine-HCL	52.48

H ₂ O	
L-Isoleucine	106.97
L-Leucine	111.45
L-Lysine HCL	163.75
L-Methionine	32.34
L-Phenylalanine	68.48
L-Proline	40.0
L-Serine	26.25
L-Threonine	101.05
L-Tryptophan	19.22
L-Tyrosine-2Na-2H ₂ O	91.79
L-Valine	99.65

Vitamins

Biotin	0.0035 mg/L
D-Ca Pantothenate	3.24
Choline Chloride	11.78
Folic Acid	4.65
i-Inositol	15.60
Niacinamide	3.02
Pyridoxal HCL	3.00
Pyridoxine HCL	0.031
Riboflavin	0.319
Thiamine HCL	3.17
Thymidine	0.365
Vitamin B ₁₂	0.680

Other Components

HEPES Buffer	25 mM
Na Hypoxanthine	2.39 mg/L
Lipoic Acid	0.105
Sodium Putrescine-2HCL	0.081
Sodium Pyruvate	55.0
Sodium Selenite	0.0067
Ethanolamine	20uM
Ferric Citrate	0.122
Methyl-B-Cyclodextrin complexed with Linoleic Acid	41.70
Methyl-B-Cyclodextrin complexed with Oleic Acid	33.33
Methyl-B-Cyclodextrin complexed with Retinal Acetate	10

5

Adjust osmolarity to 327 mOsm

Example 12: Construction of GAS Reporter Construct

One signal transduction pathway involved in the differentiation and proliferation of cells is called the Jaks-STATs pathway. Activated proteins in the Jaks-STATs pathway bind to gamma activation site "GAS" elements or interferon-sensitive responsive element ("ISRE"), located in the promoter of many genes. The binding of a protein to these elements alter the expression of the associated gene.

GAS and ISRE elements are recognized by a class of transcription factors called Signal Transducers and Activators of Transcription, or "STATs." There are six members of the STATs family. Stat1 and Stat3 are present in many cell types, as is Stat2 (as response to IFN-alpha is widespread). Stat4 is more restricted and is not in many cell types though it has been found in T helper class I, cells after treatment with IL-12. Stat5 was originally called mammary growth factor, but has been found at higher concentrations in other cells including myeloid cells. It can be activated in tissue culture cells by many cytokines.

The STATs are activated to translocate from the cytoplasm to the nucleus upon tyrosine phosphorylation by a set of kinases known as the Janus Kinase ("Jaks") family. Jaks represent a distinct family of soluble tyrosine kinases and include Tyk2, Jak1, Jak2, and Jak3. These kinases display significant sequence similarity and are generally catalytically inactive in resting cells.

The Jaks are activated by a wide range of receptors summarized in the Table below. (Adapted from review by Schidler and Darnell, Ann. Rev. Biochem. 64:621-51 (1995).) A cytokine receptor family, capable of activating Jaks, is divided into two groups: (a) Class 1 includes receptors for IL-2, IL-3, IL-4, IL-6, IL-7, IL-9, IL-11, IL-12, IL-15, Epo, PRL, GH, G-CSF, GM-CSF, LIF, CNTF, and thrombopoietin; and (b) Class 2 includes IFN-a, IFN-g, and IL-10. The Class 1 receptors share a conserved cysteine motif (a set of four conserved cysteines and one tryptophan) and a WSXWS motif (a membrane proximal region encoding Trp-Ser-Xxx-Trp-Ser (SEQ ID NO:2)).

Thus, on binding of a ligand to a receptor, Jaks are activated, which in turn activate STATs, which then translocate and bind to GAS elements. This entire process is encompassed in the Jaks-STATs signal transduction pathway.

Therefore, activation of the Jaks-STATs pathway, reflected by the binding of the GAS or the ISRE element, can be used to indicate proteins involved in the proliferation and differentiation of cells. For example, growth factors and cytokines are known to activate the Jaks-STATs pathway. (See Table below.) Thus, by using GAS elements linked to reporter molecules, activators of the Jaks-STATs pathway can be identified.

	<u>ISRE</u> <u>Ligand</u>	<u>JAKs</u>				<u>STATs</u>	<u>GAS(elements) or</u>
		<u>tyk2</u>	<u>Jak1</u>	<u>Jak2</u>	<u>Jak3</u>		
5	<u>IFN family</u>						
	IFN-a/B	+	+	-	-	1,2,3	ISRE
	IFN-g		+	+	-	1	GAS
	(IRF1>Lys6>IFP)						
	IL-10	+	?	?	-	1,3	
10	<u>gp130 family</u>						
	IL-6 (Pleiotrohic)	+	+	+	?	1,3	GAS
	(IRF1>Lys6>IFP)						
	IL-11(Pleiotrohic)	?	+	?	?	1,3	
15	OnM(Pleiotrohic)	?	+	+	?	1,3	
	LIF(Pleiotrohic)	?	+	+	?	1,3	
	CNTF(Pleiotrohic)	-/+	+	+	?	1,3	
	G-CSF(Pleiotrohic)	?	+	?	?	1,3	
	IL-12(Pleiotrohic)	+	-	+	+	1,3	
20	<u>g-C family</u>						
	IL-2 (lymphocytes)	-	+	-	+	1,3,5	GAS
	IL-4 (lymph/myeloid)	-	+	-	+	6	GAS (IRF1 = IFP
	>>Ly6)(IgH)						
25	IL-7 (lymphocytes)	-	+	-	+	5	GAS
	IL-9 (lymphocytes)	-	+	-	+	5	GAS
	IL-13 (lymphocyte)	-	+	?	?	6	GAS
	IL-15	?	+	?	+	5	GAS
30	<u>gp140 family</u>						
	IL-3 (myeloid)	-	-	+	-	5	GAS
	(IRF1>IFP>>Ly6)						
	IL-5 (myeloid)	-	-	+	-	5	GAS
	GM-CSF (myeloid)	-	-	+	-	5	GAS
35	<u>Growth hormone family</u>						
	GH	?	-	+	-	5	
	PRL	?	+/-	+	-	1,3,5	
	EPO	?	-	+	-	5	
40	CAS>IRF1=IFP>>Ly6)						GAS(B-
	<u>Receptor Tyrosine Kinases</u>						
	EGF	?	+	+	-	1,3	GAS (IRF1)
45	PDGF	?	+	+	-	1,3	
	CSF-1	?	+	+	-	1,3	GAS (not IRF1)

To construct a synthetic GAS containing promoter element, which is used in the Biological Assays described in Examples 13-14, a PCR based strategy is employed to generate a GAS-SV40 promoter sequence. The 5' primer contains four tandem copies of the GAS binding site found in the IRF1 promoter and previously demonstrated to
5 bind STATs upon induction with a range of cytokines (Rothman et al., Immunity 1:457-468 (1994).), although other GAS or ISRE elements can be used instead. The 5' primer also contains 18bp of sequence complementary to the SV40 early promoter sequence and is flanked with an XhoI site. The sequence of the 5' primer is:

5':GCGCCTCGAGATTTCCTCCGAAATCTAGATTTCCTCCGAAATGATTTCCTCCG
10 AAATGATTTCCTCCGAAATATCTGCCATCTCAATTAG:3' (SEQ ID NO:3)

The downstream primer is complementary to the SV40 promoter and is flanked with a Hind III site: 5':GCGGCAAGCTTTTGTCAAAGCCTAGGC:3' (SEQ ID NO:4)

PCR amplification is performed using the SV40 promoter template present in
15 the B-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested with XhoI/Hind III and subcloned into BLSK2-. (Stratagene.) Sequencing with forward and reverse primers confirms that the insert contains the following sequence:

5':CTCGAGATTTCCTCCGAAATCTAGATTTCCTCCGAAATGATTTCCTCCGAAATG
20 ATTTTCCTCCGAAATATCTGCCATCTCAATTAGTCAGCAACCATAGTCCCGCCC
CTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGC
CCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCTCGGC
CTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTT
TGCAAAAAGCTT:3' (SEQ ID NO:5)

25

With this GAS promoter element linked to the SV40 promoter, a GAS:SEAP2 reporter construct is next engineered. Here, the reporter molecule is a secreted alkaline phosphatase, or "SEAP." Clearly, however, any reporter molecule can be instead of SEAP, in this or in any of the other Examples. Well known reporter molecules that can
30 be used instead of SEAP include chloramphenicol acetyltransferase (CAT), luciferase, alkaline phosphatase, B-galactosidase, green fluorescent protein (GFP), or any protein detectable by an antibody.

The above sequence confirmed synthetic GAS-SV40 promoter element is subcloned into the pSEAP-Promoter vector obtained from Clontech using HindIII and
35 XhoI, effectively replacing the SV40 promoter with the amplified GAS:SV40 promoter element, to create the GAS-SEAP vector. However, this vector does not contain a

neomycin resistance gene, and therefore, is not preferred for mammalian expression systems.

Thus, in order to generate mammalian stable cell lines expressing the GAS-SEAP reporter, the GAS-SEAP cassette is removed from the GAS-SEAP vector using
5 SalI and NotI, and inserted into a backbone vector containing the neomycin resistance gene, such as pGFP-1 (Clontech), using these restriction sites in the multiple cloning site, to create the GAS-SEAP/Neo vector. Once this vector is transfected into mammalian cells, this vector can then be used as a reporter molecule for GAS binding as described in Examples 13-14.

10 Other constructs can be made using the above description and replacing GAS with a different promoter sequence. For example, construction of reporter molecules containing NFK-B and EGR promoter sequences are described in Examples 15 and 16. However, many other promoters can be substituted using the protocols described in these Examples. For instance, SRE, IL-2, NFAT, or Osteocalcin promoters can be
15 substituted, alone or in combination (e.g., GAS/NF-KB/EGR, GAS/NF-KB, IL-2/NFAT, or NF-KB/GAS). Similarly, other cell lines can be used to test reporter construct activity, such as HELA (epithelial), HUVEC (endothelial), Reh (B-cell), Saos-2 (osteoblast), HUVAC (aortic), or Cardiomyocyte.

20 **Example 13: High-Throughput Screening Assay for T-cell Activity.**

The following protocol is used to assess T-cell activity by identifying factors, such as growth factors and cytokines, that may proliferate or differentiate T-cells. T-cell activity is assessed using the GAS/SEAP/Neo construct produced in Example 12. Thus, factors that increase SEAP activity indicate the ability to activate the Jaks-STATS
25 signal transduction pathway. The T-cell used in this assay is Jurkat T-cells (ATCC Accession No. TIB-152), although Molt-3 cells (ATCC Accession No. CRL-1552) and Molt-4 cells (ATCC Accession No. CRL-1582) cells can also be used.

Jurkat T-cells are lymphoblastic CD4+ Th1 helper cells. In order to generate stable cell lines, approximately 2 million Jurkat cells are transfected with the GAS-
30 SEAP/neo vector using DMRIE-C (Life Technologies)(transfection procedure described below). The transfected cells are seeded to a density of approximately 20,000 cells per well and transfectants resistant to 1 mg/ml gentamicin selected. Resistant colonies are expanded and then tested for their response to increasing concentrations of interferon gamma. The dose response of a selected clone is demonstrated.

35 Specifically, the following protocol will yield sufficient cells for 75 wells containing 200 ul of cells. Thus, it is either scaled up, or performed in multiple to generate sufficient cells for multiple 96 well plates. Jurkat cells are maintained in RPMI

+ 10% serum with 1% Pen-Strep. Combine 2.5 mls of OPTI-MEM (Life Technologies) with 10 ug of plasmid DNA in a T25 flask. Add 2.5 ml OPTI-MEM containing 50 ul of DMRIE-C and incubate at room temperature for 15-45 mins.

5 During the incubation period, count cell concentration, spin down the required number of cells (10^7 per transfection), and resuspend in OPTI-MEM to a final concentration of 10^7 cells/ml. Then add 1ml of 1×10^7 cells in OPTI-MEM to T25 flask and incubate at 37°C for 6 hrs. After the incubation, add 10 ml of RPMI + 15% serum.

10 The Jurkat:GAS-SEAP stable reporter lines are maintained in RPMI + 10% serum, 1 mg/ml Gentamicin, and 1% Pen-Strep. These cells are treated with supernatants containing a polypeptide as produced by the protocol described in Example 11.

On the day of treatment with the supernatant, the cells should be washed and resuspended in fresh RPMI + 10% serum to a density of 500,000 cells per ml. The exact number of cells required will depend on the number of supernatants being screened. For one 96 well plate, approximately 10 million cells (for 10 plates, 100 million cells) are required.

Transfer the cells to a triangular reservoir boat, in order to dispense the cells into a 96 well dish, using a 12 channel pipette. Using a 12 channel pipette, transfer 200 ul of cells into each well (therefore adding 100,000 cells per well).

20 After all the plates have been seeded, 50 ul of the supernatants are transferred directly from the 96 well plate containing the supernatants into each well using a 12 channel pipette. In addition, a dose of exogenous interferon gamma (0.1, 1.0, 10 ng) is added to wells H9, H10, and H11 to serve as additional positive controls for the assay.

25 The 96 well dishes containing Jurkat cells treated with supernatants are placed in an incubator for 48 hrs (note: this time is variable between 48-72 hrs). 35 ul samples from each well are then transferred to an opaque 96 well plate using a 12 channel pipette. The opaque plates should be covered (using sellophane covers) and stored at -20°C until SEAP assays are performed according to Example 17. The plates containing the remaining treated cells are placed at 4°C and serve as a source of material for repeating the assay on a specific well if desired.

30 As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate Jurkat T cells. Over 30 fold induction is typically observed in the positive control wells.

Example 14: High-Throughput Screening Assay Identifying Myeloid Activity

The following protocol is used to assess myeloid activity by identifying factors, such as growth factors and cytokines, that may proliferate or differentiate myeloid cells.

- 5 Myeloid cell activity is assessed using the GAS/SEAP/Neo construct produced in Example 12. Thus, factors that increase SEAP activity indicate the ability to activate the Jaks-STATS signal transduction pathway. The myeloid cell used in this assay is U937, a pre-monocyte cell line, although TF-1, HL60, or KG1 can be used.

- 10 To transiently transfect U937 cells with the GAS/SEAP/Neo construct produced in Example 12, a DEAE-Dextran method (Kharbanda et. al., 1994, Cell Growth & Differentiation, 5:259-265) is used. First, harvest 2×10^7 U937 cells and wash with PBS. The U937 cells are usually grown in RPMI 1640 medium containing 10% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 mg/ml streptomycin.

- 15 Next, suspend the cells in 1 ml of 20 mM Tris-HCl (pH 7.4) buffer containing 0.5 mg/ml DEAE-Dextran, 8 ug GAS-SEAP2 plasmid DNA, 140 mM NaCl, 5 mM KCl, 375 uM $\text{Na}_2\text{HPO}_4 \cdot 7\text{H}_2\text{O}$, 1 mM MgCl_2 , and 675 uM CaCl_2 . Incubate at 37°C for 45 min.

- 20 Wash the cells with RPMI 1640 medium containing 10% FBS and then resuspend in 10 ml complete medium and incubate at 37°C for 36 hr.

The GAS-SEAP/U937 stable cells are obtained by growing the cells in 400 ug/ml G418. The G418-free medium is used for routine growth but every one to two months, the cells should be re-grown in 400 ug/ml G418 for couple of passages.

- 25 These cells are tested by harvesting 1×10^8 cells (this is enough for ten 96-well plates assay) and wash with PBS. Suspend the cells in 200 ml above described growth medium, with a final density of 5×10^5 cells/ml. Plate 200 ul cells per well in the 96-well plate (or 1×10^5 cells/well).

- 30 Add 50 ul of the supernatant prepared by the protocol described in Example 11. Incubate at 37°C for 48 to 72 hr. As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate U937 cells. Over 30 fold induction is typically observed in the positive control wells. SEAP assay the supernatant according to the protocol described in Example 17.

Example 15: High-Throughput Screening Assay Identifying Neuronal Activity.

When cells undergo differentiation and proliferation, a group of genes are activated through many different signal transduction pathways. One of these genes, EGR1 (early growth response gene 1), is induced in various tissues and cell types upon activation. The promoter of EGR1 is responsible for such induction. Using the EGR1 promoter linked to reporter molecules, activation of cells can be assessed.

Particularly, the following protocol is used to assess neuronal activity in PC12 cell lines. PC12 cells (rat pheochromocytoma cells) are known to proliferate and/or differentiate by activation with a number of mitogens, such as TPA (tetradecanoyl phorbol acetate), NGF (nerve growth factor), and EGF (epidermal growth factor). The EGR1 gene expression is activated during this treatment. Thus, by stably transfecting PC12 cells with a construct containing an EGR promoter linked to SEAP reporter, activation of PC12 cells can be assessed.

The EGR/SEAP reporter construct can be assembled by the following protocol. The EGR-1 promoter sequence (-633 to +1)(Sakamoto K et al., Oncogene 6:867-871 (1991)) can be PCR amplified from human genomic DNA using the following primers:

5' GCGCTCGAGGGATGACAGCGATAGAACCCCGG -3' (SEQ ID NO:6)
5' GCGAAGCTTCGCGACTCCCCGGATCCGCCTC-3' (SEQ ID NO:7)

Using the GAS:SEAP/Neo vector produced in Example 12, EGR1 amplified product can then be inserted into this vector. Linearize the GAS:SEAP/Neo vector using restriction enzymes XhoI/HindIII, removing the GAS/SV40 stuffer. Restrict the EGR1 amplified product with these same enzymes. Ligate the vector and the EGR1 promoter.

To prepare 96 well-plates for cell culture, two mls of a coating solution (1:30 dilution of collagen type I (Upstate Biotech Inc. Cat#08-115) in 30% ethanol (filter sterilized)) is added per one 10 cm plate or 50 ml per well of the 96-well plate, and allowed to air dry for 2 hr.

PC12 cells are routinely grown in RPMI-1640 medium (Bio Whittaker) containing 10% horse serum (JRH BIOSCIENCES, Cat. # 12449-78P), 5% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 ug/ml streptomycin on a precoated 10 cm tissue culture dish. One to four split is done every three to four days. Cells are removed from the plates by scraping and resuspended with pipetting up and down for more than 15 times.

Transfect the EGR/SEAP/Neo construct into PC12 using the Lipofectamine protocol described in Example 11. EGR-SEAP/PC12 stable cells are obtained by growing the cells in 300 ug/ml G418. The G418-free medium is used for routine growth but every one to two months, the cells should be re-grown in 300 ug/ml G418 for couple of passages.

To assay for neuronal activity, a 10 cm plate with cells around 70 to 80% confluent is screened by removing the old medium. Wash the cells once with PBS (Phosphate buffered saline). Then starve the cells in low serum medium (RPMI-1640 containing 1% horse serum and 0.5% FBS with antibiotics) overnight.

The next morning, remove the medium and wash the cells with PBS. Scrape off the cells from the plate, suspend the cells well in 2 ml low serum medium. Count the cell number and add more low serum medium to reach final cell density as 5×10^5 cells/ml.

Add 200 ul of the cell suspension to each well of 96-well plate (equivalent to 1×10^5 cells/well). Add 50 ul supernatant produced by Example 11, 37°C for 48 to 72 hr. As a positive control, a growth factor known to activate PC12 cells through EGR can be used, such as 50 ng/ul of Neuronal Growth Factor (NGF). Over fifty-fold induction of SEAP is typically seen in the positive control wells. SEAP assay the supernatant according to Example 17.

Example 16: High-Throughput Screening Assay for T-cell Activity

NF- κ B (Nuclear Factor κ B) is a transcription factor activated by a wide variety of agents including the inflammatory cytokines IL-1 and TNF, CD30 and CD40, lymphotoxin-alpha and lymphotoxin-beta, by exposure to LPS or thrombin, and by expression of certain viral gene products. As a transcription factor, NF- κ B regulates the expression of genes involved in immune cell activation, control of apoptosis (NF- κ B appears to shield cells from apoptosis), B and T-cell development, anti-viral and antimicrobial responses, and multiple stress responses.

In non-stimulated conditions, NF- κ B is retained in the cytoplasm with I- κ B (Inhibitor κ B). However, upon stimulation, I- κ B is phosphorylated and degraded, causing NF- κ B to shuttle to the nucleus, thereby activating transcription of target genes. Target genes activated by NF- κ B include IL-2, IL-6, GM-CSF, ICAM-1 and class 1 MHC.

Due to its central role and ability to respond to a range of stimuli, reporter constructs utilizing the NF- κ B promoter element are used to screen the supernatants produced in Example 11. Activators or inhibitors of NF- κ B would be useful in treating diseases. For example, inhibitors of NF- κ B could be used to treat those diseases
 5 related to the acute or chronic activation of NF- κ B, such as rheumatoid arthritis.

To construct a vector containing the NF- κ B promoter element, a PCR based strategy is employed. The upstream primer contains four tandem copies of the NF- κ B binding site (GGGGACTTTCCC) (SEQ ID NO:8), 18 bp of sequence complementary to the 5' end of the SV40 early promoter sequence, and is flanked with an XhoI site:
 10 5':GCGGCCTCGAGGGGACTTTCCCGGGGACTTTCCGGGGACTTTCCGGGAC
 TTTCCATCCTGCCATCTCAATTAG:3' (SEQ ID NO:9)

The downstream primer is complementary to the 3' end of the SV40 promoter and is flanked with a Hind III site:

5':GCGGCAAGCTTTTTGCAAAGCCTAGGC:3' (SEQ ID NO:4)
 15 PCR amplification is performed using the SV40 promoter template present in the pB-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested with XhoI and Hind III and subcloned into BLSK2-. (Stratagene)
 Sequencing with the T7 and T3 primers confirms the insert contains the following sequence:
 20 5':CTCGAGGGGACTTTCCCGGGGACTTTCCGGGGACTTTCCGGGACTTTCC
 ATCTGCCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCA
 TCCCGCCCCTAACTCCGCCCCAGTTCCGCCCATTTCTCCGCCCCATGGCTGACT
 AATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTC
 CAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAAAGCTT:
 25 3' (SEQ ID NO:10)

Next, replace the SV40 minimal promoter element present in the pSEAP2- promoter plasmid (Clontech) with this NF- κ B/SV40 fragment using XhoI and HindIII. However, this vector does not contain a neomycin resistance gene, and therefore, is not
 30 preferred for mammalian expression systems.

In order to generate stable mammalian cell lines, the NF- κ B/SV40/SEAP cassette is removed from the above NF- κ B/SEAP vector using restriction enzymes SalI and NotI, and inserted into a vector containing neomycin resistance. Particularly, the

NF- κ B/SV40/SEAP cassette was inserted into pGFP-1 (Clontech), replacing the GFP gene, after restricting pGFP-1 with SalI and NotI.

- Once NF- κ B/SV40/SEAP/Neo vector is created, stable Jurkat T-cells are created and maintained according to the protocol described in Example 13. Similarly, the method for assaying supernatants with these stable Jurkat T-cells is also described in Example 13. As a positive control, exogenous TNF alpha (0.1, 1, 10 ng) is added to wells H9, H10, and H11, with a 5-10 fold activation typically observed.

Example 17: Assay for SEAP Activity

- As a reporter molecule for the assays described in Examples 13-16, SEAP activity is assayed using the Tropix Phospho-light Kit (Cat. BP-400) according to the following general procedure. The Tropix Phospho-light Kit supplies the Dilution, Assay, and Reaction Buffers used below.

- Prime a dispenser with the 2.5x Dilution Buffer and dispense 15 μ l of 2.5x dilution buffer into Optiplates containing 35 μ l of a supernatant. Seal the plates with a plastic sealer and incubate at 65°C for 30 min. Separate the Optiplates to avoid uneven heating.

- Cool the samples to room temperature for 15 minutes. Empty the dispenser and prime with the Assay Buffer. Add 50 μ l Assay Buffer and incubate at room temperature 5 min. Empty the dispenser and prime with the Reaction Buffer (see the table below). Add 50 μ l Reaction Buffer and incubate at room temperature for 20 minutes. Since the intensity of the chemiluminescent signal is time dependent, and it takes about 10 minutes to read 5 plates on luminometer, one should treat 5 plates at each time and start the second set 10 minutes later.

- Read the relative light unit in the luminometer. Set H12 as blank, and print the results. An increase in chemiluminescence indicates reporter activity.

Reaction Buffer Formulation:

# of plates	Rxn buffer diluent (ml)	CSPD (ml)
10	60	3
11	65	3.25
12	70	3.5
13	75	3.75
14	80	4

15	85	4.25
16	90	4.5
17	95	4.75
18	100	5
19	105	5.25
20	110	5.5
21	115	5.75
22	120	6
23	125	6.25
24	130	6.5
25	135	6.75
26	140	7
27	145	7.25
28	150	7.5
29	155	7.75
30	160	8
31	165	8.25
32	170	8.5
33	175	8.75
34	180	9
35	185	9.25
36	190	9.5
37	195	9.75
38	200	10
39	205	10.25
40	210	10.5
41	215	10.75
42	220	11
43	225	11.25
44	230	11.5
45	235	11.75
46	240	12
47	245	12.25
48	250	12.5
49	255	12.75
50	260	13

Example 18: High-Throughput Screening Assay Identifying Changes in Small Molecule Concentration and Membrane Permeability

Binding of a ligand to a receptor is known to alter intracellular levels of small molecules, such as calcium, potassium, sodium, and pH, as well as alter membrane potential. These alterations can be measured in an assay to identify supernatants which bind to receptors of a particular cell. Although the following protocol describes an assay for calcium, this protocol can easily be modified to detect changes in potassium, sodium, pH, membrane potential, or any other small molecule which is detectable by a fluorescent probe.

The following assay uses Fluorometric Imaging Plate Reader ("FLIPR") to measure changes in fluorescent molecules (Molecular Probes) that bind small molecules. Clearly, any fluorescent molecule detecting a small molecule can be used instead of the calcium fluorescent molecule, fluo-3, used here.

For adherent cells, seed the cells at 10,000 -20,000 cells/well in a Co-star black 96-well plate with clear bottom. The plate is incubated in a CO₂ incubator for 20 hours. The adherent cells are washed two times in Biotek washer with 200 ul of HBSS (Hank's Balanced Salt Solution) leaving 100 ul of buffer after the final wash.

A stock solution of 1 mg/ml fluo-3 is made in 10% pluronic acid DMSO. To load the cells with fluo-3, 50 ul of 12 ug/ml fluo-3 is added to each well. The plate is incubated at 37°C in a CO₂ incubator for 60 min. The plate is washed four times in the Biotek washer with HBSS leaving 100 ul of buffer.

For non-adherent cells, the cells are spun down from culture media. Cells are re-suspended to 2-5x10⁶ cells/ml with HBSS in a 50-ml conical tube. 4 ul of 1 mg/ml fluo-3 solution in 10% pluronic acid DMSO is added to each ml of cell suspension. The tube is then placed in a 37°C water bath for 30-60 min. The cells are washed twice with HBSS, resuspended to 1x10⁶ cells/ml, and dispensed into a microplate, 100 ul/well. The plate is centrifuged at 1000 rpm for 5 min. The plate is then washed once in Denley CellWash with 200 ul, followed by an aspiration step to 100 ul final volume.

For a non-cell based assay, each well contains a fluorescent molecule, such as fluo-3. The supernatant is added to the well, and a change in fluorescence is detected.

To measure the fluorescence of intracellular calcium, the FLIPR is set for the following parameters: (1) System gain is 300-800 mW; (2) Exposure time is 0.4 second; (3) Camera F/stop is F/2; (4) Excitation is 488 nm; (5) Emission is 530 nm; and (6) Sample addition is 50 ul. Increased emission at 530 nm indicates an extracellular

signaling even which has resulted in an increase in the intracellular Ca^{++} concentration.

Example 19: High-Throughput Screening Assay Identifying Tyrosine Kinase Activity

The Protein Tyrosine Kinases (PTK) represent a diverse group of transmembrane and cytoplasmic kinases. Within the Receptor Protein Tyrosine Kinase (RPTK) group are receptors for a range of mitogenic and metabolic growth factors including the PDGF, FGF, EGF, NGF, HGF and Insulin receptor subfamilies. In addition there are a large family of RPTKs for which the corresponding ligand is unknown. Ligands for RPTKs include mainly secreted small proteins, but also membrane-bound and extracellular matrix proteins.

Activation of RPTK by ligands involves ligand-mediated receptor dimerization, resulting in transphosphorylation of the receptor subunits and activation of the cytoplasmic tyrosine kinases. The cytoplasmic tyrosine kinases include receptor associated tyrosine kinases of the src-family (e.g., src, yes, lck, lyn, fyn) and non-receptor linked and cytosolic protein tyrosine kinases, such as the Jak family, members of which mediate signal transduction triggered by the cytokine superfamily of receptors (e.g., the Interleukins, Interferons, GM-CSF, and Leptin).

Because of the wide range of known factors capable of stimulating tyrosine kinase activity, the identification of novel human secreted proteins capable of activating tyrosine kinase signal transduction pathways are of interest. Therefore, the following protocol is designed to identify those novel human secreted proteins capable of activating the tyrosine kinase signal transduction pathways.

Seed target cells (e.g., primary keratinocytes) at a density of approximately 25,000 cells per well in a 96 well Loprodyne Silent Screen Plates purchased from Nalge Nunc (Naperville, IL). The plates are sterilized with two 30 minute rinses with 100% ethanol, rinsed with water and dried overnight. Some plates are coated for 2 hr with 100 ml of cell culture grade type I collagen (50 mg/ml), gelatin (2%) or polylysine (50 mg/ml), all of which can be purchased from Sigma Chemicals (St. Louis, MO) or 10% Matrigel purchased from Becton Dickinson (Bedford, MA), or calf serum, rinsed with PBS and stored at 4°C. Cell growth on these plates is assayed by seeding 5,000 cells/well in growth medium and indirect quantitation of cell number through use of alamarBlue as described by the manufacturer Alamar Biosciences, Inc. (Sacramento, CA) after 48 hr. Falcon plate covers #3071 from Becton Dickinson (Bedford, MA) are

used to cover the Loprodyn Silent Screen Plates. Falcon Microtest III cell culture plates can also be used in some proliferation experiments.

To prepare extracts, A431 cells are seeded onto the nylon membranes of Loprodyn plates (20,000/200ml/well) and cultured overnight in complete medium.

- 5 Cells are quiesced by incubation in serum-free basal medium for 24 hr. After 5-20 minutes treatment with EGF (60ng/ml) or 50 ul of the supernatant produced in Example 11, the medium was removed and 100 ml of extraction buffer ((20 mM HEPES pH 7.5, 0.15 M NaCl, 1% Triton X-100, 0.1% SDS, 2 mM Na₃VO₄, 2 mM Na₄P₂O₇ and a cocktail of protease inhibitors (# 1836170) obtained from Boehringer Mannheim
- 10 (Indianapolis, IN) is added to each well and the plate is shaken on a rotating shaker for 5 minutes at 4°C. The plate is then placed in a vacuum transfer manifold and the extract filtered through the 0.45 mm membrane bottoms of each well using house vacuum. Extracts are collected in a 96-well catch/assay plate in the bottom of the vacuum manifold and immediately placed on ice. To obtain extracts clarified by centrifugation,
- 15 the content of each well, after detergent solubilization for 5 minutes, is removed and centrifuged for 15 minutes at 4°C at 16,000 x g.

Test the filtered extracts for levels of tyrosine kinase activity. Although many methods of detecting tyrosine kinase activity are known, one method is described here.

- Generally, the tyrosine kinase activity of a supernatant is evaluated by
- 20 determining its ability to phosphorylate a tyrosine residue on a specific substrate (a biotinylated peptide). Biotinylated peptides that can be used for this purpose include PSK1 (corresponding to amino acids 6-20 of the cell division kinase cdc2-p34) and PSK2 (corresponding to amino acids 1-17 of gastrin). Both peptides are substrates for a range of tyrosine kinases and are available from Boehringer Mannheim.

- 25 The tyrosine kinase reaction is set up by adding the following components in order. First, add 10ul of 5uM Biotinylated Peptide, then 10ul ATP/Mg₂⁺ (5mM ATP/50mM MgCl₂), then 10ul of 5x Assay Buffer (40mM imidazole hydrochloride, pH7.3, 40 mM beta-glycerophosphate, 1mM EGTA, 100mM MgCl₂, 5 mM MnCl₂, 0.5 mg/ml BSA), then 5ul of Sodium Vanadate(1mM), and then 5ul of water. Mix the
- 30 components gently and preincubate the reaction mix at 30°C for 2 min. Initiate the reaction by adding 10ul of the control enzyme or the filtered supernatant.

The tyrosine kinase assay reaction is then terminated by adding 10 ul of 120mM EDTA and place the reactions on ice.

- Tyrosine kinase activity is determined by transferring 50 ul aliquot of reaction
- 35 mixture to a microtiter plate (MTP) module and incubating at 37°C for 20 min. This

allows the streptavidin coated 96 well plate to associate with the biotinylated peptide. Wash the MTP module with 300ul/well of PBS four times. Next add 75 ul of anti-phosphotyrosine antibody conjugated to horse radish peroxidase(anti-P-Tyr-
5 POD(0.5u/ml)) to each well and incubate at 37°C for one hour. Wash the well as above.

Next add 100ul of peroxidase substrate solution (Boehringer Mannheim) and incubate at room temperature for at least 5 mins (up to 30 min). Measure the absorbance of the sample at 405 nm by using ELISA reader. The level of bound peroxidase activity is quantitated using an ELISA reader and reflects the level of
10 tyrosine kinase activity.

Example 20: High-Throughput Screening Assay Identifying Phosphorylation Activity

As a potential alternative and/or compliment to the assay of protein tyrosine
15 kinase activity described in Example 19, an assay which detects activation (phosphorylation) of major intracellular signal transduction intermediates can also be used. For example, as described below one particular assay can detect tyrosine phosphorylation of the Erk-1 and Erk-2 kinases. However, phosphorylation of other molecules, such as Raf, JNK, p38 MAP, Map kinase kinase (MEK), MEK kinase,
20 Src, Muscle specific kinase (MuSK), IRAK, Tec, and Janus, as well as any other phosphoserine, phosphotyrosine, or phosphothreonine molecule, can be detected by substituting these molecules for Erk-1 or Erk-2 in the following assay.

Specifically, assay plates are made by coating the wells of a 96-well ELISA
25 plate with 0.1ml of protein G (1ug/ml) for 2 hr at room temp, (RT). The plates are then rinsed with PBS and blocked with 3% BSA/PBS for 1 hr at RT. The protein G plates are then treated with 2 commercial monoclonal antibodies (100ng/well) against Erk-1 and Erk-2 (1 hr at RT) (Santa Cruz Biotechnology). (To detect other molecules, this step can easily be modified by substituting a monoclonal antibody detecting any of the above described molecules.) After 3-5 rinses with PBS, the plates are stored at 4°C
30 until use.

A431 cells are seeded at 20,000/well in a 96-well Loprodyne filterplate and cultured overnight in growth medium. The cells are then starved for 48 hr in basal medium (DMEM) and then treated with EGF (6ng/well) or 50 ul of the supernatants obtained in Example 11 for 5-20 minutes. The cells are then solubilized and extracts
35 filtered directly into the assay plate.

After incubation with the extract for 1 hr at RT, the wells are again rinsed. As a positive control, a commercial preparation of MAP kinase (10ng/well) is used in place of A431 extract. Plates are then treated with a commercial polyclonal (rabbit) antibody (1ug/ml) which specifically recognizes the phosphorylated epitope of the Erk-1 and Erk-2 kinases (1 hr at RT). This antibody is biotinylated by standard procedures. The bound polyclonal antibody is then quantitated by successive incubations with Europium-streptavidin and Europium fluorescence enhancing reagent in the Wallac DELFIA instrument (time-resolved fluorescence). An increased fluorescent signal over background indicates a phosphorylation.

10

Example 21: Method of Determining Alterations in a Gene Corresponding to a Polynucleotide

RNA isolated from entire families or individual patients presenting with a phenotype of interest (such as a disease) is be isolated. cDNA is then generated from these RNA samples using protocols known in the art. (See, Sambrook.) The cDNA is then used as a template for PCR, employing primers surrounding regions of interest in SEQ ID NO:X. Suggested PCR conditions consist of 35 cycles at 95°C for 30 seconds; 60-120 seconds at 52-58°C; and 60-120 seconds at 70°C, using buffer solutions described in Sidransky, D., et al., Science 252:706 (1991).

PCR products is then sequenced using primers labeled at their 5' end with T4 polynucleotide kinase, employing SequiTherm Polymerase. (Epicentre Technologies). The intron-exon borders of selected exons is also determined and genomic PCR products analyzed to confirm the results. PCR products harboring suspected mutations is then cloned and sequenced to validate the results of the direct sequencing.

PCR products is cloned into T-tailed vectors as described in Holton, T.A. and Graham, M.W., Nucleic Acids Research, 19:1156 (1991) and sequenced with T7 polymerase (United States Biochemical). Affected individuals is identified by mutations not present in unaffected individuals.

Genomic rearrangements are also observed as a method of determining alterations in a gene corresponding to a polynucleotide. Genomic clones isolated according to Example 2 are nick-translated with digoxigenindeoxy-uridine 5'-triphosphate (Boehringer Mannheim), and FISH performed as described in Johnson, Cg. et al., Methods Cell Biol. 35:73-99 (1991). Hybridization with the labeled probe is carried out using a vast excess of human cot-1 DNA for specific hybridization to the corresponding genomic locus.

Chromosomes are counterstained with 4,6-diamino-2-phenylidole and propidium iodide, producing a combination of C- and R-bands. Aligned images for precise mapping are obtained using a triple-band filter set (Chroma Technology, Brattleboro, VT) in combination with a cooled charge-coupled device camera
5 (Photometrics, Tucson, AZ) and variable excitation wavelength filters. (Johnson, Cv. et al., Genet. Anal. Tech. Appl., 8:75 (1991).) Image collection, analysis and chromosomal fractional length measurements are performed using the ISee Graphical Program System. (Inovision Corporation, Durham, NC.) Chromosome alterations of the genomic region hybridized by the probe are identified as insertions, deletions, and
10 translocations. These alterations are used as a diagnostic marker for an associated disease.

Example 22: Method of Detecting Abnormal Levels of a Polypeptide in a Biological Sample

15 A polypeptide of the present invention can be detected in a biological sample, and if an increased or decreased level of the polypeptide is detected, this polypeptide is a marker for a particular phenotype. Methods of detection are numerous, and thus, it is understood that one skilled in the art can modify the following assay to fit their particular needs.

20 For example, antibody-sandwich ELISAs are used to detect soluble polypeptides in a sample, preferably a biological sample. Wells of a microtiter plate are coated with specific antibodies, at a final concentration of 0.2 to 10 ug/ml. The antibodies are either monoclonal or polyclonal and are produced by the method described in Example 10. The wells are blocked so that non-specific binding of the
25 polypeptide to the well is reduced.

The coated wells are then incubated for > 2 hours at RT with a sample containing the polypeptide. Preferably, serial dilutions of the sample should be used to validate results. The plates are then washed three times with deionized or distilled water to remove unbounded polypeptide.

30 Next, 50 ul of specific antibody-alkaline phosphatase conjugate, at a concentration of 25-400 ng, is added and incubated for 2 hours at room temperature. The plates are again washed three times with deionized or distilled water to remove unbounded conjugate.

35 Add 75 ul of 4-methylumbelliferyl phosphate (MUP) or p-nitrophenyl phosphate (NPP) substrate solution to each well and incubate 1 hour at room temperature. Measure the reaction by a microtiter plate reader. Prepare a standard curve, using serial dilutions of a control sample, and plot polypeptide concentration on

the X-axis (log scale) and fluorescence or absorbance of the Y-axis (linear scale). Interpolate the concentration of the polypeptide in the sample using the standard curve.

Example 23: Formulating a Polypeptide

5 The secreted polypeptide composition will be formulated and dosed in a fashion consistent with good medical practice, taking into account the clinical condition of the individual patient (especially the side effects of treatment with the secreted polypeptide alone), the site of delivery, the method of administration, the scheduling of administration, and other factors known to practitioners. The "effective amount" for
10 purposes herein is thus determined by such considerations.

 As a general proposition, the total pharmaceutically effective amount of secreted polypeptide administered parenterally per dose will be in the range of about 1 $\mu\text{g/kg/day}$ to 10 mg/kg/day of patient body weight, although, as noted above, this will be subject to therapeutic discretion. More preferably, this dose is at least 0.01 mg/kg/day , and
15 most preferably for humans between about 0.01 and 1 mg/kg/day for the hormone. If given continuously, the secreted polypeptide is typically administered at a dose rate of about 1 $\mu\text{g/kg/hour}$ to about 50 $\mu\text{g/kg/hour}$, either by 1-4 injections per day or by continuous subcutaneous infusions, for example, using a mini-pump. An intravenous bag solution may also be employed. The length of treatment needed to observe changes
20 and the interval following treatment for responses to occur appears to vary depending on the desired effect.

 Pharmaceutical compositions containing the secreted protein of the invention are administered orally, rectally, parenterally, intracisternally, intravaginally, intraperitoneally, topically (as by powders, ointments, gels, drops or transdermal
25 patch), buccally, or as an oral or nasal spray. "Pharmaceutically acceptable carrier" refers to a non-toxic solid, semisolid or liquid filler, diluent, encapsulating material or formulation auxiliary of any type. The term "parenteral" as used herein refers to modes of administration which include intravenous, intramuscular, intraperitoneal, intrasternal, subcutaneous and intraarticular injection and infusion.

30 The secreted polypeptide is also suitably administered by sustained-release systems. Suitable examples of sustained-release compositions include semi-permeable polymer matrices in the form of shaped articles, e.g., films, or microcapsules. Sustained-release matrices include polylactides (U.S. Pat. No. 3,773,919, EP 58,481), copolymers of L-glutamic acid and gamma-ethyl-L-glutamate (Sidman, U. et al., Biopolymers 22:547-556 (1983)), poly (2- hydroxyethyl methacrylate) (R. Langer et al., J. Biomed. Mater. Res. 15:167-277 (1981), and R. Langer, Chem. Tech. 12:98-105 (1982)), ethylene vinyl acetate (R. Langer et al.) or poly-D- (-)-3-hydroxybutyric
35

acid (EP 133,988). Sustained-release compositions also include liposomally entrapped polypeptides. Liposomes containing the secreted polypeptide are prepared by methods known per se: DE 3,218,121; Epstein et al., Proc. Natl. Acad. Sci. USA 82:3688-3692 (1985); Hwang et al., Proc. Natl. Acad. Sci. USA 77:4030-4034 (1980); EP 52,322; 5 EP 36,676; EP 88,046; EP 143,949; EP 142,641; Japanese Pat. Appl. 83-118008; U.S. Pat. Nos. 4,485,045 and 4,544,545; and EP 102,324. Ordinarily, the liposomes are of the small (about 200-800 Angstroms) unilamellar type in which the lipid content is greater than about 30 mol. percent cholesterol, the selected proportion being adjusted for the optimal secreted polypeptide therapy.

10 For parenteral administration, in one embodiment, the secreted polypeptide is formulated generally by mixing it at the desired degree of purity, in a unit dosage injectable form (solution, suspension, or emulsion), with a pharmaceutically acceptable carrier, i.e., one that is non-toxic to recipients at the dosages and concentrations employed and is compatible with other ingredients of the formulation. For example, the 15 formulation preferably does not include oxidizing agents and other compounds that are known to be deleterious to polypeptides.

Generally, the formulations are prepared by contacting the polypeptide uniformly and intimately with liquid carriers or finely divided solid carriers or both. Then, if necessary, the product is shaped into the desired formulation. Preferably the 20 carrier is a parenteral carrier, more preferably a solution that is isotonic with the blood of the recipient. Examples of such carrier vehicles include water, saline, Ringer's solution, and dextrose solution. Non-aqueous vehicles such as fixed oils and ethyl oleate are also useful herein, as well as liposomes.

The carrier suitably contains minor amounts of additives such as substances that 25 enhance isotonicity and chemical stability. Such materials are non-toxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, succinate, acetic acid, and other organic acids or their salts; antioxidants such as ascorbic acid; low molecular weight (less than about ten residues) polypeptides, e.g., polyarginine or tripeptides; proteins, such as serum albumin, gelatin, or 30 immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids, such as glycine, glutamic acid, aspartic acid, or arginine; monosaccharides, disaccharides, and other carbohydrates including cellulose or its derivatives, glucose, manose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; counterions such as sodium; and/or nonionic surfactants such as polysorbates, 35 poloxamers, or PEG.

The secreted polypeptide is typically formulated in such vehicles at a concentration of about 0.1 mg/ml to 100 mg/ml, preferably 1-10 mg/ml, at a pH of

about 3 to 8. It will be understood that the use of certain of the foregoing excipients, carriers, or stabilizers will result in the formation of polypeptide salts.

Any polypeptide to be used for therapeutic administration can be sterile.

5 Sterility is readily accomplished by filtration through sterile filtration membranes (e.g., 0.2 micron membranes). Therapeutic polypeptide compositions generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

Polypeptides ordinarily will be stored in unit or multi-dose containers, for example, sealed ampoules or vials, as an aqueous solution or as a lyophilized
10 formulation for reconstitution. As an example of a lyophilized formulation, 10-ml vials are filled with 5 ml of sterile-filtered 1% (w/v) aqueous polypeptide solution, and the resulting mixture is lyophilized. The infusion solution is prepared by reconstituting the lyophilized polypeptide using bacteriostatic Water-for-Injection.

The invention also provides a pharmaceutical pack or kit comprising one or
15 more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration. In addition, the polypeptides of the
20 present invention may be employed in conjunction with other therapeutic compounds.

Example 24: Method of Treating Decreased Levels of the Polypeptide

It will be appreciated that conditions caused by a decrease in the standard or normal expression level of a secreted protein in an individual can be treated by
25 administering the polypeptide of the present invention, preferably in the secreted form. Thus, the invention also provides a method of treatment of an individual in need of an increased level of the polypeptide comprising administering to such an individual a pharmaceutical composition comprising an amount of the polypeptide to increase the activity level of the polypeptide in such an individual.

30 For example, a patient with decreased levels of a polypeptide receives a daily dose 0.1-100 ug/kg of the polypeptide for six consecutive days. Preferably, the polypeptide is in the secreted form. The exact details of the dosing scheme, based on administration and formulation, are provided in Example 23.

Example 25: Method of Treating Increased Levels of the Polypeptide

Antisense technology is used to inhibit production of a polypeptide of the present invention. This technology is one example of a method of decreasing levels of a polypeptide, preferably a secreted form, due to a variety of etiologies, such as cancer.

5 For example, a patient diagnosed with abnormally increased levels of a polypeptide is administered intravenously antisense polynucleotides at 0.5, 1.0, 1.5, 2.0 and 3.0 mg/kg day for 21 days. This treatment is repeated after a 7-day rest period if the treatment was well tolerated. The formulation of the antisense polynucleotide is provided in Example 23.

10

Example 26: Method of Treatment Using Gene Therapy

One method of gene therapy transplants fibroblasts, which are capable of expressing a polypeptide, onto a patient. Generally, fibroblasts are obtained from a subject by skin biopsy. The resulting tissue is placed in tissue-culture medium and
15 separated into small pieces. Small chunks of the tissue are placed on a wet surface of a tissue culture flask, approximately ten pieces are placed in each flask. The flask is turned upside down, closed tight and left at room temperature over night. After 24 hours at room temperature, the flask is inverted and the chunks of tissue remain fixed to the bottom of the flask and fresh media (e.g., Ham's F12 media, with 10% FBS,
20 penicillin and streptomycin, is added. The flasks are then incubated at 37°C for approximately one week.

At this time, fresh media is added and subsequently changed every several days. After an additional two weeks in culture, a monolayer of fibroblasts emerge. The monolayer is trypsinized and scaled into larger flasks.

25 pMV-7 (Kirschmeier, P.T. et al., DNA, 7:219-25 (1988)), flanked by the long terminal repeats of the Moloney murine sarcoma virus, is digested with EcoRI and HindIII and subsequently treated with calf intestinal phosphatase. The linear vector is fractionated on agarose gel and purified, using glass beads.

The cDNA encoding a polypeptide of the present invention can be amplified
30 using PCR primers which correspond to the 5' and 3' end sequences respectively as set forth in Example 1. Preferably, the 5' primer contains an EcoRI site and the 3' primer includes a HindIII site. Equal quantities of the Moloney murine sarcoma virus linear backbone and the amplified EcoRI and HindIII fragment are added together, in the presence of T4 DNA ligase. The resulting mixture is maintained under conditions
35 appropriate for ligation of the two fragments. The ligation mixture is then used to

transform bacteria HB101, which are then plated onto agar containing kanamycin for the purpose of confirming that the vector has the gene of interest properly inserted.

5 The amphotropic pA317 or GP+am12 packaging cells are grown in tissue culture to confluent density in Dulbecco's Modified Eagles Medium (DMEM) with 10% calf serum (CS), penicillin and streptomycin. The MSV vector containing the gene is then added to the media and the packaging cells transduced with the vector. The packaging cells now produce infectious viral particles containing the gene (the packaging cells are now referred to as producer cells).

10 Fresh media is added to the transduced producer cells, and subsequently, the media is harvested from a 10 cm plate of confluent producer cells. The spent media, containing the infectious viral particles, is filtered through a millipore filter to remove detached producer cells and this media is then used to infect fibroblast cells. Media is removed from a sub-confluent plate of fibroblasts and quickly replaced with the media from the producer cells. This media is removed and replaced with fresh media. If the
15 titer of virus is high, then virtually all fibroblasts will be infected and no selection is required. If the titer is very low, then it is necessary to use a retroviral vector that has a selectable marker, such as neo or his. Once the fibroblasts have been efficiently infected, the fibroblasts are analyzed to determine whether protein is being produced.

20 The engineered fibroblasts are then transplanted onto the host, either alone or after having been grown to confluence on cytodex 3 microcarrier beads.

It will be clear that the invention may be practiced otherwise than as particularly described in the foregoing description and examples. Numerous modifications and variations of the present invention are possible in light of the above teachings and, therefore, are within the scope of the appended claims.

25 The entire disclosure of each document cited (including patents, patent applications, journal articles, abstracts, laboratory manuals, books, or other disclosures) in the Background of the Invention, Detailed Description, and Examples is hereby incorporated herein by reference.

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Human Genome Sciences, Inc. et al.
- (ii) TITLE OF INVENTION: 186 Human Secreted Proteins
- 10 (iii) NUMBER OF SEQUENCES: 644
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Human Genome Sciences, Inc.
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- (C) CITY: Rockville
- (D) STATE: Maryland
- 20 (E) COUNTRY: USA
- (F) ZIP: 20850
- 25
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
- 30 (B) COMPUTER: HP Vectra 486/33
- (C) OPERATING SYSTEM: MSDOS version 6.2
- 35 (D) SOFTWARE: ASCII Text
- (vi) CURRENT APPLICATION DATA:
- 40 (A) APPLICATION NUMBER:
- (B) FILING DATE: March 6, 1998
- 45 (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- 50 (A) APPLICATION NUMBER:
- (B) FILING DATE:
- 55

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 733 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

30	GGGATCCGGA GCCCAAATCT TCTGACAAAA CTCACACATG CCCACCGTGC CCAGCACCTG	60
	AATTCGAGGG TGCACCGTCA GTCTTCCTCT TCCCCCAAA ACCCAAGGAC ACCCTCATGA	120
35	TCTCCCGGAC TCCTGAGGTC ACATGCGTGG TGGTGGACGT AAGCCACGAA GACCTGAGG	180
	TCAAGTTCAA CTGGTACGTG GACGGCGTGG AGGTGCATAA TGCCAAGACA AAGCCGCGGG	240
40	AGGAGCAGTA CAACAGCACG TACCGTGTGG TCAGCGTCCT CACCGTCCTG CACCAGGACT	300
	GGCTGAATGG CAAGGAGTAC AAGTGCAAGG TCTCCAACAA AGCCCTCCCA ACCCCCATCG	360
	AGAAAACCAT CTCCAAGCC AAAGGGCAGC CCCGAGAACC ACAGGTGTAC ACCCTGCCCC	420
45	CATCCCGGGA TGAGCTGACC AAGAACCAGG TCAGCCTGAC CTGCCTGGTC AAAGGCTTCT	480
	ATCCAAGCGA CATCGCCGTG GAGTGGGAGA GCAATGGGCA GCCGGAGAAC AACTACAAGA	540
50	CCACGCCTCC CGTGCTGGAC TCCGACGGCT CCTTCTTCCT CTACAGCAAG CTCACCGTGG	600
	ACAAGAGCAG GTGGCAGCAG GGAACGTCT TCTCATGCTC CGTGATGCAT GAGGCTCTGC	660
	ACAACCACTA CACGCAGAAG AGCCTCTCCC TGTCTCCGGG TAAATGAGTG CGACGGCCGC	720
55	GA CTCTAGAG GAT	733

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

10 Trp Ser Xaa Trp Ser
1 5

15

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 86 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

25 GCGCCTCGAG ATTTCCTCGA AATCTAGATT TCCCGAAAT GATTTCCTCG AAATGATTTC 60
30 CCCGAAATAT CTGCCATCTC AATTAG 86

(2) INFORMATION FOR SEQ ID NO: 4:

35

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

45 GCGGCAAGCT TTTTGCAAAG CCTAGGC 27

(2) INFORMATION FOR SEQ ID NO: 5:

50

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 271 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

60 CTCGAGATTT CCCGAAATC TAGATTTCCT CGAAATGATT TCCCGAAAT GATTTCCTCG 60

AAATATCTGC CATCTCAATT AGTCAGCAAC CATAGTCCCG CCCCTAACTC CGCCCATCCC 120
GCCCCTAACT CCGCCAGTT CCGCCATTC TCGCCCAT GGCTGACTAA TTTTTTTTAT 180
5 TTATGCAGAG GCGAGGCCG CCTCGGCCTC TGAGCTATTC CAGAAGTAGT GAGGAGGCTT 240
TTTTGGAGGC CTAGGCTTTT GCAAAAAGCT T 271

10

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
15 (A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GCGCTCGAGG GATGACAGCG ATAGAACCCC GG 32

25

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GCGAAGCTTC GCGACTCCCC GGATCCGCCT C 31

40

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
45 (A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GGGGACTTTC CC 12

55

(2) INFORMATION FOR SEQ ID NO: 9:

60 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GCGGCCTCGA GGGGACTTTC COGGGGACTT TCCGGGGACT TTCCGGGACT TTCCATCCTG 60

10 CCATCTCAAT TAG 73

15 (2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

25 CTCGAGGGGA CTTTCCCGGG GACTTTCCGG GGACTTTCCG GGACTTTCCA TCTGCCATCT 60

CAATTAGTCA GCAACCATAG TCCCGCCCCT AACTCCGCCC ATCCCGCCCC TAACTCCGCC 120

30 CAGTTCGGCC CATTCCTCCGC CCCATGGCTG ACTAATTTT TTTATTTATG CAGAGGCCGA 180

GGCCGCCTCG GCCTCTGAGC TATTCAGAA GTAGTGAGGA GGCTTTTTTG GAGGCCTAGG 240

CTTTTGCAA AAGCTT 256

35

(2) INFORMATION FOR SEQ ID NO: 11:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GGCACGAGGT AATTCTACC AGAAATTTCC AGAGCATTAT GTAGGTAGAA AAAAATGCAA 60

50 GCAAGCTGTT AAAGATCTTG GATCCATTA TATAGTATGT ATAGCTGAAA TCTGTAATTC 120

AATCACITTT TCTCTTTTAT CCTCTAACCA AAAAATGTT TAATTTTGCA TCCCAAATGT 180

55 TTTTAATCTT TGTATATTTT TTA AAAATCC TTTTCTCCTC ATCATGCGCT TTTTGTGGT 240

TGTAATAGA CTTACTTGCA CTTGAAGAT GAGTACTCC TTGTCATCTT ACAAATATGT 300

GATATGGTAA TTTTCATAAC AGATGTCAGT TTTGAACCA GAATTGGTGA TTTGTTTATA 360

60 AGAAAAAAC TGGCTTCATT TCTGTGAAAT TGCTCTTTGA AAATTTCTTT TTACACGTGT 420

5 AAGCCAACTG AGATACCGTG ATGGTGTGA TTCTTTCAA TGATGCTTAC CATCTATTTT 480
AGCCACTGAG CCTTTTATTA TTGTCTATT TGTAAGTTT ATTGTCTTA ACTCATTTAA 540
TAAATATACT GTTTATCTGT TTCTGAAAAA AAAAAAAAAA AA 582

10

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
15 (A) LENGTH: 465 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GTITGGGGT GAGGCCGAGC TGCTGCGGG CTTCTCGCC GGCCAGGACA CAGCTACTCG 60
CAGCGCGGG GCGCCTGGCT ATGATGTTCC TCACCCAGGG CCGGCCTCTG CCTCTACTTC 120
25 GTGCCAGGCC CACTTGCCAG GCAGGAGCCC TCCCCAAGCC TTCAGGGCTG CTCGGAGTCA 180
CCTGTTGGAA TGGACTAAAA GGACCCCTGT GTGGGAACAG GTGCTCCCCA AACACCCTGC 240
TGCTGGCTGC CAGGCAGGCC CTCTGGAAGG GAAGGGGCG GACTCATCAG GACCTCCCTG 300
30 GACCCCTGCA GGCAGGCAG CTTGGGCCG AGCCCAAGCA TTTGGCTCTG CTGCCCCCAA 360
GGGACAGGA AGCCTCTTGG GCCTCTTCCC TTCTGGACA AGGCCCCCTG CCTTTGCCTC 420
35 ACATAAACTG TACAGTATTT TCATTAAAG CCTCTTTCAT AAAAA 465

40

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
45 (A) LENGTH: 474 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

50 ATGCAATTCC TGCTCACAGC CTTTCTGTTG GTGCCACTTC TGGCTCTTTG TGATGTCCCC 60
ATATCCCTAG GCTTCTCCCC CTCTAGAAG GGCTTCTTGA TAGATTAGAA AATAAGAATG 120
AGTGACATTT CCTATGTGCA TATAAGAAGG AGCCACAAGA CATGTCTTTT AAATAAAGG 180
55 ACAGTGTCCT TCCTTTTAGC TGCCGAATAG AACCTTGGTC TCATCCTCCT GGAGCTAGGC 240
CTTTAAACA GCTTCTGTGT TTCTCATTTG TCTCAGTGT TTGCCAGGGT TTTATCGGAA 300
60 AGATAATGTT CCGTTTAAAA TATTTCTTAA TGAGGCOGGG CGTGGTGGCT CAGGCCTGTA 360

ACCCTAGCAM TTGGGGGCTG AGCGGGTGA TCACGAGGTC AGGAGATCGA GACCATCCTG 420

5 GSTAACATGG TGAAACCCCG TCTCTACTAA AAATACAAAA AAAAAAAAAA AAAA 474

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 314 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

20 TTATGTTGGG GAGCAAGACC TGATAGCCAG CCTTACATG GGAGTATAAT TCTGTCTCC 60
ATCTCATAAG CCCAGTACC TGAGCCAGAA TGATTATAAC CAACCACACT GTCTCTTTAT 120
CATGGATGGC TTTAGCAGTA GGTATTATTC ATCATTGCCA TTGTAGCTC TACAGTGGTT 180
25 TATAGTAATT TCTCATCTT TAAGTCTCTC CCTCAGTGCC TGTGTATATC AAATCATTG 240
CTCTCTCANG CAGTTGAGCT CTGCATTCTC CCYTATGGG GAGAGCTGTG TTGGAGAGAG 300
AGAATATNAC TTCC 314

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 613 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

45 CTCATATTGC CGTCTGGCTA AAAGTGAACA TGCCATTGAT CAATCTGCTT TTATTATATT 60
ATGTTCTTAA TGGTGGCAAG CAAGACAAGA AGTAGAAAGA AAGATGGTGT AAGCTCAAGA 120
ACCCACTAAA TCTATCCTAT GGCTGGGTT CACCCAGCCT GCTTTGTGGA TTTTGTCTCA 180
50 CTATAACAGA GCTCCCAAGG AGACTGCAGA GTCAGCTCCC TTAAGCACTG TAACTAAAGC 240
CTAACTCTTC CGTTCCACCC AACATGTYC CCAGCTCATC CTCTTTCCCR AAGTCCCTTT 300
TCTGCCCCAG ATGCGAATTG CATTTAACTA ATCTCAAGT GAAATGTCCA CACAGRATTC 360
55 CATTTTAATT AGCATACCAT AGTTTTTGTG CAAATTTGCT TTCAGARGAC TCCCATTGCA 420
GCTGCTCAGA GACGCTAAG GCAGGGCCTC TTGAWGCTTT CCCGATAGCT TTCAGCTGCA 480
60 ATAGCTCTTA GGCAGAATGC CATGAGGTC CTGCCCACT GTATTACTGG GGAACACCTG 540

ATTGGCTAGA AGTTGATCCT CCTGTAACCTT TTCTGAGTTC TTTACATTTA CTCGTGAAAC 600

CCAAATATGC CAC 613

5

(2) INFORMATION FOR SEQ ID NO: 16:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 356 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

20 CCCCCCCAT TGAACCCCTGG GCTGTGAAAG TTTTTCCTG TGTGGGTCGT TCTGTGTGGC 60

GCCTGGTGTG TGGKTCCCAA CTCCTGTTGC AAAGTGGCAG CAGCCAATCA TGAAGCGCCC 120

TTATTTTATG TTGCAGATGA CCAGGTCTCC CCCCCACAGC CTCTGTCTGG TCCCTCATTG 180

25 GTGAGTGGTC TGCCTGCCCA AGGAGCCTGA TTGGTGGGAA ATGGCATCAT CTAATATGAT 240

GGGAAGGCAT TTGGTCCTGG TTATGTTTAT TACAACATCA TTGCACTCTG GGACTCCAGT 300

30 CCCTGAAAAC GTAATTGTG GTGTTACCAA AGGACCACAG GGGAAAAAAA AAAAAA 356

(2) INFORMATION FOR SEQ ID NO: 17:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 414 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

40

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

45 GAAACTANAT CCGGGGCTT TTAACNGGTA CTGGGAAAT AAGTATTGGG TAATCACTAA 60

GNGGACATTG ACTGCACCAA ACCAAAGCTA TAGAAAGAAA TGATTGACTT TTAAAAATAT 120

ATTACATTA ACTGTCCTAG GATACTTCTC TTGAGGCTTT GGAAACTTC TTCCTTGAAA 180

50 TTGTCATATC CACTCCAGTT CTGTCACCAA AGATTTTAAT CTTCAGATCG CAATTTCTCTC 240

TCTCCAGAA AAAAGTACTA CAACAGGCTC AAGGGATATG CTTTGGTGGT CAAGGGATTA 300

55 CACTATGGTT TTCCTTCTGT TCACAATGGT ATTTACAGGA GACCTGTCA TCAGAGGACG 360

TACTGAACTA TCTTTATGAC TTTGGATTG ATCAGAGGTT TAAAAAAA AAAA 414

60

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 469 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

10 AATCACCATT GCAATACAAA TGATCTGCCT GGTGAATGYT GAGCTGTACC CCACATTCTG 60
CAGGAACYTC GGAGTGATGG TGTGTTCTC CCTGTGTGAC ATAGGTGGGA TAATCACCCC 120
15 CTTCATAGTC TTCAGGCTGA GGGAGGTCTG GCAAGCCTTG CCCCTCATTT TGTPTGCGGT 180
GTTGGGCTG CTGCGCGG GAGTGACGCT ACTTCTTCCA GAGACCAAGG GGGTCGCTTT 240
GCCAGAGACC ATGAAGGACG CCGAGAACCT TGGGAGAAAA GCAAAGCCCA AAGAAAACAC 300
20 GATTTACCTT AAGGTCCAAA CCTCAGAACC CTCGGGCACC TGAGAGAGAT GTTPTGCGGC 360
GATGTCGTGT TGGAGGGATG AAGATGGAGT TATCCTCTGC AGAAATTCCT AGACGCCTTC 420
25 ACTTCTCTGT ATTCTTCTC ATACTGCCT ACCCCCAAT TAATATCAG 469

30 (2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 550 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

40 CCCCCCCCC CCCCACACT TTCAGGAGTC ACCCCCCAGC ATTTGGGGTT GGGTTGGCCC 60
TACTCCAGCC TGGAGCTCCC TGAGGGAGCC TGCACTCCCT GCTCCCAATC CCCGCTACTG 120
GTGCAGGGAT GCAGCCTGGA GCTGGCGTCC TTGTTCTGGG CCTGCTGCTG CCGCCACCCC 180
45 AGAGCCCCAG CCTGTCCTGA ATTGACATCA GTGCTTCCT GAACTGCCTC CCCACCCCT 240
GGGCATTATC CCAGGAACT TTATGTTTTC TAGAAGCTAA GCAGCTGCTG GGACTCAGGG 300
50 ACTGGTGCAG GTAGGCTGAG TGGCAGCTCA GTCCTAGAAG GTCTCTGAAG ATCTGGACTG 360
AGGACCTTGC TACTCCCCAA GCCAGAGCCC ATCAGCCAGG OCTGCTGTGA GCCACCTGCC 420
TGTGGAGTGC TGAGCTCAAC CAAAGGCTGG CAAGCTCTGG GCCTCATTTA AGGGATTCTG 480
55 ATGAGCCGAT GGGCCCTGGA GGCAGCCCAT TAAAGCATCT GGCTCGTTTT TGGAAAAAAA 540
AAAAAAAAA 550

60

(2) INFORMATION FOR SEQ ID NO: 20:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 741 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

TCTTGAAGAG TGTACAGTAC AGGATTATTA TAATGAAAGT TTATATCAAC AGGGTTTCGT 60
15 TGGCTCTGCA TATATTATAA GCAAAAGAGA TTGGTAAAGT GCCACAGTAT TCCAGATAAC 120
TTTTTCAGTTG CGGCCTTTCT TCTCGTTCTT TAATTTGAAA CCTAGATACA TGCAGTAAAA 180
20 ACTAGGAGAA TGACTTTTAC CCTTGGGGAC AGCCAAGTTT TGTTGATAAA CCTATTTTCT 240
AGCATGCCTT CAGGAAGTTG TGCCAGACCC TAGATTGTGA AGGACCCACT GTTCTTCTGT 300
TGTACGAGCT CCCTGAACCA TTGTTTCTGAG GACCAATGTC ACATCGCTTC ATGGGCATGG 360
25 NCCATGGGAG CATCTGGGTG ATAYCTGTCT ACAGTATTGG CTCTTCTGCG AGGCTGATAC 420
ACAAGGCCTC TCTTCCACAT GATCATTTGC AAACCTCCCC CAGCCCCTAC CATCCAATGT 480
GGAAGGAAAA CAAGAACTGC CTGAAGAAGA GTCCAAGCTA CAGATACACA GCGTGTGCAT 540
30 TGGGGCTGTC ACCTTCCTCC TCCCACTTCT GTATCTCTCAG AGATGCTGCG TGGATGTTTC 600
CTTAACCTCA GCTGACTTCC CTGTGAATGT CTAATGCTAG TTCAGGGCCT CCAGGCATTG 660
35 ATTTGTACAG TGGTAACTCC CAATGAGGCT TCTGTTATCA TTTGGTGTGC TTTTCTGTGC 720
ATTAAAAGAA ATGATTTTCC C 741

40

(2) INFORMATION FOR SEQ ID NO: 21:

- 45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 991 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GGCACGAGTC TCCCTGGGG AAGTTTCTTCT TTTCAGGAG GGAGGAGGCG TTTCACAGGT 60
55 AATGTGTCTA GAGTGTGGG CAGAAAATCT GGGACCACAC CACACCAGTT CTCTCCTTAA 120
TCCACGTCAT TTGCCTTCTA TCCAGCTAT GTTTCAGTG TCCTCTGGGT GTTCCAAGA 180
GCAACAAGAA ATGAATAAAT CTCTGGTGAG TTGTTTATTT GTTCTTCACT TTGTTTACA 240
60 CTGTATTTTC TGAGTTTATG GGTGTCTGTG AATTAAAAAG GAAAAGTAGA AATAAGTAA 300

ACTCAGGTTG AAGGAAATAT ACATAAATAA GATAAAGCTG ACCTGTAGAT ATAGCAGGTT 360
 5 ATAAAGCTTA GAGTTGTCTA AGTTGAGTGC AAATTTTCCT CTGATCTTTC TGATGCCGAA 420
 CAAAAAGCA GTCATGTTTG TTATGTGATT GGAATGGAAC CCGAGAAGAG AGCATGCTGT 480
 GTTCTTGTGG GACAGGAAAG CTTGCGTGCA CCAAGTCTGA ACCACCACCT TCATGGTGAC 540
 10 ATAGATTATG TGCTGGAACA TATTTACAC CCGCCTGGCA GTAAACACTT GTAGTGTGT 600
 GCAGTGAAA CCGTCATCTT CCGCTAAAGC ACGGCGTGT GTGCAGCGGA AATGGTCATC 660
 15 TGCTGCTAAA ACACAGCTTC CATCGTAATG TATGCTCCTT ACTCAAAGAG TGTGGTCCCA 720
 AACAGCCTTT GGGAGGTCCT CCTTGATTCA TGGATGAAAC CTGGAACATC TTGAGGACTG 780
 AGTTAACCAT AGGTCCTTAA ATAACTCTCC ACACGTTTTT CTTAGTTTAT CTCTACATGC 840
 20 AGGGTGTGCA GCAGCCTGTT CAAAGTCATA TTTCTGGA AATATTCCA GTGTTTATTT 900
 GCACTTTAGC CCACTCTGTG TAGCCTTATT TCTCTAAAC TCACCATTAA TCTGAATAAT 960
 25 AGTCAAATTT AGGGGACTG TATTTGCCTT A 991

30 (2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 653 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

40 CCACGCGTCC GGAATTCCCC TGAGGATCTT GGGCTATCTT TGACAGGGGA TTCTTGCAAG 60
 TTGATGCTTT CTACAAGTGA ATATAGTCAG TCCCCAAGA TGGAGAGCTT GAGTTCTCAC 120
 AGAATTGATG AAGATGGAGA AAACACACAG ATTGAGGATA CGGAACCCAT GTCTCCAGTT 180
 45 CTCAATTCTA AATTGTGTC TGCTGAAAAT GATAGTATCC TGATGAATCC AGCACAGGAT 240
 GGTGAAGTAC AACTGAGTCA GAATGATGAC AAAACAAAGG GAGATGATAC AGACACCAGG 300
 50 GATGACATTA GTATTTTAGC CACTGGTTGC AAGGGCAGAG AAGAAACGGT AGCAGAAGAA 360
 GTTTGTATTG ATCTCACTTG TGATTGGGG AGTCAGGCAG TTCCGTCACC AGCTACTCGA 420
 TCTGAGGCAC TTTCTAGTGT GTTAGATCAG GAGGAAGCTA TGGAAATTAA AGAACCCAT 480
 55 CCAGAGGAGG GGTCTTCAGG GTCTGAGGTG GAAGAAATCC CTGAGACACC TTGTGAAAGT 540
 CAAGGAGAGG AACTCAAAGA AGAAAATATG GAGAGTGTTC CGTTGCACCT TTCTCTGACT 600
 60 GAAACTCAGT CCCAAGGGTT GTGTCTCGG AGGCATCCAA AAAAAAAAAA AAA 653

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1486 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

5	GGCAGGCTGA CGACCTGCAA GCCACAGTGG CTGCCCTGTG CGTGCTGCGA GGTGGGGGAC	60
10	CCTGGGCAGG AAGCTGGCTG AGCCCCAAGA CCCCAGGGGC CATGGGCGGG GATCTGGTGC	120
15	TGGCCTGGG GGCCTTGAGA CGCOGAAAGC GCTTGCTGGA GCAGGAGAAG TCTCTRGCCG	180
20	GCTGGGCACT GGTGCTGGCA SGARCTGGCA TTGGACTCAT GGTGCTGCAT GCAGAGATGC	240
25	TGTGGTTCGG GGGGTGCTCG GCTGTCAATG CCACTGGGCA CCTTTCAGAC AACTTTGGC	300
30	TGATCCCCAT CACATTCTTG ACCATCGGCT ATGGTGACGT GGTGCCGGGC ACCATGTGGG	360
35	GCAAGATCGT YTGCTGTGC ACTGGAGTCA TGGGTGTCTG CTGCACAGCC CTGCTGGTGG	420
40	CCGTGGTGGC CCGAAGCTG GAGTTTAACA AGGCAGAGAA GCACGTGCAC AACTTCATGA	480
45	TGGATATCCA GTATACCAA GAGATGAAGG AGTCCGCTGC CCGAGTGCTA CAAGAAGCCT	540
50	GGATGTTCTA CAAACATACT CGCAGGAAGG AGTCTCATGC TGCCCGCANG CATCAGCGCA	600
55	ANCTGCTGGC CGCCATCAAC GCGTCCGCC AGGTGCGGCT GAAACACCGG AAGCTCCGGG	660
60	AACAAGTGAA CTCCATGGTG GACATCTCCA AGATGCACAT GATCCTGTAT GACCTGCAGC	720
65	AGAATCTGAG CAGCTCACAC CGGGCCCTGG AGAAACAGAT TGACACGCTG GCGGGGAAGC	780
70	TGGATGCCCT GACTGAGCTG CTTAGCACTG CCCTGGGGCC GAGGCAGCTT CCAGAACCCA	840
75	GCCAGCAGTC CAAGTAGCTG GACCCACGAG GAGGAACCAG GCTACTTTCC CCAGTACTGA	900
80	GGTGTGGGAC ATCGTCTCTG CCACTCTGTA CCCAGCCCTG AACAAAGCAC CTCAGTGCA	960
85	AGGACCAAAG GGGGCCCTGG CTTGGAGTGG GTTGGCTTGC TGATGGCTGC TGGAGGGGAC	1020
90	GCTGGCTAAA GTGGGKAGGC CTTGGCCAC CTGAGGCCCC AGGTGGGAAC ATGGTCACCC	1080
95	CCACTCTGCA TACCCTCATC AAAAACACTC TCACTATGCT GCTATGGACG ACCTCCAGCT	1140
100	CTCAGTTACA AGTGCAGGCG ACTGGAGGCA GGAATCCTGG GTCCCTGGGA AAGAGGGTAC	1200
105	TAGGGGCCCG GATCCAGGAT TCTGGGAGGC TTCAGTTACC GCTGGCCGAG CTGAAGAAGT	1260
110	GGGTATGAGG CTGGGGCGGG GCTGGAGGTG GCGCCCTCTG GTGGGACAAC AAAGAGGACA	1320
115	CCATTTTTC AGAGCTGCAG AGAGCACCTG GTGGGGAGGA AGAAGTGTAA CTCACCAGCC	1380
120	TCTGCTCTTA TCTTTGTAAT AAATGTTAAA GCCAGAAAAA AATAAAAAAA AAAAAAAAAA	1440

AACTCGAGGG GGGCCCRKAC CCAATCWCCC TATAGTAKAC GTANNN

1486

5

(2) INFORMATION FOR SEQ ID NO: 24:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2323 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

CTTCGCGGTT TCTCCTGCCA GGGGAGGTCC CGGCTTCCCG TGGAGGCTCC GGACCAAGCC	60
CCTTCAGCTT CTCCCTCCGG ATCGATGTGC TGCCGCGGCC GCGCCGCGG TCCCGCGTCC	120
TTGCGTCTCT GCTCCCGGA CCCGGCTCCG CGCAGCCAGC CAGCATGTGC GGGATCAAGA	180
AGCAAAGAC GGAGAACCAG CAGAAATCCA CCAATGTAGT CTATCAGGCC CACCATGTGA	240
GCAGGAATAA GAGAGGGCAA GTGGTTGGAA CAAGGGGTGG GTTCCGAGGA TGTACCGTGT	300
GGCTAACAGG TCTCTCTGGT GCTGGGAAA ACAACGATAA GTTTTGCCCT GGAGGAGTAC	360
TTGTCTCCCA TGCCATCCCT GTTAATTCCT GGATGGGGAC AATGTCCGTC ATGGCCTTAA	420
CAGAAATCCC CAGATGGCTT CATGGCCCC AAAGCATGGA AGGTCCTGAC AGATTATTAC	480
AGGTCCCTGC AGAAGAACTA AGCCTTTGGT CCAGAGTTTC TTCTGAAGT GCTCTTTGAT	540
TACCTTTTCT ATTTTATGA TTAGATGCTT TGTATTAAAT TGCTTCTCAA TGATGCATTT	600
TAATCTTTTA TAATGAAGTA AAAGTTGTGT CTATAATTAA AAAAATATAT ATATATATAC	660
ACACACACAT ATACATACAA AGTCAAACTG AAGACCAAAT CTTAGCAGGT AAAAGCAATA	720
TTCTTATACA TTTCATAATA AAATTAGCTC TATGTATTTT CTACTGCACC TGAGCAGGCA	780
GGTCCCAGAT TTCTTAAGGC TTTGTTTGAC CAGTGTCTTA GTTACTTGCT GAAAAGTGAA	840
TATATTTTCC AGCATGTCTT GACAACCTGT ACTCTTCCAA TGTCATTTAT CAGTTGTAAA	900
ATATATCAGA TGTGTCTCT TCTGTACAAT TGACAAAAA AAAAATTTTT TTTTCTCACT	960
CTAAAAGAGG TGTGGCTCAC ATCAAGATTC TTCTGATAT TTTACCTCAT GCTGTACAAA	1020
GCCTTAATGT TGTAAATATA TCTTACGTGT TGAAGACCTG ACTGGAGAAA CAAAATGTGC	1080
AATAACGTGA ATTTTATCTT AGAGATCTGT GCAGCCTATT TCTGTCACAA AAGTTATATT	1140
GTCTAATAAG AGAAGTCTTA ATGGCCTCTG TGAATAATGT AACTCCAGTT ACACGGTGAC	1200
TTTTAATAGC ATACAGTGAT TTGATGAAAG GACGTCAAAC AATGTGGCGA TGTCGTGGAA	1260
AGTTATCTTT CCCGCTCTTT GCTGTGGTCA TTGTGTCTTG CAGAAAGGAT GGCCCTGATG	1320

	CAGCAGCAGC GCCAGCTGTA ATAAAAATA ATTCACTA TCAGACTAGC AAGGCACTAG	1380
	AACTGGAAAA GACCACAGAA AACAAAGAAT CCAACCCCTT CATCTTACAG GTGAACAAAC	1440
5	TGTGATGATG CACATGTATG TGTTTTGTAA GCTGTGAGCA CCGTAACAAA ATGTAAATTT	1500
	GCCATTATTA GGAAGTGCTG GTGGCAGTGA AGAAGCACCC AGGCCACTTG ACTCCCACTC	1560
10	TGGTGCCCTG TCTACACCAG ACAACACAGG AGCTGGGTCA GATTCCCTC AGCTGCTTAA	1620
	CAAAGTCTCT CGAACAGAAA GTGCTTACAA AGCTGCCTTC TCGGATACTG AAAGGTCGAG	1680
	TTTTCTGAAC TGCACTGATT TTATTGCAGT TGAAAAAAA AAAAAGCTAT TCCAAAGATT	1740
15	TCAAGCTGTT CTGAGACATC TTCTGATGGC TTTACTTCCT GAGAGGCAAT GTTTTTACTT	1800
	TATGCATAAT TCATTGTTGC CAAGGAATAA AGTGAAGAAA CAGCACCTTT TAATATATAG	1860
20	GTCTCTCTGG AAGAGACCTA AATTAGAAAG AGAAAACTGT GACAATTTTC ATATTCTCAT	1920
	TCTTAAAAAA CACTAATCTT AACTAACAAA AGTCTTTTG AGAATAAGTT ACACACAATG	1980
	GCCACAGCAG TTTGCTTTA ATAGTATAGT GCCTATACTC ATGTAATCGG TTACTIONACTA	2040
25	CTGCCTTTAA AAAAAAAAC CAGCATATTT ATTGAAAACA TGAGACAGGA TTATAGTGCC	2100
	TTAACCGATA TATTTTGTGA CTTAAAAAAT ACATTTAAAA CTGCTCTTCT GCTCTAGTAC	2160
30	CATGCTTAGT GCAAATGATT ATTTCTATGT ACAACTGATG CTGTCTCTTA TTTTAATAAA	2220
	TTTATCAGAG TGAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	2280
	AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA	2323
35		

(2) INFORMATION FOR SEQ ID NO: 25:

40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 683 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:	
	GGCAGAGCC TGTGTGGTCA TGTTCTCGT GGTGCAGTAC CTGACATGAG CCAGCCACGC	60
50	TCAGTGGCTG AACAGCATTC CCACAGCTG CAAGTGTGTG TGTGTGTGAA AGAGAGAGGG	120
	GGGCCAGAG CCGCCTTTTG AAATGTTTGC CTGTCTGAAC TGTGAAGACA CTGGGAGTG	180
55	ATTGTGGTCT AATTTCCAAC CTGCTCTGTT TTCTGTGACA TCTTGGAGGG GAGCTAGTGC	240
	CACACCATGC GCGGTGCTTA GAAATGAAAA AGTCCCGGT CTGTCTCTCT CACTCTCGCT	300
	CTCATGGGGG AGGGAAGAA TGGCTTTGGT GGCTTTGTTT ACACAGCTGA TCGGTGCTGG	360
60	GAAGGTGTCC ACAGTGAGCC TGTGTGCAGG ACTGTCCACA CGGTTACAC TTGTCACCAT	420

CAGGCCTTTC TGGTCCTGAT AGGGTGGAGC AAAAGTGGAA AGGAAAGGAA AGAGGCTTTT 480
 CTCACAGCCA TTATATTAAA TAGTAGGTCG ATTCACATCT CGTGCTCCTG GCCACCTTCC 540
 5 CCTGTGCCCTC AGTGACATGT AGATGACTGA CTGCCAATAC TTGTCACCAT TCCCTGGAAG 600
 CAGCTACCTA GGGGAAACAA GATGTAGTGC TATTGCCGAT AACAAAGTAAG ATTTTCCACA 660
 10 CTAAAAAAAA AAAAAAAAAA AAA 683

15 (2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2036 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

25 CTGAGAAAGG AAAGCATTCG GATCTGCTGC AAAACACAT ATATCCATAA AGACTCATGT 60
 TATTTCAGAAA ACAGATTGTG AACACAATCA CATTGCGATG AATCCTTTAA AAGGAAGAAG 120
 ACCTTAAAGT ATCTGCAAAT CTGAATTCTT ATTTATTCCT TCACTGAATA TAGAAACAAT 180
 30 GGTATCTGA TTATTAGAGA TATTATTTTG GATATGTTAC TTATTAACIT GCTATGGCTG 240
 GTAACCATGA TAAAGTCTGT TATTAATAAC AACATAATTC TTTTTTTAAA GAAGAAAAGC 300
 35 TTATTTTTC TTAGCAGTGT ATAGATTAT CTACTTAGIT GGTGTTTGCT ATTAGTGTTT 360
 TAATTTTITT TTTAAGTTGA GTGTTTGATA AATTTTAAGA CCTGTGCCCC ACCTTGTTTT 420
 GAGTCCGTG TTAGCTACAG GTATATAGCY CAWTTTAAAA ATCCTAAAGC AAAAGAATTT 480
 40 TATTTATAAA AGAATCMAMC MGTGTCATGC ATGAGGCTGT GAAGTCAGAT ATTTAGTAAT 540
 AAAAGCAGCA GTGCCTTTTT TTGTATTTAC CCAITGACCC CCACCAAATG CAACTGTTTT 600
 45 ATATTAAGAA AATAGTAACA ATTTTAAAAT CTCAGAGTAA AATCTATTT ACTACATGCT 660
 TTTCCCCCT TGTCTGATT TAAGCAGTGT GTACTTGGCA TCTCTACATT GTCCTAGGGA 720
 CAGTGGTGTT CTACAATATT ATCATGTATG ATGTTTATT GGTGCTTTTT ATTCATAGTG 780
 50 GCTTCTTACC AGAAACAGTA GGAAGAAACA CATGAACTGT GTACAAGACA TGAAACATG 840
 CTGCTGATAT GTTGTTTTTT CACATGCTTT TGAGTTTTCA CTTTTTAAAC GAGAGCCAGC 900
 55 AAGCAAATA GATGTGGCTG GGTCTGCCTG TCCGGGCGGC TTTTTGCACC GAGCTCTCAA 960
 ATCCTGTGTA TTGAGGGTTC CTTTTTGTA CTCAGGATG GAGCTACAGC TGGGCCCCC 1020
 TCTCTCCAT TCGTTTGAAG AGACACTGAG GGAACAAGG GTTCTTTTG AGGTGTCCTT 1080
 60

	GGCTGCCTTT TACGGGATGG GAGCCTTCTC CGGATCTTTT GTTCTTCTGC ACCTCTTGTA	1140
	GCTACTGCCG GTGCAAGGTT GTAGATGTTA TTCCCCAGGA GCCTGGGCTK GGGGGCTGAG	1200
5	CTGGGCTGAA TGCAAAAGCA TGCAACCAGA AGGCGGGCAA GGGGAGGAAA AGCAGGCCTG	1260
	GCCTCATGGG TCCCCTGGAG ATGTCTGTAG CAGTCAGCTC CAGCTTGGGC CTGGGGAAGC	1320
10	AGCCTGACCA AGGCGCTCAG GTGTGCCTGT TACAAGAAGA ACCTGCAGAA GGATAATTTG	1380
	CACATGGAGC TGTGATAACA CTAATGTTGA TTTTTTTTTT TTTTACAAGT CATCAGRGAT	1440
	GTTTGCAAAG TGAGTTTTAT TTTTTTGTAA TTCTTTTATC TTTACTTAAA GGTGAATGTG	1500
15	TATTCCTCTG GGAGGAATAG GAAGAAAACA GGAATGTTAA TAATGTCGAA CAGAAAACCT	1560
	CCTCCCTTAT TAATATATAA TCYTATGTA TTTATGCCNT AATGTAAGCT GACTTTTAAA	1620
	AAGCTTCTTT TTGTTGCATG CCCTGTGCAG GCATCTGTAT TGTACATGCA TGCCTTTTCGT	1680
20	CCTGTTTTCC TGTATAAAGT TAGTGAACAA AGAAATATTT TTGCCCTAGT TCATGTTGCC	1740
	AAGCAATGCA TATTTTTTAA ATTTGTCATA TATGGAAAGA GCATGTTTGT TACATGTAAA	1800
25	AGCTTTACTG ATATACAGAT ATACTAATGT TTGAAGATGC TGTCTTTTGC AAGTGTACAG	1860
	TTTTCAAATG TTGTTACCAG TGAAACACCC TTGTGGTTTA AACTTGCTAC AATGTATTTA	1920
	TTATTCATTT CCTCCCATGT AACTAAGAAT CATGGCTATA TTTTCATATCA ACGTTATATT	1980
30	GAAAGTGAAG GGAAATGATT AATACAAGGT TTGTAACAA AAAAAANAA ANNAAA	2036

35

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 717 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

45

	GGCACGAGAT AACATAGGCA CAATAATACT GTATGTCTAC TTCTAGGATT ATAAGGAATT	60
	AACATGAGA TGACATTTCC ATTTGAGAAG AAAATAGTTG CTTTCAGTGC CTTTATTTG	120
50	ATTCTGAGAG AGAGCAGACT CGCACCAACA TTCAACCCCA GCGCTGATAT GACAGTAATC	180
	CTCAGAGGCA GAGCCCAGCA CAAAACAGCA ATGCTAGAAA GTTACAATTG GAAAGTTTCC	240
55	TGCCAGCTTC GGAATGACA CTGCAAGCT GATGCCAGAA ACTGCCAGAG TAATTCTCCT	300
	CATTACTGCT CTACCCACCC ACTTTCAGCT CCCCAAATTA ACTAGTGCAG TTGACTAATC	360
	CTCTTTACCT TTATCATTTA GGTGAGGCAT TGCACAAAAA CTCTCGACTT TGCCATATAA	420
60	GGGCTGTGGT TCTCTGTGGT CCTGGATAAG AGGCATCACC ATTATCTGGA AACATGCAGT	480

5
 10
 AAATGCAGAT TCTTCATCTT CTCGCCAGAC CTCCTGAGTT AGAAATTCAC AAGTTCTCCA 540
 GGTGATCTCA TACATGCTAA AGTTTGAGAA CCATTGAGTA AAGTTAATGC ATTAAGAAGA 600
 GATTAGATAG GGATGGTGGC GTATCTTCCT ACAGTTTCCC TGTTAACAAG AAAGTCAGAG 660
 GTCAGTTGAT CAGACATTAG ATTATTTATT GCTAAACTA AAAAAAATTA AAAAAA 717

(2) INFORMATION FOR SEQ ID NO: 28:

15
 20
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 495 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

25
 30
 35
 40
 GAATTCGGCA CGAGCAGCAT CCTAATTTTA GTTTGGAGAT GCATTCTAAA GGATCTTCTC 60
 TATTGCTTTT TCTCCACAA TTAATCTTGA TTCTGCCTGT CTGTGCACAT TTGCATGAGG 120
 AACTGAACTG TTGTTTTCAT AGGTAAATGA GAGACTGAGT TTTTTCATT CTGAAGAGAA 180
 AGGGCATTTG CTCCTACAAG CTGAAAGGCA CCCCTGGGTG GCTGGGGCCC TCGTGGGAGT 240
 TTCTGGGGGA TTGACCCCTA CAACATGCAG TGGCCCTACA GAAAAACCTG CAACTAAAAA 300
 TTATTTTTTA AAAAGGCTCC TCCAGGAAAT GCATATAAGG GCTAATCACC CAGTATTTTG 360
 ARGCTTCGAA GARGTAATAR AMCCCTGGAG AGAGAACTG AGACATGTAA GAGGGTGGGA 420
 ATGACTCAGT GGTGGCACAC TATGGAGTCC TGCCCAAG TAGCACACAT CAACCCACTA 480
 CACAGAAATC CTAGG 495

(2) INFORMATION FOR SEQ ID NO: 29:

45
 50
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 556 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

55
 60
 AGCTTAACGT CATGATTCAT TAGGGGAATG CAAGGCAAAA CCATGATGAG AATGCCCTTA 60
 GACACCTCTT AGAAGAGCTG CTAGAAAGGC AGACAGCACC AAGCGCTTAA ATGAGATGGG 120
 GGCACGGTG CTTCTTCTGT GCCTACTGGT AGGGGTGCAG CAGAGTGGTT CAGTCTGGGA 180
 CAGTTAGCTG GACATCACGT GGACCAACA CACGCATTTC CTGGGTACT TACCAAGGAG 240

AATAGAAAGC AGGCAGATCT TTACAGCAGC TCTTACCTGW TTGCAAAACA ATGGAAATGC 300
 CCACATGTCC ACAAACAAGT KTGTGGTCTG CCTGTGCCAT GAAGCACAGT GTGGCTGAGC 360
 5 GTCAAGAGTC CCCACACTCA AAGGAGGCAG CAGATACAGG GCTGCACACT GTGTGATTCC 420
 ACACATGTGA CATTTCTGGAC ACGGACATGC TGGATGGCAA AACGAGCATC GGGCTGAGAG 480
 10 GACTGCTGAG AAGGGGAACG GGGCTGCTGG GATGTGGGTT GATTGTAGCA GTAGCTCATG 540
 GAGATGTGAC CTCAA 556

15

(2) INFORMATION FOR SEQ ID NO: 30:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 434 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

CTAAATGGTG ACTGTGGCTT TGTCGAGACA GGCCCCAAAT GGTAGGTGTG AACACAACAT 60
 GCACAGAATG AGGAGACATG CAGAGTGCTG AAATACTGTC CTGGACAGAT GTGTTACATG 120
 30 ACTTTCTTTT CAGCTTATTT CTGTGGCCTG CCTTTGAAGA TAGAGCTTTG TTGATATTTA 180
 CATTAAACCA AATTGTATAA YTATGTTCCA TTCTGACATG TTATTTAGCA AARGAAAAAR 240
 35 GAGTAATTCT ACATCAGCAT CTTTAGTGCA TGCTAAAAGA TTAAAAATGT CTTTGGGGA 300
 ACATGTTTTG TATACATAAA TGTTTAGATA GAAATATTTA TAGAATNCTC TATGTGAGTA 360
 TTNATCTCCC TATGTATATT TATATCTAGA TGTGTCAATC TTTGTATTGA TATGAAATGC 420
 40 TATGAATAGT GAGA 434

45

(2) INFORMATION FOR SEQ ID NO: 31:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 715 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

CCACGGGTCC GATCTCACAG CTCCGACACT ATGCGAGCC ATACACAACC TGGTGTGAGG 60
 AAACGTACTC CCAAATAAG CCCAAGATGC AAAGTTTGGT TCAATGGGGG TTAGACAGCT 120
 60 ATGACTATCT CCAAATGCA CCTCCTGGAT TTTTTCGAG ACTTGGTGTT ATTGGTTTGG 180

CTGGCCTTAT TGGACTCCTT TTGGCTAGAG GTTCAAAAAT AAAGAAGCTA GTGTATCCGC 240
CTGGTTTCAT GGGATTAGCT GCCTCCCTCT ATTATCCACA ACAAGCCATC GTGTTTGCCC 300
5 AGGTCAGTGG GGAGAGATTA TATGACTGGG GTTTACGAGG ATATATAGTC ATAGAAGATT 360
TGTTGAAGGA GAACTTTCAA AAGCCAGGAA ATGTGAAGAA TTCACCTGGA ACTAAGTAGA 420
10 AAACTCCATG CTCTGCCATC TTAATCAGTT ATAGGTAAAC ATTGGAATC CATAGAATAA 480
ATCAGTATTT CTACAGAAAA ATGCATAGA AGTCAGTATT GAATGTATTA AATTGGCTTT 540
CTTCTTCAGG AAAAAGTAGA CCAGACCTCT GTTATCTTCT GTGAAATCAT CCTACAAGCA 600
15 AACTAACCTG GAATCCCTTC ACCTAGAGAT AATGTACAAG CCTTAGAACT CCTCATTTCT 660
ATGTTGCTAT TTATGTACCT AATTAAACC CAAGTAAAA AAAAAAAAAA AAAAA 715
20

(2) INFORMATION FOR SEQ ID NO: 32:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 486 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

GAGCCAGTGC CGGCGAAAGG GGACCTTCCT CTACTTCCTG CCACAGACCC TGTCCCCACA 60
35 CACTTCCTGC CCCTGCTCTG CTGGGAGGCC ACTTCCTCCC CCAGTGCTGG ATTCCACCCC 120
CAGCTCACCC TCAAACATGG CCCCCTCTCT CCTCTGCTT GCCCTCTCT GCTCCCTGGA 180
40 GGCTGTTCTG TCCTCCCCTC TTGAAAAGCA ATGCCAGCTT CCTGGGATCT TCTGCCAACT 240
CCAGCTACCA TGCCCTTTGC TCCTGTGAGC TCAGCTCCTC AAGGGAATTG TCTAMCCTCG 300
GTGTCTGCT TCCCTCCCTC AACCTCCTCA CCTGCTCCA AGCTGGCATC TGCCCTCCA 360
45 CTGCACAGAA CGGNTCCCC ACCACCTGCC TTTACAGGA GGAAGCAGCA ACATGGAAGA 420
ANCGAACTAT AGGGGCTACA ANGATGCTCA GCTCTGATCC CGAAGGCAAA AAGNATCTTT 480
50 GGGCAC 486

(2) INFORMATION FOR SEQ ID NO: 33:

55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 725 base pairs
(B) TYPE: nucleic acid
60 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

5 GTTCCTCTGG TAATAATTAG GTTATTCOCA GAAGCACAGT GTCATTCTTT AAATAAAAGC 60
 TTTCCTGTTT AAAGCTTTTC AAAGGAGCAG ACCACCTTGA AGATTCCCC TAGGGTTGAT 120
 ATGTGTCTAA TTCATTTTAT AAAAATTATT CTGTCTTCA TTTTAAAGCT TTGGCTATAT 180
 10 AGTCAGAAAT GTCCTAAATA ACAAATATT TTGTATTTAA TTTAGGGAAG ACTAAAGGGA 240
 AGAAAAATGA AAATCAGTC TTTATGTAAG CTCCAAGGAT ATTAGGGCTT AAAGGGCTTT 300
 15 TCTAGTTTGA TGAGAATTG TACTACTGAT TTTTATATAT TCCTGTTTTT GATGAACAGA 360
 TCTCTGGGGA AATTGTTGAG TTACAATGGC ATTTCACTGT GATCCCTCTC AAGCTCAGAT 420
 CAGTCTATA ACCCAATGAC AACCTGTCTC TTTGGTTTAC TGTCCTGTGA AATGTCAGCT 480
 20 CAAGTTTCCC AGAAGTCGTG TGTTATGAT GAGTCAGAGT GCTTTTCCTC GGTGGGACAG 540
 TTGCTGGCCC TCTTAATTTT GGTGTATGTG CTTCCAAGTA TCTAAACCTC CAGTCTGATC 600
 25 TGTATATGCT ATCCTAACTG TTAATTGTAT TATTGATTAT GTTGATTATC TTGCTTGAAG 660
 GTTCATACTT TTCAATTGTA TAGAAATAAA GTTTTTTCT GCTTATAAAA AAAAAAAAAA 720
 AAAAA 725

30

(2) INFORMATION FOR SEQ ID NO: 34:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 437 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

CACACAGCAT GCTGCCCTCA GACGTGTCCA TCCTGTACCA CATGAAAACG CTGCTGCTCC 60
 45 TGCAAGATAC TGAGAGATTG AAGCATGCTC TGGAAATGTT CCCAGAACAT TGCAAGATGC 120
 CTCCTGCTTT TATTGGCTCT TGTCGAAATC AAATTGGAAG ATCTTCAGTC CCAGCTGCAC 180
 50 CCAACGTGGA AAAGTATTCC AGGTCCATCC CCAAGGAACC AACACCGATG ACATGGACTC 240
 AGGAATCTTA TAACCTACGT GGACTCTTTC CATCCGTACA TTGTCGTGCA CATGCCACTC 300
 ATCACCTGGC GTGCCCAGAT CCTCGCARGG CAACACCCTG TGATAATTCC AGGTGATTCT 360
 55 CTACATCTGC AGCTTGAGGT TAGCCTCATA TCACATTACA TTCTCACTAN AAACNAAAAA 420
 AAAAAAAAAA AACTCNA 437

60

(2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:
- 5 (A) LENGTH: 943 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

GGCACGAGCT GGAACAGAGA CTAAATCCCA CGAAACTGAC ATTGTTAAAC AACTAAAAAC 60
AGAAGTACTT ACCTCTTGAA GATTTAATAT ATAATGGTTG ACATGATACA TGTACATGAT 120
15 GAATGACCAG ATGCTTATGG TCTACATTTT CCTTTATCCT GTTAGTATTA CCTTCCTTAA 180
TCTTGTGTTCA TTAACATGCT AATTCCTCTT CAGTGTTTAT TTCTAGTGA CAGAATGCTA 240
20 ACATTTCTTA CACCCCTGGCA GAAGGGAGAG AAATGTGTTT TGGGGTGGGT AACTAAATTT 300
TTGAGTGAAA TATCATAAGA TGANAATGA AANAAGGAGA CACAAANAGT TATNACAAAA 360
AAACAATGGT TTTTTTAGCC ATTGACTGG CTCTTTAAAT AGTCTACAAG ACATTCACGT 420
25 TTAACATCAC TTTTAGTGAA ATAAAATGTG CCATACTAGT ATGTGCTTCA AAAGGGCAAA 480
TGTGCTTTAG TGCCCTAAGG CTAAATTTTG GTCATTTGAC ATCAGAGATG TTGTAAGTAT 540
30 TGCACCTAAT ACGCACCTAT TTNICAATAG TGTTATTTT TGGNTAGCAT TTTTTTTACC 600
ACTATNTTGT TGATAGCTTT TTGTTCTNIN AGGTTGNAAN ATGACAGTGC TNATNCAAA 660
CAGATTACCC ATNTGCAGAA CTAAGGGAAG CNATTTATGT ATGAAAGNAA TTNITGAATT 720
35 NGTCATTNFC AACCNITGNA TTAAAGCTTA GACTAAATAG TAATATATNG TGGGNAGGAT 780
TTTGGTTTTG TGATATTTNT GTGNATTAAG GNATAGATGT TAACNITAT TTTGTAGNAA 840
40 AGTGANITGT ATGTGGITAA TTATAATAA AACTGGTACC AGNAAAAAA AAAAAAAAN 900
NAAAAAAAA AAAAAAAAA AAAAAAAAA AAAAAAAAA AAA 943

45

(2) INFORMATION FOR SEQ ID NO: 36:

- (i) SEQUENCE CHARACTERISTICS:
- 50 (A) LENGTH: 604 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

GGCACGAGAA ATCTTCATGC TGTAAGTCACT CCAGACCATG GAGTGGCTTT CCAGCTGAAT 60
GAATCCTATG TCTCGCGTGC AGGTGGTTGG TTTTCAATGT TCTTGCTAAT TTTTTTTCTA 120
60

TTGGATCTTG GGAGTTTCT TGTGTTGCTC CTGTGTTTGC CCAGCTTTAA TAAAACCAGG 180
 CGCAAACAAA AACCATAGCA TTCTGAACAA TAGGGGGGCC ACATTGGACC CAGTATGTCA 240
 5 CTTTAATGGA CTTCAAGAAA AAATCTGAAT GGGAAAAATG ACACTAGGAA TGTATACTCC 300
 ACACATTTTA TGCCATATAA TGGTGTGTTT TCTTAATTTT GTTCTGTG GCGAAATGTG 360
 GCTTTCAAAT TAAATGACC TTTTCTTCTT TGAAACTTTT TGTTTTGA CTGTATAATTA 420
 10 AGGGTTTGA AAGATTCATA ATTCTGAGAG AGGTTTGCAA CCAGGAGATA CAAAGAAGTC 480
 TCAGTAGTAA TCTGTTCAT GTGCTTTTAC AGCCAGCTAC ATTTAAGGAT GTATTAGTTA 540
 15 CAGAAATTAT ATGTCTGTGT ATGTGTCTCT ACTCAATAAA GTACATGCCT CCACAAAAAA 600
 AAAA 604

20

(2) INFORMATION FOR SEQ ID NO: 37:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 349 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

GTGAGTGCCC GGGAGCCCG AGGCCCTGCC CCTAAGAAGG ATATCTYTRA CGCTCCCTT 60
 GTCCACACCC TAACCCCCCA GCTGCTCAGG CAGTGGGCAC ATGGCAGGGG CCTCACTGGG 120
 35 GGCACATAGA GCATTTGGGG GACTGCGAGT GCTCACCTTT GACTTCCTGC AGGTCGGGGG 180
 AAAACCAGAT CATGATGACC AAAGTYTACA TATCTTGAT CTTTCATGGT CTGATCCTGC 240
 40 CCTCCCTGGG TCTCACCAGG TATATGCCAC CACYTTCGTG TCTAAATTCA GAATAAGAGT 300
 CACATCAGGA GAGCACTGTC CCCAGGANAA TGCAAACGGG TTGGCAGCA 349

45

(2) INFORMATION FOR SEQ ID NO: 38:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 672 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

GTAGTCGTTG CGGTTGCCCG GATGGCGAAG ATCTGCCCGT TTGAAGTCGT AAAACGCACC 60
 TCGGTACCGG TGCTGTGTGG TTTGGTGATT GTWATCGTTG CTACAGAGCT GATGGTGCCA 120
 60

GGAACGGCAG CAGCGGTCAC AGGCAAGTAA ATAGTAATGC CGGAGCAAGT TTCTTCCGGC 180
 TTTATCATGT CACCCACTGT GGTATATGCG TTGTGGTCTG CCAACTTTGC CGTGAACAAT 240
 5 TTCAGCAATA ATCAGATGGC GGCTGGCGCA ATATTCAAGA TAAAGCCTGG CAGTGGTGGC 300
 GCTGATGGTT CAGTGCCTGC GSCACCGTTT YTGCCGTATG TTGCACACCA GGNTCTTTAA 360
 ACAGTTTTTCG SACCOCGTTC AGCGTCAAGG GTTCAATGCC GGTCCGTAGC TCGTCCTTAG 420
 10 GTTCACCCCG AGCATAAGCA TTAAACATCT CATCAATTTC CTCTGGCTG GCGCTATCAA 480
 TACTTCCAG CATATGTTTA CGCTGGCGGA AACGGGTTAG CGTTTGCCCC ARCMGWTCTAT 540
 15 AGGCAATGGG CTTAATGAGA TAATCAAATA CACCACAACG TACGGCTTCA GACACCGTTT 600
 CCATATCGCT GGCTGCAGTG GTAAACACCA CGTCGCCGGG ATAATGCCCC TGCACCAGTT 660
 CATGCAGTAA AT 672
 20

(2) INFORMATION FOR SEQ ID NO: 39:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1908 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

AGAGTTGATA TTTTGTAGAA CAGTAATTTT ACTTTTAAGG AAATTGGCTA GCTCTTTGAC 60
 35 TNNAGAGCTG TAGGAAGCTC AACATTTCTT TGTAGAGAAC GTTGCTTTTT TTGGATTGTA 120
 CAGGTATAAA AACATTGCTT TTGTTGAATT GTATAGGTGT AAAAAGGGAA TAACTGTATG 180
 40 CAGGTTTGAA AAGGAAATGT GCTTTAGGCA TGAGTCATAA GATGCCATTG TACTTGTAGG 240
 CATTTTATTT TCCTTTAGAA ATGGACATCA GCTCTTCTCT TCTGACTGGT AACACATAGC 300
 CCCAAAGCAT GAGATTATTT TTCATTGGGT TTTTATGTT GTTTAGTTT GGTTTGTTAC 360
 45 GCCAGCCCG TCTGTCTGCG GAACACTGAC TCTGCTCTCT AATGAGAACA AAGTTAGAAA 420
 TCTGCCGATA ACCTAAAATA ATTTAGAAAT GAATTAAAAA TGTGAAATCG GGTAAAGTG 480
 50 ATGATGATAA AATAGCATGC AAGAAACAAG CTCCTTCCAT CAGACTTGGC TACTGTTTTT 540
 TTCTGGTACG ATTTGGTTTG GAAGAGCTC TTGTTTCCTT CTCTTTGGGG TATGCTTTCG 600
 TTCTTAATA TGTTTGTAAC ATTATTGAGA TATAATTCAC ATACCTTACA ATTCACTTAT 660
 55 TTAAAGGGTA CAATTTAGTG GTTTTATAGT TATTCACAAA GTTGTGTAAC CGTGACCACA 720
 GTCAATTTTA GAACATTTTC TTACCCCAAA AAGAAACCCT GTACCCTTGA GCAGTCACCT 780
 60 CTCATTTTCT CCCAGTGCCC ACCCATCCC CGAGCCCKG GAACCACTAA TCTATTTCTC 840

5 TCTCTGTAGA TTTGCTTATT CTGGTCATTT CATATAAATG GAATTCCTACA ATATTCCGGTC 900
 TTTTGGGACT GGCTTCCCAA ATATGATTTT CTATATGGAG TGAGAAAATT CTTCTCATCT 960
 TGAGAACTCT TATTGCTGTG AAAGGGAGTG GTTGGTAAAA TCAATAGATT TCAGGCAAGA 1020
 GGGCCAGATA CCTAACAGGT TTTTCTCCGT GAATCTTATG CTGAGTAGTT TTTCTCATA 1080
 10 ACCAAGCATT TATGATATAT TACTACTTAT AATACTGTGG CTAGTCTCTA GAATGGATGT 1140
 TGAAATCTTT GCCTCCTCAG TCGGGAAGAG TCCTGCTAAA AATCAGGCTA AAAATCAGGC 1200
 CAAAAATCAG GCCAAATGAC TTGGCAAATA ATTGACAAAG TGGTTTTCAC GTGTGTCTAT 1260
 15 CTTTGCTAGC AGCTTGTATA CCTCAGGCCA GGTGAGCTCC CCAAATTTCT TTTTTCATTT 1320
 ACTCCAGTGA GTTCTGCTG TCTTTTTCAA GTATGTACCA TAGGACTTAA AGGTGATTTG 1380
 20 GATGCGTTGT AACACTGCTA AATATGCTAA GTACAGAATT TTATCTACAG TACTGTGAGA 1440
 CAGTCAATTA TTGCCTAGGG TAGTTCAAAA ATATGATGTG AGCTAGTTAA GCCTTTGCTT 1500
 GACTGATTTT AGTGATATTC AGAAGTGTGT ACCAATCAAG GCTCTTTAAA ATACGGAACG 1560
 25 ACTCACTTAA TAACCAGGGA ACCAGCCAAA TACTGTGCAG CCGCAGAATA TGCATATCAA 1620
 TGAGTTGGAG GTGATTATTC TCTGTAACCT CCTAATGATT GTTTTCTAAG CATTGTGGCT 1680
 30 TCTCAGTGGC TTGACAGCAT CTTCTGGT GTATGTGGCC TGTTTACATG ATGTATTGAA 1740
 TAATGTTGTT TGTGTGAGC ATCAATGCCT GTAACACCAA ACTAAACAG TGTTTTGGG 1800
 ATATGTTTCC AATCTTTAAA TGACCTTGCC CTGTCCAATA AATAAATGAT TGTCTCACCC 1860
 35 TGTTAAAAA AAAAAAATT AAAAAACTG GNGGGGGGC CCGGTACN 1908

40

(2) INFORMATION FOR SEQ ID NO: 40:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 458 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

CCTCAAAAAA AAAAANGAAA GGAAAGAGGT CTCTACACAA GCCCGTGATT CTTCATGGCA 60
 AGGGATAACA TCAGAAATGT TTCATTYCK GCTATTAGTT TCCATTCTT TCCCCATCCA 120
 55 GGCATAAAGA GAAACAAAAG ACAATGATGG TATCTCTGT GTCCTCAGCT TTGGCACTTT 180
 TGTGTGATTT GCTAAGGAGC AGTGACCTTG CTAAAAAGAC TGAATAATCC ACCCACTGAA 240
 60 TAGCTAACCT GGGGAGGAAA TGAAAATTTT CTTTGTGGAT CTCCTCAAAT CCATTGTTGT 300

	CACCAGGCCC TCCAGAAC TCCTCAGTTC CTTACAGTG CAACCTGTG TACTTGCCCC	360
	GCAACCCAAT AGTATTGTGC CTCATTTCAC CTTCCATGGG CAACTGCCCT CCCTTCTGGA	420
5	CATAAAACCT CATATTTTAA ATNAAGTTGA AATTTGAA	458
10	(2) INFORMATION FOR SEQ ID NO: 41:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1153 base pairs	
	(B) TYPE: nucleic acid	
15	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:	
20	GGCACAGAGC CTCGACCCA GGTGGTCTGG AGCCTGCCGG GAGAGTGGTG GCATCTGAGA	60
	GGCTGGTCGT GGACTGTGGT TGGGGGAGGT GGGAGCTGTT TTAACCGTGT GCCCCCTCTC	120
	CTGTGCCGGC GTGGGCATCC CCCGGGGCAG TGGAAACCCG GCGCTCCTCC AGCTTCCGAG	180
25	TCCAGCCAGC CTGGGCGGGG GCGCGCCCCC GAGACACCCG AGGAGTCCGT TCCTCCCTGG	240
	TTACGTGGAC TGTGGAGCTG GTCTCTTGTG GCTCAGCGCC GTGCGGAGGT TGAAGCGTAC	300
30	CTGCGGAGGT CGCACCAGGG CGTGAGGAGG AGGAGGAAGG GCATGAGCCG AGCTTGAGGA	360
	ATCCGTGCTC CAAACTCTAC ACTCAAGGAT GCACTGCGCA ACTCTGGTGG CGATGGGCTG	420
	GGGCAGATGT CCTTGGAGTT CTACCAGAAG AAGAAGTCTC GCTGGCCATT CTCAGACGAG	480
35	TGCATCCCAT GGGAAGTGTG GACGGTCAAG GTGCATGTGG TAGCCCTGGC CACGGAGCAG	540
	GAGCGGCAGA TCTGCCGGGA GAAGGTGGGT GAGAACTCT GCGAGAAGAT CATCAACATC	600
40	GTGGAGGTGA TGAATCGGCA TGAGTACTTG CCCAAGATGC CCACACAGTC GGAGGTGGAT	660
	AACGTGTTTG ACACAGGCTT GCGGGACGTG CAGCCCTACC TGTACAAGAT CTCCTTCCAG	720
	ATCACTGATG CCCTGGGCAC CTCAGTCACC ACCACCATGC GCAGGCTCAT CAAAGACACC	780
45	CTGCCCTCTG AGCGTCGCTG GATCTCTGGG AGCTCCTTGA TGGCTCCCAG ACCTTGGCTT	840
	TTGGGAATTG CACTTTTGGG CCTTTGGGCT CTGGAACCTG CTCTGGGTCA TTGGTGAGAC	900
50	TTGGAAGGGG CAGCCCCGCG TGGCTTCTTG GTTTTGTGGT TGCCAGCCTC AGGTCATCCT	960
	TTTAATCTTT GCTGACGGTT CAGTCTGCC TCTACTGTCT CTCCATAGCC CTGGTGGGGT	1020
	CCCCCTTCTT TCTCCACTGT ACAGAAGAGC CACCAC TGGG ATGGGGAATA AAGTTGAGAA	1080
55	CATGAGTTTG GGCTGAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1140
	AAAAAAAAAA AAA	1153
60		

(2) INFORMATION FOR SEQ ID NO: 42:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1983 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

	GGCACGAGAG GGGCCGAGCC GACAAGATGT TCTTGCTGCC TCTTCCGGCT GCGGGGCGAG	60
15	TAGTCGTCCG ACGTCTGGCC GTGAGACGTT TCGGGAGCCG GAGTCTCTCC ACCGCAGACA	120
	TGACGAAGGG CTTGTTTTA GGAATCTATT CCAAGAAAA AGAAGATGAT GTGCCACAGT	180
	TCACAAGTGC AGGAGAGAAT TTTGATAAAT TGTTAGCTGG AAAGCTGAGA GAGACTTTGA	240
20	ACATATCTGG ACCACCTCTG AAGGCAGGGA AGACTCGAAC CTTTTATGGT CTGCATCAGG	300
	ACTTCCCCAG CGTGGTGCTA GTTGGCCTCG GCAAAAAGGC AGCTGGAATC GACGAACAGG	360
25	AAAAGTGGCA TGAAGCAAA GAAAACATCA GAGCTGCTGT TGCAGCGGGG TGCAGGCAGA	420
	TTCAAGACCT GGAGCTCTCG TCTGTGGARG TGGATCCCTG TGGAGACGCT CAGGCTGCTG	480
	CGGAGGGAGC GGTGCTTGGT CTCTATGAAT ACGATGACCT AAAGCAAAAA AAGAAGATGG	540
30	CTGTGTGGC AAAGCTCTAT GGAAGTGGG ATCAGGAGGC CTGGCAGAAA GGAGTCTGT	600
	TTGCTTCTGG GCAGAACTTG GCACGCCAAT TGATGGAGAC GCCAGCCAAT GAGATGACGC	660
35	CAACCAGATT TGCCGAAATT ATTGAGAAGA ATCTCAAAAG TGCTAGTAGT AAAACCGAGG	720
	TCCATATCAG ACCCAAGTCT TGGATTGAGG AACAGGCAAT GGGATCATTC CTCAGTGTGG	780
	CCAAAGGATC TGACGAGCCC CCAGTCTTCT TGGAAATTCA CTACAAAGGC AGCCCAATG	840
40	CAAACGAACC ACCCCTGGTG TTTGTTGGGA AAGGAATTAC CTTTGACAGT GGTGGTATCT	900
	CCATCAAGGC TTCTGCAAAT ATGGACCTCA TGAGGGCTGA CATGGGAGGA GCTGCAACTA	960
45	TATGCTCAGC CATCGTGTCT GCTGCAAAGC TTAATTGCC CATTAATATT ATAGGTCTGG	1020
	CCCCCTCTTG TGAAAATATG CCCAGCGGCA AGGCCAACA GCGGGGGGAT GTTGTITAGAG	1080
	CCAAAAACGG GAAGACCATC CAGGTTGATA ACACTGATGC TGAGGGGAGG CTCATACTGG	1140
50	CTGATGCGCT CTGTTACGCA CACACGTTTA ACCCGAAGNT CATCTCAAT GCCGCCACCT	1200
	TAACAGGTGC CATGGATGTA GCTTTGGGAT CAGGTGCCAC TGGGGTCTTT ACCAATTCAT	1260
55	CCTGGCTCTG GAACAACTC TTCGAGGCCA GCATTGAAAC AGGGGACCGT GTCTGGAGGA	1320
	TGCCTCTCTT CGAACATTAT ACAAGACAGG TTGTAGATTG CCAGCTTGCT GATGTTAACA	1380
60	ACATTGGAAA ATACAGATCT GCAGGAGCAT GTACAGCTGC AGCATTCTCG AAAGAATTCG	1440

TAACTCATCC TAAGTGGGCA CATTTAGACA TAGCAGGCGT GATGACCAAC AAAGATGAAG 1500
 TTCCCTATCT ACGGAAAGGC ATGACTGGGA GGCCCAACAAG GACTCTCATT GAGTTCTTAC 1560
 5 TTCGTTTCAG TCAAGACAAT GCTTAGTTCA GATACTCAAA AATGCTTCA CTCTGTCTTA 1620
 AATGGACAG TTGAACITAA AAGGTTTTTG AATAAATGGA TGAAAATCTT TTAACGAGA 1680
 CAAAGGATGG TATTTAAAAA TGTAGAACAC AATGAAATTT GTATGCCTTG ATTTTITTTT 1740
 10 CATTCACAC AAAGATTTAT AAAGGTAAAG TTAATATCTT ACTTGATAAG GATTTTAAAG 1800
 ATACTCTATA AATGATTAAA ATTTTATAGAA CTTCTAATC ACTTTTCAGA GTATATGTTT 1860
 15 TTCATTGAGA AGCAAAATTG TAACTCAGAT TTGTGATGCT AGGAACATGA GCAAACTGAA 1920
 AATTACTATG CACTTGTCAG AAACAATAAA TGCAACTTGT TGTGCAAAAA AAAAAAAAAA 1980
 AAA 1983
 20

(2) INFORMATION FOR SEQ ID NO: 43:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1406 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

ATGATGATGA CTTTGAAGAC GATTTTATTC CTCTTCCTCC AGCTAAGCGC CTTGAGGTTA 60
 35 ATAGTTGGAA AAGACTCTAT AGATATTGAC ATTTCTTCAA GGAGAAGAGA AGATCAGTCT 120
 TTAAGGCTTA ATGCCTAAGC NCTTGGTCTT AACTTGACCT GGGATAACTA CTTTAAAGAA 180
 40 ATAAAAAATT CCAGTCAATT ATTCTCAAC TGAAAGTTTA GTGGCAGCAC TTCTATTGTC 240
 CCTTCACTTA TCAGCATACT ATTGTAGAAA GTGTACAGCA TACTGACTCA ATTCTTAAGT 300
 CTGATTGTG CAAATTTTTA TCGTACTTTT TAAATAGCCT TCTTACGTGC AATCTGAGT 360
 45 TAGAGGTAAA GCCCTGTTGT AAAATAAAGG CTCAAGCAAA ATTGTACAGT GATAGCAACT 420
 TTCCACACAG GACGTTGAAA ACAGTAATGT GGCTACACAG TTTTTTTAAC TGTAAAGACA 480
 50 TCAGCTGGCT CTTTAATATA TGACTAAACA ATAATTTAAA ACAATCATA GTAGCAGCAT 540
 ATTAAGGTT TCTAGTATGC TAATATCACC AGCAATGATC TTTGGCTTTT TGATTTATTT 600
 GCTAGATGTT TCCCCCTTGG AGTTTGTGCA GTTTCACACT GTTGTCTGGC CCAGGTGTAC 660
 55 TGTGTGTCG CTTTGTAAAT ATCGCAAACC ATTGGTTGGG AGTCAGATTG GTTCTTAAA 720
 AAAAAAAAAA AAAACGACAT ACGTGACAGC TCACTTTTCA GTTCATTATA TGTACCGAGG 780
 60 GTAGCAGTGT GTGGGATGAG GTTCGATACA GNCGTATTTA TTGCTTGTCA TGTAAATTAA 840

5 AAACCTTGTA TTAACTCTT TTCAATCCTT TTAGATAAAA TTGTTCTTTG CAAGAATGAT 900
 TGGTGCTTAT TTTTTCAAAA ATTTGCTGTG AACAACTGA TGACAACAAG CAACATTTAT 960
 CTAATGAAC ACAGCTATCT TAATTGGTT CTCAAGTTT TCTGKTGCAC TTGTAAAATG 1020
 CTACAAGGAA TATTAATAAA ATCTATTCAC TTAACTTAT AATAGTTTAT GAAATAAAAA 1080
 10 CATGAGTCAC AGCTTTTGT CTGTGGTAAC CTATAAAAA AGTTTGTCTT TGAGATTCAA 1140
 TGTAAGAAG TGAAAACAAT GTATATGTTG TAAATATTG TGTGTTGTA GAAATTTTG 1200
 TCATAAGAAA TTAAAAGAAC TTACCAGGAA GGTTTTAAAG TTAGAAATAT TCCATGCCAA 1260
 15 TAAAATAGGA AATTATAAT ATATAGTTT AAGCCTGCAT CAGTGGGAGT CTGGCTATG 1320
 TAGTTATGTA GTTATTATGN AACCACCAAG ATTTTGTG CTATTACCG TAACCAAAGG 1380
 20 GGCCGATTAA NTGGTTTGAA GNCTTG 1406

25 (2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 1391 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

35 GGGCCTGAAG GCGGCRGCGC AGTCCCAGAG AGTGCTCGCT CCTGCTCGGG GCGCTCGGGC 60
 CCCGGGCGTC GCCATGACCA GTGAGCTGGA CATCTTCGTG GGAACACGA CCCTTATCGA 120
 CGAGGACGTG TATCGCCTCT GGCTCGATGG TTAATCGGTG ACCGACGGG TGGCCCTGCG 180
 40 GGTGCGCTCG GGAATCCTGG AGCAGACTGG CGCCACGGCA GCGGTGCTGC AGAGCGACAC 240
 CATGGACCAT TACCGCACCT TCCACATGCT CGAGCGGCTG CTGCATGCGC CGCCCAAGCT 300
 45 ACTGCACCAG CTCATCTTCC AGATTCCGCC CTCCCGGCAG GCACTACTCA TCGAGAGGTA 360
 CTATGCCTTT GATGAGGCCT TTGTTGCGGA GGTGCTGGGC AAGAAGCTGT CCAAAGGCAC 420
 CAAGAAAGAC CTGATGACA TCAGACCAA AACAGGCATC ACCCTCAAGA GCTGCCGGAG 480
 50 ACAGTTTGAC AACTTTAAAC GGTCTTCAA GGTGGTAGAG GAAATGCGG GCTCCCTGGT 540
 GGACAATATT CAGCAACACT TCCTCCTCTC TGACCGGTTG GCCAGGGACT ATGCAGCCAT 600
 55 CGTCTCTTT GCTAACAACC GCTTTGAGAC AGGGAAGAAA AACTGCAGT ATCTGAGCTT 660
 CGGTGACTTT GCCTTCTGCG CTGAGCTCAT GATCCAAAAC TGGACCCTTG GACCCGTCGA 720
 60 CTCACAGATG GATGACATGG ACATGGACTT AGACAGGAAT TTCTCCAGGA CTTGAAGGAG 780

	CTCAAGGTGC TAGTGGCTGA CAAGGACCTT CTGGACCTGC ACAAGAGCCT GGTGTGCACT	840
	GCTCTCCGGG AAAGCTGGGC GTCTTCTCTG AGATGGAAGC CAACTTCAAG AACCTGTCCC	900
5	GGGGGCTGGT GAACGTGCCG CCAAGCTGAC CCACAATAAA GATGTCAGAG ACCTGTTTGT	960
	GGACCTCGTG GAGAAGTTTG TGGAAACCTG CCGCTCCGAC CACTGGCCAC TCAGCGACGT	1020
10	GCGGTTCTTC CTGAATCAGT ATTCAGCGTC TGTCCAATCC CTCGATGGCT TCCGACACCA	1080
	GGCCCTCTGG GACCGCTACA TGGGCACCTT CCGCGGCTGC CTCTGCGCC TGTATCATGA	1140
	CTGAGGTGCC TCCCAACGTC CGCCACGCT GACAATAAAG TTGCTCTGAG TTTGGAGACT	1200
15	GGTCTCGCT CCGGGGAGCA AGTGGGGGCG GTGCAGATGT GCCTGTGTCT GTCTCTGAGC	1260
	ACCTGGTGTC CGTGACAAG GATGGATGTG TNCNGTGGCT CCTTGGGAAC TGAGACATAT	1320
20	CTCAGGAAT GGTGTCTGTG CTCAGCCCAT CCACCAGAAG AGTCTGCTCA CAAAAAAAAA	1380
	AAAAAAAAA A	1391

25

(2) INFORMATION FOR SEQ ID NO: 45:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1569 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

35

	GGCAGGATG GAGATGGCTG CGCGGTGGC GGGGATGCTG CGAGGGGGTC TCCTGCCCCA	60
	GGCGGGCCGG CTGCCTACCC TCCAGACTGT CCGCTATGGC TCCAAGGCTG TTACCCGCCA	120
40	CCGTGCTGTG ATGCACTTTC AGCGGCAGAA GCTGATGGCT GTGACTGAAT ATATCCCCC	180
	GAAACCAGCC ATCCACCCAT CATGCCTGCC ATCTCTCCC AGCCCCCAC AGGAGGAGAT	240
45	AGGCCTCATC AGGCTTCTCC GCCGGGAGAT AGCAGCAGTT TTCCAGGACA ACCGAATGAT	300
	AGCCGTCTGC CAGAATGTGG CTCTGAGTGC AGAGGACAAG CTTCTTATG CGACACCAGC	360
	TGCGGAAACA CAAGATCCTG ATGAAGGTCT TCCCCAACCA GGTCTGAAA GCCCTTCCTG	420
50	GAGGATTCCA AGTACCAAAA TCTGCTGCCC CTTTTGTGG GGCACAACAT GCTGCTGGTC	480
	AGTGAAGAGC CCAAGGTCAA GGAGATGGTA CGGATCTTAA GGGACTGTGC CATTCCTGCC	540
55	GCTGCTAGGT GGCTGCATTG ATGACACCAT CCTCAGCAGG CAGGGCTTTA TCAACTACTC	600
	CAAGCTCCCC AGCCTGCCCC TGGTGCAGGG GGAGCTTGTA GGAGGCCTCA CCTGCCTCAC	660
	AGCCCAGACC CACTCCTGTC TCCAGCACCA GCCCTCCAG CTGACCACCC TGTGAGACCA	720
60	GTACATCAGA GAGCAACGCG AGRAAGGATT CTGTATGTC GGCCAATGGG AAGCCAGATC	780

	CTGACACTGT TCCGGACTCG TAGCCAGCCT GTTTAGCCAG CCCTGCGCAT AAATACACTC	840
5	TGCGTTATTG GCTGTGCTCT CCTCAATGGG ACATGTGGAA GAACTTGGGG TCGGGGAGTG	900
	TGTTTGTAC TTTGTTTCA CTAGTAATGA TATTGTCAGG TATAGGGCCA CTGGAGATG	960
	CAGAGGATTC CATTTAGAT GTCAGTCACC GGCTTCGTCC TTAGTTTTC CAACTTGGGA	1020
10	CGTGATAGGA GCAAAGTCTC TCCATTCTCC AGGTCCAAGG CAGAGATCCT GAAAAGATAG	1080
	GGCTATTGTC CCCTGCCTCC TTGGTCACTG CCTCTTGCTG CACGGGCTCC TGAGCCCACC	1140
15	CCCTTGGGGC ACAACCTGCC ACTGCCACAG TAGCTCAACC AAGCAGTTGT GCTGAGAATG	1200
	GCACCTGGTG AGAGCCTGCT GTGTGCCAGG CTTTGTGCTG AGTGCTGTTA CATGTATTAG	1260
	TTCTTTACT GCTGACCACA TTGTACCCAT TTCACAGAGA AGGAGCAGAG AAATTAAGTG	1320
20	GCTTGCTCAA GGTCATGCAG TTAGTAAGTG GCAGAACAGG GACTTGAACC AAGCCCTCTG	1380
	CTCTGAAGAC CGCGTCTGA ATTTCTTCAC TAGAGCTTCC TCATCAGGTT ACCCAGAAGT	1440
25	GGGTCCCATC CACCATCCAG GTGTGCTTGG ATGTTAGTTC TCCACCCTCG AGGTGTACGC	1500
	TGTGAAAAGT TTGGGAGCAC TGCTTTATAA TAAAATGAAA TATATTCTAA AAAAAAAAAA	1560
	AAAAAAAAA	1569

30

(2) INFORMATION FOR SEQ ID NO: 46:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1924 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

	GGGCCCCCCC WGWKTITTTT TTTTTTTTTT TTTAATTAGG ATAATGCCTT TATTAAAGAG	60
45	AATGAAACGT TCATTCTCTC TTCCACTCCT TCTCGTTGGT TTTCTGGACA CAGCTCACCT	120
	GATCCTGCTA GAAACGTTGT CAGTCTGCTT GTGGCTTCCC TCCTTGATTG ACTCACGCTG	180
50	TGTGATGTCT TGAGAAGTAT CTATCCACTT CATGTGAATG AGCACTCCAA TATCAGCCAA	240
	CATCAATCAT TCTTACCTAA AGAATAATAA GAAAAAGTTA ATATAAAGA CAAGGTATA	300
	AAATAAAGGT TTGAAAATGC TAGTCAACTT CAAAATTTAA AGAGTAAAAA TCCAGAGATA	360
55	AAGATTGGGG GTAAGTTACA GCATAAAAAA ATAGGAAGAA ACTTCATGGT GGGGGGGA	420
	TCTAAATTA TTCTTACATA AAATAAGTAG ACACCTGAAT TAGAATGAAA ACTGTATTTT	480
60	CTTTAAAATG TAAAAGCCTG ACTCTCAGTT TCACCAGTCT GAGCACAGT TTGACTGCAA	540

CCCAAAATAT ACTATCCCTT ATGTGAAGGT ATGTGACAAC GTTGACCTCA CCAAATGAGT 600
 TTAAACATCA GCTCTTTTTT CATATGAAAG CACATACCCT GCTCCCCATT CAAGTATGTC 660
 5 TTCCATTGTC AGGCAGGCTG ACCACCTTCA GCAGGAGTCC TCCAAGAGTG CCCAACTCCC 720
 CTTCCACAG TACACAACGC TGTAGTTGTT GTCTGCAAT CCTTTGTATT TACCTCATTC 780
 10 TTTCCCATCT AAGTCTCAC TGAGTTTAA AGTTAGGGCT GGAAAAGCTA TGCCTTACTG 840
 GGACAGCAAG GAACCAATTT TTTTCTGAGG GAGAAGACAT TCACCTTCAC TATATGCCTG 900
 GCAGGGCCAC AGTGCACAAA ACAAGATCA GCCTTCATTC AAGTCCAGG TTTTCTTCC 960
 15 TCCCTGAATG ATTACTGCAA AGGGTATATG AAGTAAGAGT TCCCTGTGTC ACATGTACCA 1020
 TCCATAAGGG ATACTATATC GTTTGCAAT CTTCCTCCCA TTCTCCACAT TGTCTTATCT 1080
 TAAGTCCAAG CCTTTTTCAC TCTCAAAAAA AAAAAAAAAA TATTTTTTTC AGCACTGGTG 1140
 20 TTCAAAAGCA ACGTTTTTAT GGTTAATGGT TTACCAGCAA CTGTTGAGAT TTCCAGTTGA 1200
 GTCTTAAAAA TTGCCAATCA TTATCTAGCA GCAATGACAG ATGATTAGGA GCAGTCAAAT 1260
 25 CCTCTGAATT CTTCCTCTAA TAGGCAGCCA TTTGAGAACT GCACTAGCTG ACATCACTAA 1320
 AACATTATCA GCTAAAGCCA AAACCAATA AAGGCCCAGA CCAACATCCT GGCTCTCTAA 1380
 AACCTGTCCA AAATCATTA A GTGAAAGGCA GTAAATGCAG GACTGTGGAT CATGTCACTG 1440
 30 CAGCTGACAA TGATTAACAA TAGGAGACAT GCAACCCCA TTAAGGTAA AAGTCCAAA 1500
 CTAGTCACAC GCATCTCTTT ATTGGGGAAA AGTGAGACTA TTATGCATTC TTGGTAGGTT 1560
 35 TGCAACCTTG CATGAAGAGC ACCCATGCA TTTCTTTCAT CTTCAGAAA GCACCGGTAT 1620
 CTGTTCCAAG GGCCTAACAG TACGAAATA CATTCTGGCA TCACACCTCT GAACCCAAGA 1680
 CTGTCTCAT TAAAAATAAT TTTGGTTGT AACAAATTA TGAAATACAA TGCAAGCACC 1740
 40 TCGGTATAGC ATTATTACTG AAACCACTTA ATTCCAGCT TTTTGAGTTT TTTAAAAAA 1800
 CCCACTGCAC TAAGATTCAC AATTCATTGC TACATACAAA TTAAAGCTAG TAAGAACACA 1860
 45 CTAACGTCAC AAGTTTCTCA TTCTAAAGTG CAAAAGCCTA ATCATCTGAA AGTGAACAGG 1920
 GTAA 1924

50

(2) INFORMATION FOR SEQ ID NO: 47:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 475 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

TGGTGTGGGG CCCAGAAAMC AAGGGACCAG TGAAACAMC CCCAGAGACT TGTATCCGCC 60
 5 AGGAAAGCCA TTGCCAMTYC TGAGCCCTTG AAGGCAAGG AGGGAAACAG TGTTACCAGA 120
 GCCCAGTAAG AACTGCTGTC ATGAAGGAGG GGCCACCTTG TAAGAGACAT CATTACTACC 180
 AGAACTGTGG TGCCAAATG CTGGTGTCTC TCTTTGGAGA AACCAACCAG ATACATCTGC 240
 10 TGGAGACCCA GGTGGGCACA GAGAAGGGTG GAGAGAGAAT CTGGGAAGAG AAATGGAGAA 300
 TAAGCAGCAC AGTGTATTC ATTTCTGTAA ATTCTATGT AGAAGGCTCA GTGTTAGAAA 360
 15 TAAAGTTATT CTACTAGTTG CAAGTTAAGT GTTCTGTTT GTTCTGCTTT CCTGTTAGCA 420
 TAAGTAAACT CCCTTTGGAA CTACACAGGT ATGTCCTCC TTCAACATGT GTGAA 475

20

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 346 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

AAGGGACAGA GACCTGGATT CAGATCTCAT TTTACAATGA AGACCCCAAT GCAGAAAGTC 60
 ATGTCTGAAA TTCTGAGCTT ACTCTCTGTC CTGCTGGGAC CTGCTCTGGA TGAGAGAAGG 120
 35 GAGGAAAAGG ACTAATCAGA GGAGCCAATG AAGTCACTCC ATGAGTTTCC TGAACCTGTC 180
 CCAGCTAGAG ATTAACGTYT GACOWTCAAC GTAGGACACT GTGCAGATGG CTACTTGCTG 240
 GCGCACATGA AGACCAAAGC CAGGACCAAG CCCCMASCCT GCTWAACACG GCAGARTCTT 300
 40 GCCCAGCCMA CYTCTGTGAR AATCTGCTTC CCTCCACAGC TGACCC 346

45

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 1366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

TAGGTGTCAG CCGCCACCCC CCCCCATAT GCAGATTTAC TSGGCATGGT AGTGGCCAGC 60
 TTCTAACACA GCTGGTATTT CAAGTCTCCT GGGACCTCAC TCAGGAATGA TACCCCTCA 120
 60 GTAGAAGCAG CAGGTGATCT TAACTCCTTT CAAAGAGCAG GCCTGTCTGG GAAGCCATGT 180

	CCTCAGCAGG CACAGCAACC CCTCTGGAAA TGGATCACAA ACTCACTTCT CAGCCAGGCA	240
5	GGCCAAGCTT CTATTGTAAC AGTAGGCACA GTATAGTCGG ATCATCACAT CAGCTGGGTT	300
	TTTGGTTTAG TCATCTAGAG TCGTCTGGAC TAAAGGTCTT TCAGGTCTCC TTGCCCTGTG	360
	AGTGCGTGAA CCTCCCCACC CGAATTGCCT CAGTTGTCCT GAGCCTCATG TCTCTCCTGG	420
10	TGGTGGGCCA GGCCCTTGCA TGGGAAGGGA GCCTGCTGCG GGCAGGCCA GCTGGGGGTG	480
	CTCACCTATG CGCAATGANA GTTATTGAAG GACTGGTTGT TGATGTGGT GAGCGTATCC	540
15	TTTATGGCCA GCGCGAAGTC GGCCAGGTCA GCCAGGTGCT GCCAGGCTC TCTCTCGGAC	600
	TTGTCTTCCT GTGCCAGGGG ACCGTGGAGA AAGTGTGAGG GGCCGCTCAC TGCAGCAGCC	660
	TGCTCTGCTG CCTTCCCTGG CAGTGTCTG GGGGTGGATT CCTACAMCT AGATGTTCAA	720
20	GGCCTTACTT TTCCTCCAC AAAGGAGTCG CAGCCACGCT AGCTCTGACT TGCCACTGTG	780
	ACAAAGTTCA CGTAGCAGGT CTAGGCAAAG ACTGGGCAAT TGAGCAGAGG AGACGGACCT	840
25	GTGAGTCTGA CCRYGAGSCG GRCCCTTCA CCTTGGCTGG GCTGGTCTG GTCCTTAGGT	900
	TTTGTGAGGT TGTCTTGTG TGGATCCCTC AACTAGGTGA TAAGCACTGG AGGGGGATGA	960
	CCGCCCTTGG ACGTGTCTT TTAACCTCAT CCATATAATA GGGCCGTGGG ATGGTTGTAG	1020
30	AGGTAAAGCA GGATGATGGT GTTTTAAGAC CAGAGCTTGG GACCAGGGCT CCTACACCTA	1080
	ATTTTCTCTC CTGGTAGCTG AACAAAGTC TAAATTAGCT TAACAAAAGA ACAGGCTGCC	1140
35	GTCAGCCAGA GTTCTGAAGG CCATGCTTTC AGTTTCCCTT GTTGACAATT GCTCTCCAGT	1200
	TCCTATGAAA GCACAGAGCC TTAGGGGGCC TGGCCACAGA ACACAACCAT CTTAGGCCTG	1260
	AGCTGTGAAC AGCAGGGGGT TGTGTGTCTG TTCTGTTTCT CTGCTTGCCG AACTTTCTCA	1320
40	ATAAACCTTA TTTCTTATTT ATAAAAAAAA AAAAAAAAAA AAAAAA	1366

45 (2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1405 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

55	GCAGTAATTC CTGTAGCCA CTGCATCCAC CAAACTAGT TTATTTTCC CCTCAAATTC	60
	ATGATTTTAA CGTCTGTAC AAAGGGAATT TTGCTGATAG CTCTTTGGGT CCCACTGTTC	120
60	CATTTTATGC TAATAGATTC CATCTAGGG CCCAGCCGTC TCTTGACTGA TGGTGTCC	180

	TTTAACCCCTT GGCATGTATA ATAGAATTTT GGTGAATGAA AGAACCCAAA TAGGCCAGAT	240
	AGTCCCCCA GGCCTGATA TCCATAAAAG GCTTGGGAAT GCATTATGTA ATTGTCCTTA	300
5	GTCTTTTGT TGTMTTAGAA AAAAAAACA AGATGGGCTC AGATGGATGC CTACGTAAAA	360
	ATGGTTCCTA GCTGTGTACT CATAACTTTT CTTTGAATTG AGTAGTGAAA GGAAGGAGGA	420
10	GGAAAGGAAA TTAAATGTCC TTCTAGTATT CTCTGGACTC AAGTCTGACA TATGAGATAA	480
	TAACCTATAT TGAAATGCCA AGAATTGTAT CTGAAACAAG AGAACAGTTT GACACATTTA	540
	TCATGCCTTC ATATTACATA TTAAGTAAA CCAATTAATA AACATATGAA ATATCCATTG	600
15	CACAAGGCAA AGGCACCTAA ACCTTTTGT TCTTTTCTA CATAGCAGAA ATTGATTTTT	660
	TTTTTATTTT TTTAGGGGAA CCTATATAAT TATGACCCAG TGATGTCTTT TGGTGACTTA	720
20	AGCTTATGAA TTCAGGTAC AATTGAGTTG ATTCTAGATG GTTACTACCT TGAAAAGGAT	780
	GTTGGTGCC TATGTGACAC GAGCCAGAGC CTGCTGGGGA ATAAACAAAG CAGGTTCAT	840
	GCCAACACCA ACTCGTAGCT TTAGTGGGCA GATGGGGAGT GGTTCACAGA CTTCCCAAAA	900
25	TGTGGGGCT TTGGGATTTT CCACACCATC CCAAGTGTGT TGTTCATTCT TCCTCTTTTC	960
	ACACTCTTGG ATGGATWATT TGRAAATGGT GRAAWMMCY YYKRAATTIG CCCAATAGCC	1020
30	WIGRCCACC ATTCTTWATG ACACCATAAC CAAATAGTTC CWTAAATGTTG AAATATTAGA	1080
	AACCTGTTAC CAGCCYKSMA KTWACCCWVA WTTTTCCCAT GTTTGTGGAA TTGATATTGA	1140
	AATAGCAGGG CTAAGGAATT ACTGGCAAGT TTTAGCCTGT GGGTAATACC TTAGGGTTAT	1200
35	TTAAATATTT GTAATTTTAT TTAATGTTC ATGAATGTTT GAAAGGAACA AAATTATCAG	1260
	GGATGGCTCT TTGCCATGGG TCTTATTTTC ACCCTCTTTT CTGTAAGAAA AAAGAACAAT	1320
40	GTCTTAATGT ATTTTAAAG TTTTGGTAT AGTTTCTAAT TCCAATTTTA ATAAAAGTTT	1380
	TWTRTAAAAA AAAAAAAAAA AAAAA	1405

45

(2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

55

	CGGATTTTCT AGGACCCCAA AAAAAAAAAA AGGGNAAAAA AAACCCNCAA AACCAACCAA	60
	AACCCCAAAA AAAAAAAAAA TCCACAAAAA CAAAAAACT ATAAAAAGA AAGAATTAAA	120
60	AACTTTCAGA GAATTACTAT TTACTTTATT AACTTACGGA TTTATTATAT AAATATATAT	180

TCACCTAGCA ACATATCTCT GCCGTCTCTC CTGCTCTCAT AATGAAGACA TAGCCGATTC 240
TCTGCCCGGG CCCCTTGCTG ATGCTCTCTC GGGTCTGCGT CGGCGGTGGG TCTCTGGGA 300
5 CCTCCAGAG GTGGAGGTGG GCTGATGGCC TGGCTGCCTG GTGGTTGATG GTTTTGCTCC 360
CCCTACCTTT TTTTGTGAG TTTATTCTGA TTGATTTTTT TTCTTGGTTT CTGGATAAAC 420
10 CACCTCTGG GGACAGGATA ATAAACATG TAATATTTTT AAGAAGGAAA AAAAAAAAAA 480
AAAAAACTNG GGGGGGCCC CGAA 504

15

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 777 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

NAAGTATCTT GGCCAGTTTA TTACAGAGGA CGATAAATGA TTCCATGTGG ATAGGGCATA 60
ACATACAGAG AATGAGACTA TGCCAGAAAT GGGAGGAGGC ATTTGAAACA ACATGAGTAT 120
30 CTCAGGGACA GATGGATTGA TTCTGCTATT GGTAGGCCTG GAAGCAANGG TCAGAAGTAG 180
CAAAAATGG ATACCAAAAG CACTATTWGT CACCCAAGCT AAGTGAATA GCTGGCCCAG 240
35 TAGGAGAAAT GCAGGTTTTG CTCTACACTA AGTTCTCCAA CTCTTGATAA GCCTCCAAAA 300
ACAAATGTTA GGGGAAAAA ACGCAGCTGG TTATGAAAAG ATATATCTCA TTTCATTAAA 360
AAATCAATGT CAATGCTGTT AATAGAATCC TTTTATCTTC AGGACAGAGG CAATGCCCTA 420
40 AACAAACACC AGCTCAAGAG CCTCTGATGC CAACCTAGAG GGTACCCAAA CACAACTTA 480
GCATAGAGGT AAGAATCTCT ATGTCTTTTG GTGGAGGCAA AGCCATTTGG TTGGTACTTC 540
45 ACAGGAACAT CTTTCTACCA AGTCTTCATC ATATGGTATG TGCCACGAGT CTCCAGTTGT 600
TTGCACCACT GTGTCATAGC TGAGAATACG CTGAAAGGTT AGTTTGTATC CTGGAACCT 660
ATTTACAATT GCCAGCTGAT GTCCCTGCTG CCACTTAAAA AAGGCTTGGG TCTGGCATAG 720
50 GCAGAMAGGC CTGTGGTCCC CTCGTGCCGA TTCTNGGCTC GAGGCCAATT NCCTTAT 777

55

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:
60 (A) LENGTH: 602 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

5
 ATGACTACAG TGTATATACCC TCCAATCTTT GCAGGTGGGC ATGGAACACT GCTTGTATCA 60
 CTCTGTGCAC GGTATAAATC CATATATCCA CAAAACACA CATCCATCCA TCAACATATA 120
 10 CATGGTTTGG GATGAGCAGG TCAATAGTTT TGAGAGGGAG TTGTTCCTT TTTTTTTTCT 180
 CATTATACTC TTAAATTGTT GTCAGTTATC AAACAAACAA ACAGAAAAAT TGTTTGGAAA 240
 AACCTTGCAT ACGCCTTTTC TATCAAGTGC TTTAAATAT AGACTAAATA CACACATCCT 300
 15 GCCAGTTTTT TCTTACAGTG ACAGTATCCT TACCTGCCAT TTAATATTAG CCTCGTATTT 360
 TTCTCACGTA TATTACCTG TGACTTGTAT TTGTATTTA AACAGGAAAA AAAACATTCA 420
 20 AAAAAAGAAA AATTAAGTGT AGCGCTTCAT TATACTATTA TATTATTATT ATTATTGTGA 480
 CATTTTGGAA TACTGTGGAA GTTTTATCTC TTGCATATAC TTTATACGGA AGTATTACGC 540
 CTTAAAAATA CGAAAATAAA TTTTACAAGG TTCCGGTTTT GGTGGTGGAA AGAGTAAATT 600
 25 GA 602

30

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 1749 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

40
 AGTCACTGAC TTGGAGCCGC TCGGGGAAG TCCGCCCAG ACAGGCGGTG GGTGGGAATG 60
 CCTCACTTCA GTTTGAAGAG GTTCCGATC CAAAGGGTT AAAACGAGCG AACCCCGATC 120
 45 CCGACCACA CTTCCCGCCT CCTAAAACG CACACCCGC TAGCCATGGG CAGCCGCGAC 180
 CACCTGTTC AAGTGCTGGT GGTGGGGAC GCCGAGTGG GCAAGACGTC GCTGGTGCAG 240
 GATTATTCCC AGGACAGCTT CAGCAAACAC TACAAGTCCA CGGTGGGAGT GGATTTTGCT 300
 50 CTGAAGGTC TCCAGTGGT TGAATAGAG ATAGTGGGC TTCAGCTGTG GGATATTGCA 360
 GGGCAGGAGC GCTTACCTC TATGACACGA TTGTATTATC GGGATGCCTC TGCCTGTGTT 420
 55 ATTATGTTG ACGTTACCAA TGCCACTACC TTCAGCAACA GCCAGAGGTG GAAACAGGAC 480
 CTAGACAGCA AGCTCACACT ACCCAATGGA GAGCCGGTGC CCTGCCTGCT CTTGGCCAAC 540
 AAGTGTGATC TGTCCCTTG GGCAGTGAGC CGGGACCAGA TTGACCGTT CAGTAAAGAG 600
 60

	AACGGTTTCA CAGGTTGGAC AGAAACATCA GTCAAGGAGA AAAAAAATAT TAATGAGGCT	660
	ATGAGAGTCC TCATTGAAAA GATGATGAGA AATTCCACAG AAGATATCAT GTCTTTGTCC	720
5	ACCCAAGGGG ACTACATCAA TCTACAAACC AAGTCTCCA GCTGGTCTG CTGCTAGTAG	780
	TGTTTGGCTT ATTTTCCATC CCAGTTCTGG GAGGTCTTTT AAGTCTCTC CCTTTGGTTG	840
10	CCCACCTGAC CATTTTATTA AGTACATTG AATTGTCTCC TGACTACTGT CCAGTAAGGA	900
	GGGCCCATG TCACTTAGAA AAGACACCTG GAACCCATGT GCATTTCTGC ATCTCCTGGA	960
	TTAGCCTTTC ACATGTTGCT GRCTCACATT AGTGCCAGTT AGTGCCTTCG GTGTAAGATC	1020
15	TTCTCATCAG CCCTCAATTT GTGATCCGA ATTTTGTGAG AAGGATTAGA AATCAGCACC	1080
	TGCGTTTTAG AGATCATAAT TCTCACCTAC TTCTGAGCTT ATTTTCCAT TTGATATTCA	1140
20	TTGATATCAT GACTTCCAAT TGAGAGGAAA ATGAGATCAA ATGTCATTTT CCAAATTTCT	1200
	TGTAGGCCGT TGTTCAGAT TCTTCTGTC TTGGAATGTA AACATCTGAT TCTGGAATGC	1260
	AGAAGGAGGG GTCTGGGCAT CTGTGGATTT TTGGCTACTA GAAGTGTCCC AGAAGTCACT	1320
25	GTATTTTGA AACTTCTAAC GTCATAATTA AGTTTCTCTT GTCTTGGCAT CAAGAATAGT	1380
	CAAGTTTTTT GGCCGGGCAT GGTGGCTCAT GCCKGTAATC CCAGCACTTG GGGAGGCCAA	1440
30	GGCAGGCGGA TCACATGAGG CCAGGAATTC GAGACCAACC TGGTCAGCAT GGCAAAACCC	1500
	CGTCTCTACT AAAAGTACAA AAATTAGCCA GCGTGATGG CACGTGTCTG TAATCCCAGC	1560
	TACTCTGGAG ACTGAGGTGG GAGAATGCTT TGAGACTGGG AGGCAGAGGT TGCACTGAAC	1620
35	CGAGATCATG CCACCGCACT TCAGCCTGGG TGACAGAGAA GGACTCCGTC TCAAAAAAAA	1680
	AAAAAATAAA AAAACTCGAG GGGGGGCCCC GTACCCAAAT CGCCSTGATA GTGATCGTAW	1740
40	ACAATCNAA	1749

(2) INFORMATION FOR SEQ ID NO: 55:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1896 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

50

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

55	AAAGAGATGG GCTCTTTATT TTCTGAAAA ACCAATTTGG AGTTACTCAT TTTTCCATAA	60
	CATTAAATTT CTTACAGTGA ACTACATATT GTCCATAAGT GCTTCATCAG GACTCATCCG	120
	CCTCCTGTCT ACTGGCTCCA AATAGACCAT GTCAGCTTCA CCCCCTGGCT TTGTGTCTAT	180
60	GGGTGGCCTG TGGTATATGG AAAAGTAGCA GGGTGGTCAG GGTGGGAGAC ACAAGATGTT	240

	TTTATAGTCT AGAGCCTTTA AAAAACCCAG CAGAATGTAA TTCAGTATTT GTTTATTGGC	300
5	TGTTTTTTGA CAGATTGTTG AAATTAAATG AATTGAAAGG GAAACTCAGA GTACTAGGAC	360
	GTTTATTAAA AGGAAAAAAA TGTCTTGCAA TGTGCTGTAA TCACAAGAGG AGAAAAATAC	420
	TTGTTTCCTT GATCTGTGAG AGGTCACAGT AACCTGGGCC GAGCTGTAT TATTTATTAT	480
10	ATAATAGTAG TAGGAAGTA ATAAGTGGTT CTCTGTGTTT CAAGCACAAT ATTACAACCT	540
	CTTTTGAACC GTAAATATCA GAATGAATCC TCTTCCCAGG GGATTGAACA GAAGCTTAAT	600
15	GTTTACAAGT GTTTGAATTT GTGATCTGAA ATAACACAAA ATTAATAACA TGATTTCTCT	660
	AATTTTCCAA CTAGAGGAAG AGAACTTGT GGAAAAGTTC TTTTMTTTC TTTTMTTTC	720
	CTTAAAGAAG GGCAGCCAAG GTAGTAACCT AAAAATAGTG CCCAGGCATA TGAGAGTTGT	780
20	CCTACGAGGT TAAAGAACAC ACTGTTCCAC TGTATGGCTT TGGCCCTGAG TGGCCAGGGA	840
	GGTCAACTTG ACCCTGCCAT GTTGGTTTGA CTACTAAGA CACAGGAATC ATTGTTTTC	900
25	TTGACCAGGG TCTCACACC TGGAGGAATG TTAAGTAAGA GAAAGAACCT CTTTCTGAA	960
	TATTGACATG TAAAGACCA AAGTAATTTT TCTGAACTTC TGCAATTCTG AGAACTCTCC	1020
	AAGGAATTTA CAGTGATTTT AGTGCTTGTG AGCATTTTTC CATGAGGACT TTCATACATT	1080
30	TGACTCTTTA GTTCACAGGT TCCCATTGAT TGTGAGCAAG ATATTTATCT CTTTAGCCCT	1140
	TGGGGATCCA GCTGAGAGCA ATCTCTTGCA TTTTMTTACC CGTGATGTA CAGATATCAT	1200
35	TTCTTGTTGA TGCCATGACT TGAAAAAGTT TGGGAAGCTC TTTAGCAATA TCAGCTAAAA	1260
	GGATATGAAA TCACAGGTGA TAGCAGTTGT CATTCAGTAA TTTCTACAA GCAGCACCCC	1320
	AAAGGAAATA TAGTCCTAAT CTTTACTATC CACTTCTAAA TTAAATGTGA ATTTCATACA	1380
40	TGTTATTAGT TGTTTTCTTT ATAATTTTAT AAAAATTATT CATCGGAGT TTAACCTCCA	1440
	CTTCCATGCT ATCGGATGTG TTGGGCTCCA TGCAAGAACT TGGAAGAAAA ACAGGCAGGA	1500
45	ATGCATTTGC ATAATGACCC AGATCATCAT TTTCTGCAAC TGAGAATTAT ATTTTCATCAT	1560
	TGCTTCTAGA AGTCTGCAAT TCTTTACTTT TCTTTGGTGC ATTATTATCT AGGTGCCATC	1620
	ACTGGATAAT GTGGAGTGAC TAGAGAAGTC AYATATCACT GTAAGGTACA GTTAGGGTA	1680
50	ACACTTTAGA GGTTTATTAT TTTTAAAAA CTTTCTTGA ACTCCTGGGC CAACATGGGT	1740
	GAAACCCCGT CTTCTTACTT AAAAATACCC AAAATTAGGC CAGGGGCGTG GATGGGTGGG	1800
55	GTGCCTGTTA ATCTTCAGCT ACTTNGGGGA GGGCTTGAAG CCAGGGAGGA ACTGCCCTGG	1860
	ANCCCCGGGG NGGCCAGNA GGTTCGCCAG TTGAGT	1896

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1753 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

10 TCTTTTAA ATAGACATTT GTGGGCTCA CACAATATAT GAAATAGTAC CCTCTAAAA 60
AGAGAAAAA AAAATCAGGC GGTCAAAC TT AGAGCAACAT TGTCTTATTA AAGCATAGTT 120
15 TATTTCACTA GAAAAAATTT AATATCAAGG ACTATTACAT ACTTCATTAC TAGGAAGTTC 180
TTTTTAAAT GACACTTAAA ACAATCACTG AAAACTTGAT CCACATCACA CCCTGTTTAT 240
TTTCCTTAAA CATCTTGAA GCCTAAGCTT CTGAGAATCA TGTGGCAAGT GTGATGGSCA 300
20 GTAAATACC AGAGAAGATG TTTAGTAGCA ATTAAAGGCT GTTGCACCT TTAAGGACCA 360
GCTGGGCTGT AGTGATTCTT GGGGCCAGAG TGGCATTATG TTTTACAAA ATAATGACAT 420
25 ATGTCACATG TTTGCATGTT TGTGCTCTG TTGAATTTT GAACAGCCAG TTGACCAATC 480
ATAGAAAGTA TTACTTTCTT TCATATGGTT TTTGGTTCAC TGGCTTAAGA GGTTCCTCAG 540
AATATCTATG GCCACAGCAG CATACCACTT TCCATCCTAA TAGGAATGAA ATTAATTTTG 600
30 TATCTACTGA TAACAGAATC TGGGTCACAT GAAAAAAT CATTTTATCC GTCTTTTAAG 660
TATATGTTTA AAATAATAAT TTATGTGTCT GCATATTGCA GAACAGCTCT GAGAGCAACA 720
35 GTTTCCTATT AACTCTTTCT GACCAATAGT GCTGGCACC GCTGCTCCTC TTTGGGAAGA 780
GGAAAGGGTG TGTGAACATG GCTAACAATC TTCAAATACC CAAATGTGA TAGCATAAAT 840
AAAGTATTTA TTTTATGCCT CAGTATATTA TTATTTAATT TTTTAGGTAA TGCCTATCTC 900
40 TTGGTCTATT AAGGAAAGAA GCAATCAGTA GAGAATTCAG GATAGTTTTC TTTAAATTC 960
TGCAGATTAC ATGTTTTTAC AGTGGCCTGC TATTGAGGAA AGGTATTCCT CYATACAACT 1020
45 TGTTTTAACC TTTGAGAACA TTGACAGAAA TTATGCAATG GTTGTGTGAG ATACGGACTT 1080
GATGGTGCTG TTTAATCAGT TTGCTTCCAA AGTGGCCTAC TCAAGAGGCC CTAAGACTGG 1140
TAGAAATTAA AAGGATTTCA AAAACTTTCT ATTCCTTTCT TAAACCTACC AGCAAACCTAG 1200
50 GATGTGATA GCAATGAATG GTATGATGAA GAAAGTTTGA CCAATTTTGT TTTTGTGTG 1260
TTGTGTGTG TTTGAATTTG AATCATTCT TATTCCTTTT AAGAATGTTT ATGTATGAGT 1320
55 GTGAAGATGC TAGCGAACCT ATGCTCAGAT ATTATCGTA AGTCTCCCTT CACCTGTTAC 1380
AGAGTTTCAG ATCGGTCAC TATAGTATGT ATTTCTTTAG TAAGAATGTG TAAAATTAC 1440
AATGATCTTT TAAAAGATG ATGCAGTTCT GTATTTATTG TGCTGTGTCT GGTCTTAAGT 1500
60

GGAGCCAATT AAACAAGTTT CATATGTATT TTTCCAGTGT TGAATCTCAC AACTGTACT 1560
 TTGAAAATTT CCTTCCATCC TGAATAACGA ATAGAAGAGG CCATATATAT TGCTCTCTTA 1620
 5 TCCTTGAGAT TTCCTACCT TTATGTTAAA AGTTGTGTAT AATTGTTAAA ATCTGTGAAA 1680
 GAATAAAAAG TGGATTTAAA TTAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1740
 10 AAAAAAAGG GGG 1753

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1220 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

GCGGAAGTTA CTGCAGCCGC GGTGTTGTGC TGTGGGGAAG GGAGAAGGAT TTGTAAACCC 60
 25 CGGAGCGAGG TTCTGCTTAC CCGAGGCCGC TGCTGTGCGG AGACCCCGG GTGAAGCCAC 120
 CGTCATCATG TCTGACCAGG AGGCAAAACC TTCAACTGAG GACTTGGGGG ATAAGAAGGA 180
 30 AGGTGAATAT ATTAACTCA AAGTCATTGG ACAGGATAGC AGTGAGATTC ACTTCAAAGT 240
 GAAATGACA ACACATCTCA AGAACTCAA AGAATCATAC TGTCAAAGAC AGGGTGTTC 300
 AATGAATTCA CTCAGGTTTC TCTTTGAGGG TCAGAGAATT GCTGATAATC ATACTCCAAA 360
 35 AGAACTGGGA ATGGAGGAAG AAGATGTGAT TGAAGTTTAT CAGGAACAAA CGGGGGGTCA 420
 TTCAACAGTT TAGATATTCT TTTTATTTT TTTCTTTCC CTCATCCTT TTTTATTTT 480
 40 AAAAATAGTT CTTTGTGAAT GTGGTGTCA AAACGAATT GAAACTGGC ACCCCATCTC 540
 TTTGAAACAT CTGGTAATTT GAATTCCTAGT GCTCATTTAT CATTATTGTT TGTTTTCATT 600
 GTGCTGATTT TTGGTGATCA AGCCTCAGTC CCCCTCATAT TACCCTCTCC TTTTAAAAA 660
 45 TTACGTGTGC ACAGAGAGGT CACCTTTTC AGGACATTGC ATTTTCAGGC TTGTGGTGAT 720
 AAATAAGATC GACCAATGCA AGTGTCATA ATGACTTTCC AATTGGCCCT GATGTTCTAG 780
 50 CATGTGATTA CTTCACTCCT GGAATGTGAC TTTCAGTGGG AGATGGAAGT TTTTCAGAGA 840
 ACTGAAGTGT GGAAAAATGA CCTTTCCTTA ACTTGAAGCT ACTTTTAAAA TTTGAGGGTC 900
 TGGACCAAAA GAAGAGGAAT ATCAGGTTGA AGTCAAGATG ACAGATAAGG TGAGAGTAAT 960
 55 GACTAACTCC AAAGATGGCT TCACTGAAGA AAAGGCATTT TAAGATTTT TAAAAATCTT 1020
 GTCAGAAGAT CCCAGAAAAG TTCTAATTTT CATTAGCAAT TAATAAGCT ATACATGCAG 1080
 60 AAATGAATAC AACAGAACAC TGCTCTTTT GATTTTATTT GTACTTTTTC GCCTGGGATA 1140

5 TGGGTTTTAA ATGGACATTG TCTGTACCAG CTTCATTAAA ATAAACAATA TTTGTAAAAA 1200
TCAWAAAAAA AAAAAAAAAA 1220

10 (2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1049 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

20 TCGCGCCTGC AGACACAGCA TCTACTCAGC GTGGGTCACC TCTGTGAACA TCACTGACTG 60
CAAGCCTCCC TCAATTTCTG GTGCAGCCCA TCAGGGACCC ACAGCGCCTG GGAGGATGGT 120
GCGGATCTTG GCCAATGGGG AAATCGTGCA GGACGAGAC CCCCAGTGA GGACCACTAC 180
25 CCAGCCACCA AGAGGTAGCA TTCCTCGACA GAGCTTCTTC AATAGGGGCC ATGGTGCTCC 240
CCCAGGGGT CCTGGCCCCC GCCAGCAGCA GGCAGGTGCC AGGCTGGGTG CTGCTCAGTC 300
CCCCTTCAAT GACCTCAACC GGCAGCTGGT GAACATGGGC TTTCGCGAGT GGCATCTCGG 360
30 CAACCATGCT GTGGAGCOGG TGACCTCCAT CTGCTCCTC TTCCTGCTCA TGATGCTTGG 420
TGTTCTGTGC CTCTCCTGG TTGGCCTTGT CTACCTGGTG TCCACCTGA GTCAGCGGTG 480
35 ACCTCTGAGG GCTGATAGGG GTGGGTTTGT TGAGAGGGAC TTGCTGGGCC TTGGTGTGAG 540
AGCAGGCATA TTTGGAGGGG ATCTGGTGGT GCCTTGAAGG TATGATCAGA GAGGGGACCA 600
CAGGTGTGTG TTTCCCCTTT GTGTTAAGCG TGAGGCAGAG GGAGACGTTA GTCCCAGCAT 660
40 TTCCCAAAGT GTGGGTGGGT CCGTTGGTTC CCGAGATACT TTTAGGTGGT ATGGGGCCTG 720
CATTAAAGTG CACAAAATCA GAGCAAGAAA GCGATGCCCT TCCCAATTCT CTCAATCCTT 780
45 TTATGCCGAG AAGATCTCAG CTGGATGCCA ACATGTTCCG ATGCCTGTGG AAGACATGCC 840
GACGTCTCCT CTGCCTAGGG AGCAGGACTT GGGCTTAGGG CAGGTGGAAA AAATTCCAGA 900
CTTTTITAGC ACTGTTTTTG TTTTAATGGT ATATTTTAT TGGCTACTTT ATTGTTTAGG 960
50 ACAAGTGGA GTGGCATCTT ATTTATTTG ACCTTTTCAA TAAATAGATT TAAGTAAAAA 1020
AAAAAAAAA AAAACTCGAG GGGGGCCCC 1049

55

(2) INFORMATION FOR SEQ ID NO: 59:

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1776 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

	AAAGAGGATG TGMAGCTAGA GGTCCCCGAT GGCTGGTCGG ATGGGAAGCA CAAGGCTGAG	60
10	GGACTGGATT GTAAAGGCAC TAAGTCGTTC TCGGTGAGA ATCAGACATG GGGGACCTCT	120
	AGCTTCACAT CCTCTTTCCT TGCAGSTCTG GACATCCTGA GCCCAAGTCC CCCACACTCA	180
15	GTGCAGTGAT GAGTGGCGAA GTGAAGGTGA CAGGGCAGAA CCAGGAGCAA TTTCTGCTCC	240
	TAGCCAAGTC GCGCAAGGGG GCAGCGCTGG CCACACTCAT CCATCAGGTG CTGGAGGCCC	300
	CTGGTGCTCA CGTGTTTGA GAACTGCTGG ACATGCCCAA TGTTAGAGAG CTGGCTGAGA	360
20	GTGACTTTGC CTCTACCTTC CGCTGCTCA CAGTGTTCG TATATGGACA TACGCTGACT	420
	ACTTAGCTGA AGCCCCGAAT CTTCCTCCAC TAACAGAGG TCAGAAGAAT AAGCTTCGAC	480
25	ACCTCTCAGT TGTACCCCTG GCTGCTAAAG TAAAGTGTAT CCCATATGCA GTGTTGCTGG	540
	AGGCTCTTGC CCTGCGTAAT GTGCGGCAGC TGAAGACCT TGTGATTGAG GCTGTGTATG	600
	CTGACGTGCT TCGTGGCTCC CTGGACCAGC GCAACCAGCG GCTCGAGGTT GACTACAGCA	660
30	TCGGGCGGGA CATCCAGCGC CAGGACCTCA GTGCCATTGC CCGAACCCCK AANAAAAACC	720
	ATTAAAGTGA CGACGGCAGC AGCAGCGCA GCCACATCTC AGGACCCCTGA GCAACACCTG	780
35	ACTGAGCTGA GGAACACAGC TCCTGGCACC AACAGCGCC ASCCAGCAAG AAAGCCTCAA	840
	AGGGCAAGGG GCTCCGAGGG ANCGCCAAGA TTTGGTCCAA GTCGAATTGA AAGRACTGTC	900
	GTTCCTCCC TGGGGATGTG GGTCCACAGC TGCTGCCTG CCTCTTAGGA GTCTCAGAG	960
40	AGCCTTCTGT GCCCTGGCC AGCTGATAAT CCTAGGTTCA TGACCCCTCA CCTCCCCTAA	1020
	CCCCAACAT AGATCACACC TTCTCTAGGG AGGAGKCAA TGTAGGTCAT GTTTTGTGTG	1080
45	GTACTTTCTG TTTTGTGTA CTTCATGTGT TCCATTGCTC CCGCTGCCA TGCTCTCTCC	1140
	CTGTCTCTCT TAAGAGCTCA GCATCTGTCC CTGTTCAATTA CATGTCATTG AGTAGGTGGG	1200
	TAGCCCTGAT GGGGTGCT CTGTCTGGAG CATAACCCAC AGGCGTTTTT TCTGCCACCC	1260
50	CATCCCTGCA TGCTGATCC CCAGTTCTTA TACCTACCC CTGACCTATT GAGCAGCCTC	1320
	TGAAGAGCCA TAGGGCCCCC ACCTTTACTC ACACCCCTGAG AATTCTGGGA GCCAGTCTGC	1380
55	CATGCCAGGA GTCAGTGGAC ATGTTTCATC TAGAATCCTG TCACACTACA GTCATTCTCT	1440
	TTCTCTCTCT TGGCCCTTGG GTCCCTGGAA TGCTGCTGCT TCAACCCAG AGCCTAAGAA	1500
	TGGCAGCGGT TTCTTAACAT GTTGAGAGAT GATTCTTTCT TGGCCCTGGC CATCTCGGGA	1560
60	AGCTTGATGG CAATCCTGGA AGGGTTTAAT CTCCTTTTGT GAGTTTGGTG GGAAGGGAA	1620

GGGTATATAG ATTGTATTAA AAAAAAAG GTATATATGC ATATATCTAT ATATAATATG 1680
ACGCAGAAAT AAATCTATGA GAAATCTATC TACAAAMWAA AAAAAAAAAA AAAAAAAAAA 1740
5 AGGAATTCTGA TMTCAAGCTT ATCGATACCG TCNACC 1776

10

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 443 base pairs
15 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

ACAGATAAAT AAATAAATAA TAAATTAAAT TAAATAAAAA ATCTGAGCTA ATCTGAATAA 60
ATTGAGAGAT TTCACATGAA AGCCAGGATT TCTGGCTTCC CAGGAACAGT CAGAAGAGCT 120
25 AGCTAGCAAC ACTGGTCTGC TTGGCTACCT TCTTTGGAAC AACATGAAAT CTAGCTCCCT 180
TTTTTTTTTT TTTTGGCCC ACTTCATCCA TTCACATGAC CTGCCTGGCC TCTGCAGGTA 240
AGTGAGTATG CAACAAAAAT GTAGCACAGG TTTTGTGCTT GAACTACGTG GTTTCAGGTC 300
30 CAGCTCTGCC ACTTGCTAGC ATGACCTCGT GCCGAATTCC NGCAGCAAGT TTTTTTTTTT 360
TTTTTCAGTG CTCCAGTCCC CCTATTGGAG AATCCTGCCC CCCCTGGGA CAGAAATGTC 420
35 ACCCTGGCCC CGCGANTCCC TGA 443

40 (2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2888 base pairs
(B) TYPE: nucleic acid
45 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

50 TTAATGTTGT CAATAACCAC CAGGCCAAAC AGAATTATA TGACCTGGAT GAAGATGATG 60
ATGTTATAGC TTCCGTTCTT ACTAAACAGA TGAAGTTTGC AGCCTCAGGC GNCCTTCTCC 120
ACCACATGGC TGGGCTAAGC AGTTCCAAGC TTTCCATGTC CAAGGCCCTC CCTCTACCA 180
55 AAGTGGTTCA GAATGATGCA TACACAGCTC CTGCTCTCCC TTCTCTATT OGAACAAAAG 240
CCTTGACCAA CATGTCCCGG AACTGGTGA ACAAGGAAGA ACCCCCCAAA GAGCTGCCAG 300
60 CTGCTGAGCC TGTCTCAGC CCATTGGAAG GCACCAAGAT GACTGTGAAT AATCTGCACC 360

	CTCGAGTCAC TGAGGAGGAC ATTGTTGAGC TTTTCTGTGT GTGTGGGGCC CTCAAGCGAG	420
5	CTCGACTGGT CCATCCTGGG GTAGCGGAGG TGGTGTTTGT GAAAAAGGAC GATGCCATCA	480
	CCGCATATAA GAAGTACAAC AACCGGTGTC TGGACGGGCA GCCGATGAAG TGCAACCTTC	540
	ACATGAATGG GAATGTTATC ACCTCAGACC AGCCCATCCT GCTGOGGCTG AGTGACAGCC	600
10	CATCAATGAA AAAGGAGAGC GAGCTGCCTC GCAGGGTGAA CTCTGCCTCC TCCTCCAACC	660
	CCCCTCGYGA AGTGACCCTT GACACCATCC TGAAGGCACT CTTCAAGTCC TCAGGGGCTT	720
15	CTKTGACCAC GCAGCCCACA GAATTCAAAA TCAAGCTTTG AGCAGGGGAG TGAGGCAGCC	780
	AGAAGTGGGG GCAGAGGAGG GTGGCTCTGT TTCCCAAGG CAAAGCTTAT GACCAATGGG	840
	CCATCGGACT GGAGACCCCT GATTGTGGGA AGGGTTGCCA GGGATAAAGA GCTTCCTCAC	900
20	TGGATGGGAC CCGCCTTTCT GTGTTGTGTT CTGCCCTGTG CTCTCTCTC TACGTTAACG	960
	TTTCCTGTAG TATGTTCTT CATCTCATCG CCAAGGTAGG CTTGTGTTTT TCAGTGTGTG	1020
25	CCTCCCGAG CCTCAGCCCC AAGCTGATTT CTTATCTGGA AATGGTACAC TGAATCTCT	1080
	GGGTGGCTTT CTTGTGGCCC CATGGGATGC AGCGTGGGG CTGTCTGAAG GACCCGTCTT	1140
	TTTCCAGGGG CCGAGGGGCT GCCTTTCTCT TGTGTGTATT AAGCTTTTCA ACAAATGGAG	1200
30	GGGATGGAGA GCCCTGGTGT CCTGACGGGA GCCAGGTGG CCTGAGAGCT GTGCCGCTCC	1260
	TCTGTCTGT CAGTGGAGGT GCCTGGGTGG GGAGCAGGTC TCAGGCCCTCT TGTCTCTCC	1320
35	CCAGTGGCTC CAGGCCTCAC TAGTGGCAAG GGCAGGATGA GGCTGCACCG CTGGGAAGAG	1380
	TCTATCTAAG YTCTTGGCTT GGAGTCCCGT GTCGTCTCCR CCCAGAGGAA GTTCTCCAGA	1440
	GTTACCTTT CCCTTTTCTT TGAGTTGTGC TGAATGCCCC ACCCCAGCTC TCTTTCCCTT	1500
40	CTGGGTGTCT TTGCTGGAG GGGGCTGTGT TGTGAGCCCT CCCGGTTCTC ACCTCGCCTG	1560
	GCACTTAACC ACACCTGGT TTTGTGTAGC CGCCAGCTCT CTTCTGGTTG GGCCTTTGAA	1620
45	AGGCTCAGCC TCCCATTTGT CAGTGCTTGG GTTTGGAGCT TATTTGAATG GAAGAGGTCA	1680
	GTTTGTTCCT GGCTCTCCAT TTCTGGCCTC AGTTGTCTAC AGGACAGTGG TCAGGGATGC	1740
	CTGGAGGCAT ATATCCAGCT GCCACCAAG GGCAGTGTG GTTCCCACTT ATGTGAGTGA	1800
50	CCCCATCCAT CCATGACCAG AGGATTATTT TCCTGCCTTG GCAGAGGAGG AGGAGTCAAG	1860
	GGAGCAGGGC AGCTCTACCA GGCAAGGTGT TTCCCCAGCA TAGGCGCAGA CAGTTGGGAC	1920
55	GAAACTTCAG AGCCCAGGCA GTCCCTGAAT GACCAGGCCA GTGTTGTAC TGAGTGGTCC	1980
	CCTGCTGGTT GGGAGTGAAG AGAATCCAGG CTGGCAGAGC TGGAGCCAGT TGGGGAGCAC	2040
	GGTTCTGGGA GCTCTGAAA ATCAGTAGCA AGTGCTGGAA AAGGCACATG CCGAAGATAC	2100
60	TCAAGAGCTC CCAAGATTTG CTTGAGGCTA GCCCAGTGAA RAAAACCAGA GACTCATGTT	2160

	TCCAGGGGTC AGTCTGTGAG GCAGGAAGGA CCCAGGATTT GAAOCCAGCT TCAGTGTGCA	2220
5	GGCTCTGAGG CTGCCCAGGA CGGGAAAGTC CAAGGAAGGG GCCTGGTGGT GCTCCACTTG	2280
	CAGTCTCTTA AAGAATGCTG CTTTTTATTC TCCTAACCCCT TTCAAGTGGG TGCAGACTTC	2340
	TCGTTAGCAG CTGGAAGACA TTCCTCCAC ACTTTTCCCT TCCTGGCCCA AGAGAGCATC	2400
10	CAGAAGGCAG TAGGACCTGG TTTTTCAGGT ACTGGGAGCC GGGGGCTCAC TGCTTGCACT	2460
	GTGCTTAGGG TAGGGATGGT AAATATCCTC CCTGCATGGC TTTATCCTCC CTCTCATCCC	2520
15	AAAGCAGGTA TCTTCTGGTT GTCACAGAGT TTCATTGAGT CCAGCTGCAG CCACGTGGCC	2580
	ATCTGGAGCT GGTGCTATAG GTGACCATCT GGTACATTGA GGGGACCTGT TTGCCTCCTC	2640
	CACTCTATAA GCAGTCATCT TGGGAGACCG GGAGGAGAAG GTGGTGGGCT AGTCTCTGTGT	2700
20	CCTCCTCCAC TTCCCATGCC TCTATGTTAC CCATCTGTGT CTCTGTGCA GAAGGAGAGG	2760
	AAGGGGCATT AAGAGATGAA GGGTGATTAT GTATTACTTA TCCATTTCTG AATAAACATT	2820
25	TGTTATTCTCT AAAAAAAAAA AAAAAAACT CGAGGGGGGG CCCGGWACCC AWATCGCCSK	2880
	AAAGTGAG	2888

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(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 1851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

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	CACTAGTATA ATTTATAATT ATAACCTATT CTGATTTCCT TTCAAATATT AGGTGTCTTA	60
	GTGCGCTATG AAGGTTTGCC ACTTCATCTT GCACTGTTCC CCAAACCTTG GACTGAGCTA	120
45	TGCCAGACTC AGTCTGCTAT GTCAAAAAC TGCATCAAGC TTTTGTGTGA AGATCCTGTT	180
	TTGCGAGAAT ATATTAAATG TATCCTAATG GATGAAAGAA CTTTTTTTAA CAACAACATT	240
50	GTCTACACGT TCATGACACA TTTCTTCTA AAGGTTCAAA GTCAAGTGTT TTCTGAAGCA	300
	AACTGTGCCA ATTTGATCAG CACTCTTATT ACAAACCTGA TAAGCCAGTA TCAGAACCTA	360
	CAGTCTGATT TCTCCAACCG AGTTGAAATT TCCAAAGCAA GTGCTTCTTT AAATGGGGAC	420
55	CTGAGGGCAC TCGCTTTGCT CCTGTGAGTA CACACTCCCA AACAGTTAAA CCCAGCTCTA	480
	ATTCCAACCT TGCAAGAGCT TTTAAGCAAA TGCAGGACTT GTCTGCAACA GAGAACTCA	540
60	CTCCAAGAGC AAGAAGCCAA AGAAAGAAAA ACTAAAGATG ATGAAGGAGC AACTCCCAT	600

	AAAAGGCGGC GTGTTAGCAG TGATGAGGAG CACACTGTAG ACAGCTGCAT CAGTGACATG	660
	AAAACAGAAA CCAGGGAGGT CCTGACCCCA ACGAGCACTT CTGACAATGA GACCAGAGAC	720
5	TCCTCAATTA TTGATCCAGG AACTGAGCAA GATCTTCCTT CCCCTGAAAA TAGTTCTGTT	780
	AAAGAATACC GAATGGAAGT TCCATCTTCG TTTTCAGAAG ACATGTCAAA TATCAGGTCA	840
10	CAGCATGCAG AAGAACAGTC CAACAATGGT AGATATGACG ATTGTAAAGA ATTTAAAGAC	900
	CTCCACTGTT CCAAGGATTC TACCCTAGCC GAGGAAGAAT CTGAGTTCCC TTCTACTTCT	960
	ATCTCTGCAG TTCTGTCTGA CTTAGCTGAC TTGAGAAGCT GTGATGGCCA AGCTTTGCCC	1020
15	TCCCAGGACC CTGAGGTTCG TTTATCTCTC AGTTGTGGCC ATTCCAGAGG ACTCTTTAGT	1080
	CATATGCAGC AACATGACAT TTAGATACC CTGTGTAGGA CCATGAATC TACAATCCAT	1140
20	GTCGTACAA GGATATCTGG CAAAGGAAAC CAAGCTCCTT CTTGACATTA GGTGTAGCAT	1200
	GTCTACTTTT AAGTCCCTCA CCCCCAACC CCATGCTGTT TGTATAAGTT TTGCTTATTT	1260
	GTTTTGTGC TTCAGTTTGT CCAGTGCTCT CTGCTTGAAT GGCAAGATAG ATTTATAGGC	1320
25	TTAATTCCTG GTCAGGCAGA ACTCCAGATG AAAAAAAGT GCATCTTCAG TATACTTCCT	1380
	AAAGGGCAAT CAGATAATGG ATATGTTTTA TGTAATTAAG AGTTCACTTT AGTGGCTTTC	1440
30	ATTTAATATG GCTGCTCGG AAGAACAGGG TTGCCTAGCC CTGTACAATG TAATTTAAAC	1500
	TTACAGCATT TTTACTGTGT ATGATATGGT GTCCTCTGTG CCAGTTTTGT ACCTTATAGA	1560
	GGCAGATTGC CTCCGATCGC TGTGGTCTTT ATTATCAAAA TTAAGTTTAC TTGTATACGG	1620
35	AACAACCACA AGAAATTGA TTCTGTAAAG AATCCTCTTT AGCTGTGGCC TGGCAGTATA	1680
	TAAATGGTGC TTTATTTAAC AGAATACCTG TGGAGGAAAT AAAGCACACT TGATGTAAAA	1740
40	ATAATGTTT TATTTTATT GACATGACTG ATTGATTGCT ATTCTGTGCA CTTAATTAAA	1800
	CTGATTGTGA TGAATTWAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA A	1851

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(2) INFORMATION FOR SEQ ID NO: 63:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3542 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

60	TCCAATGCTG ATGAGCGTCT TCGCTGGCAG GCCAGCTCCT TGCCTGCTGA TGACCTTTGC	60
	ACAGAAAATG CCATCATGCT GAAACGATTC AATAGGTATC CGCTGATCAT TGACCCCTCT	120
	GGACAGGCCA CAGAATTCAT TATGAATGAA TATAAGGWTG GTAAGATCAC ACGGACCAGC	180

	TTCTCTGGATG ACGCCTTCAG AAAGAACTTA GAGAGTGCAC TGAGATTTCG TAACCCCTT	240
5	CTGGTCCAGG ATGTGGAAAG CTACGATCCA GTTTTGAACC CGGTGCTGAA CCGTGAAGTG	300
	CGGCGAACAG GGGGAGAGT GCTGATCACT CTCGGGGACC AGGACATAGA CCTGTGCGCA	360
	TGTTTGTCA TCTTCTGTC CACCCGGGAT CCAACTGTGC AGTTCACAC AGATCTCTGT	420
10	TCCCCGGTTA CTTTGTAAA CTTACAGTT ACCCGTAGCA GTTTACAAAG CCAGTGTCTA	480
	AATGAAGTAC TTAAAGCAGA AAGACCTGAT GTGGACGAGA AACGATCTGA TCTTCTTAAA	540
15	CTTCAAGGGG AATTTACAGT CCGTTTGCCT CAGCTGGAAA AATCTCTACT ACAAGCTCTG	600
	AACGAGGTGA AAGGGCGCAT TTTGGATGAC GACACGATCA TAACCACTCT GGAGAACCTG	660
	AAGAGAGAGG CTGCAGAGGT CACCAGGAAA GTTGAGGAGA CGGACATTGT CATGCAGGAG	720
20	GTGGAGACCG TGTCCAGCA GTACCTCCCG CTCTCCACCG CCTGCAGCAG CATCTACTTC	780
	ACCATGGAGT CCTCAAGCA GATACACTTC TTGTACCACT ACTCCCTCCA GTTTTTCCTG	840
25	GACATTTATC ACAACGTCCT ATACGAGAAC CGGAACCTGA AGGGTGTAC CGACCACACA	900
	CAGCGCCTGT CCATTATAAC AAAGGACCTC TTCCAGGTGG CGTTTAACCG AGTGGCTCGA	960
	GGCATGCTGC ATCAGGACCA CATTACCTTT GCCATGCTGC TGGCAAGAAT CAAACTGAAG	1020
30	GGCACCGTGG GGGAGCCAC CTACGATGCA GAATTCACG ACTTCTTGAG AGGAAATGAG	1080
	ATTGTCTGA GTGCTGGCTC CACCCCCAGG ATCCAGGGCC TGACTGTGGA GCAGGCGGAG	1140
35	GCGGTGGTGA GGCTGAGCTG CCTTCCCGG TTTAAGGACT TGATTGCAA GGTTCAGGCA	1200
	GACGAGCAAT TTGGCATCTG GCTGGACAGC AGCTCCCCG AGCAGACTGT GCCCTACCTC	1260
	TGGAGTGAAG AAACACCTGC AACACCCATT GGCCAGGCCA TCCACCGCCT GCTCCTGATC	1320
40	CAGGCTTTCC GGCCGATCG CCTGTGGCC ATGGCCACA TGTTTGTTT AACAAACCTT	1380
	GGGAGTCTT TCATGTCCAT CATGGAGCAG CCGCTCGACC TGACCCACAT TGTGGSCACA	1440
45	GAGGTGAAGC CCAACACTCC TGTCTTAATG TGCTCTGTGC CTGGTTATGA TGCCAGTGGA	1500
	CATGTCGAGG ACCTTGCAGC CGAGCAGAAC ACGCAGATCA CTTCAATTGC AATCGGCTCT	1560
	GCAGAAGGCT TTAACCAAGC AGATAAGGCA ATAAACACCG CTGTAAAGTC GGGCAGGTGG	1620
50	GTGATGCTGA AGAATGTGCA TCTGGCCCCA GGGTGGCTGA TGCAGCTGGA GAAGAAGTTG	1680
	CATTCCCTGC AGCCGATGC CTGCTTCCGA CTCTTCCTCA CCATGGAGAT CAACCCCAAG	1740
55	GTGCCTGTGA ATCTGCTCCG TGCGGGCCGC ATCTTTGTGT TCGAGCCACC GCCAGGGKTG	1800
	AAGGCCAACA TGCTGAGGAC GTTCAGCAGC ATTCCCGTCT CACGGATATG CAAGTCTCCC	1860
	AACGAGCGTG CCCGCTTGTA CTTCTGCTG GCCTGGTTTC ATGCGATCAT CCAAGAACGC	1920
60	TTACGATACG CACCACTGGG GTGGTCAAAG AAGTATGAAT TTGGAGAGTC TGACCTGCCG	1980

	TCANYTTGCG ATACGGTGGA CACGTGGCTG GATGACACGG CCAAGGGCAG GCAGAACATC	2040
5	TCACCGGATA AGATCCCGTG GTCTGCACTA AAGACCTTAA TGGCCCGATC CATTTATGGC	2100
	GGGCGCGTGG ACAACGAGTT TGACCAGCGT CTGCTCAACA CCTTCCTGGA GCGCCTGTTC	2160
	ACAACCAGGA GTTTCGACAG TGAGTTTAAG CTGGCATGCA AGGTCGACGG ACATAAAGAC	2220
10	ATTCAAATGC CAGATGGCAT GCAGGCGAGA GGAGTTTGTG CAGTGGGTGG AGTTGCTCCC	2280
	CGACACCCAG ACGCCCTCCT GGCTGGGCCT GCCCAACAAC GCCGAGAGAG TCCTCCTTAC	2340
15	CACACAGGGT GTGGACATGA TCAGTAAAAT GCTGAAGATG CAGATGTTGG AGGATGAGGA	2400
	CGACCTGGCC TACGCAGAGA CTGAGAAGAA GACGAGGACA GACTCCAGT CCGACGGGCG	2460
	CCCTGCCTGG ATGCGGACAC TGCACACCAC CCGCTCCAAC TGGCTGCACC TCATCCCCCA	2520
20	GACGCTGAGC CACCTCAAGC GCACCGTGGA GAATATCAAG GATCCTTTGT TCAGGTTCTT	2580
	TGAGACAGAA GTGAAGATGG GCGCAAAGCT GCTTCAGGAC GTTCGCCAGG ACCTTGCAGA	2640
25	TGTCGTCCAG GTGTGCGAAG GAAAGAAGAA GCAGACCAAC TACTTGCGCA CGCTGATCAA	2700
	CGAGCTAGTG AAAGGGATCT TGCCTCGGAG CTGGTCCAC TACACGGTGC CTGCCGGCAT	2760
	GACCGTCATC CAGTGGGTGT CCGACTTCAG CGAGAGGATC AAACAGCTGC AGAACATCTC	2820
30	ACTGGCAGCT GCATCTGGTG GCGCCAAGGA GCTAAAGAAC ATCCAAGTGT GCCTGGGTGG	2880
	CCTGTTGGTG CTTGAGGCGT ACATCACTGC CACCAGGCAG TATGTGGCCC AGGCCAACAG	2940
35	CTGGTCCCTG GAGGAGCTCT GCCTGGAAGT CAAAGTCACC ACCTCAGAG GCGCCACCCT	3000
	TGACGCTTGC AGCTTCGGAG TCACGGGTTT GAAACTTCAA GGGGCCACGT GCAACAACAA	3060
	CAAGCTGTCA CTGTCCAATG CCATCTCAAC CGCCCTTCCC CTGACGCAGC TGGCTGGGT	3120
40	CAAGCAGACA AACACCGAGA AGAAGGCCAG TGTGGTAACC TTACCTGTCT ACCTGAACTT	3180
	CACCGTGCA GACCTCATCT TCACCGTGGA CTTGAAAATT GCTACAAAGG AGGATCCTCG	3240
45	CAGCTTCTAC GAGCGGGGTG TCGAGTCTT GTGCACAGAG TAAACTTTTC TAGCTGCCCC	3300
	TTTCTGTAAT AGTGAAAGTT GGTATTTAAC ATTTATTCAT TTTTAAAATA TTTGGAAGGT	3360
	CTGAGCTTGT GAAAAGAAAG TGGTTGGTCT GAGGTGGAG GAAGCTGAAT GGAATCTGAC	3420
50	GGTGGGAGT GGTGGAAATT GGAAGGATAC CAGGAGGTAT TTGGGAAGGC CAATGGCGTG	3480
	GCTCCTTTGA GGAAATAAAA CACTAAGCAT GAAAAAATAA AAAAACTTA CAANCCNCAA	3540
55	GG	

60 (2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 883 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

10 AGGTGATTTT AATGATAGGT GTCATATATA GGACGGATAA TCTGTTTACA TTCTGTTCTT 60
CTCGATGCAC TCACAAGCGG GTAAGTAGGT GACAAGAAAA CAAAGATCTT ATTCAAAGA 120
GGTCTTACAG CAACCCAACG TCTCATCTTC CCATAGTAAA GATGACGGCG CCTTGAGGTA 180
15 AGCTACAGGC AACACCACTT CCGCGTTTCT CTGCGCCCT GGTCCAAGAT GGCGGATGAA 240
GCCACGGAC GTGTTGTGTC TGAGATCCCG GTGCTGAAGA CTAACGCGG ACCCGGAGAT 300
CGTGAGTTGT GGGTGACGG ACTGAAGGAG GAATATCAGT CCCTTATCCG GTATGTGGAG 360
20 AACACAAGA ATGCTGACAA CGATTGGTTC CGACTGGAGT CCAACAAGGA AGGAAGTCGG 420
TGGTTTGGAA AATGCTGGTA TATCCATGAC CTCCTGAAAT ATGAGTTTGA CATCGAGTTT 480
25 GACATTCCTA TCACATATCC TACTACTGCC CCAGAAATTG CAGTTCCTGA GCTGGATGGA 540
AAGACAGCAA AGATGTACAG GGGTGGCAA ATATGCCTGA CGGATCATTT CAAACCTTTG 600
TGGGGCCAGG AATGTGCCA AATTGGACT AGCTCATCTC ATGGCTCTGG GGCTGGGTCC 660
30 ATGGSTGGCA GTGGAATCC CTGATCTGAT TCAGAAGGGC GTCATCCAAC ACAAGAGAA 720
ATGCAACCAA TGAAGAATCA AGCCACTGAG GCAGGCAGA GGGACCTTTG ATAGGCTACG 780
35 ATACTAWTTT CCTGTGCATC AACTTAACT CATCTAAGT TCCCCCGAC ANCTCCACT 840
CTAGTTGTTA CTAAGTANTG CAGTAGCATT MTGGGAAGA ACA 883

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(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1541 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

GGCAAGAGGT GGCCTCTACC CTGGGCTCAT CTGGCTACAC AGGGACTCTA AACGCTTCCA 60
GATTCCTTGG AAACATGCCA CCCGGCATAG CCCTCAACAA GAAGAGGAAA ATACCATTTT 120
55 TAAGGCCTGG GCTGTAGAGA CAGGGAAGTA CCAGGAAGGG GTGGATGACC CTGACCCAGC 180
TAAATGGAAG GCCCAGCTGC GCTGTGCTCT CAATAAGAGC AGAGAATTCA ACCTGATGTA 240
60 TGATGGCACC AAGGAGGTGC CCATGAACCC AGTGAAGATA TATCAAGTGT GTGACATCCC 300

TCAGCCCCAG GGCTCGATCA TTAACCCAGG ATCCACAGGG TCTGCTCCCT GGGATGAGAA 360
 5 GGATAATGAT GTGGATGAAG AAGATGAGGA AGATGAGCTG GATCAGTCGC AGCACCATGT 420
 TCCCATCCAG GACACCTTCC CCTTCCTGAA CATCAATGGT TCTCCCATGG CGCCAGCCAG 480
 TGTGGGCAAT TGCAGTGTGG GCAACTGCAG CCCGGAGGCA GTGTGGCCCA AAAGTGAACC 540
 10 CCTGGAGATG GAAGTACCCC AGGCACCTAT ACAGCCCTTC TATAGCTCTC CAGAACTGTG 600
 GATCAGCTCT CTCCCAATGA CTGACCTGGA CATCAAGTTT CAGTACCGTG GGAAGGAGTA 660
 CGGGCAGACC ATGACCGTGA GCAACCCTCA GGGCTGCCGA CTCTTCTATG GGGACCTGGG 720
 15 TCCCATGCCT GACCAGGAGG AGCTCTTTGG TCCCGTCAGN CTGGAGCAGG TCAAATTCCC 780
 AGGTCCTGAG CATATTACCA ATGAGAAGCA GAAGCTGTTC ACTAGCAAGC TGCTGGACGT 840
 20 CATGGACAGA GGAATGATCC TGGAGGTCAG CGGTTCATGCC ATTTATGCCA TCAGGCTGTG 900
 CCAGTGCAAG GTGTACTGGT CTGGGCCATG TGCCCCATCA CTGTGTGCTC CCAACCTGAT 960
 TGAGAGACAA AAGAAGGTCA AGCTATTTTG TCTGGAAACA TTCTTTAGCG ATCTCATTCG 1020
 25 CCACCAGAAA GGACAGATAG AGAAGCAGCC ACCGTTTGAG ATCTACTTAT GCTTTGGGGA 1080
 AGAATGGCCA GATGGGAAAC CATGTGAAAG GAAACTCATC TTGGTTTCAGG TCATTCCAGT 1140
 30 AGTGGCTCGG ATGATCTACG AGATGTTTTC TGGTGATTTC ACAOGATCCT TTGATAGTGG 1200
 CAGTGTCCGC CTGCAGATCT CAACCCAGA CATCAAGGAT AACATCGTTG CTCAGCTGAA 1260
 GCAGCTGTAC CGCATCCTTC AAACCCAGGA GAGCTGGCAG CCCATGCAGC CCACCCCCAG 1320
 35 CATGCAACTG CCCCTGCCC TGCTTCCCA GTAATTGTGA ATGCCATCTT CTCTCTCTC 1380
 TTTTATATAA TATTGTACAT ATGGATTTTT TTAATTGTTA GATTTAACCA GCTTTTAAAT 1440
 40 CTCTGTTTTT TGTGACAGTG TTAGAAGTTT GTGATCTCC AAATATGCCT AGATTTAAAG 1500
 CTGATTTAAT TTATGGAAAA AAAAAAAAAA AAAAAAAAAA A 1541

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(2) INFORMATION FOR SEQ ID NO: 66:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 732 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

AGAAAAATGAA TGTTAGAAGG TGCTGCCGA GGCGGACAG AGTGTTCGCT CGCGCTGGAG 60
 60 AAGGCTCTGC TCAGCCCTGA GAGTCCCTTC CTGCCCCACC GATACTGGCA CTTTAAAAAG 120

GAAGCTGACC GCACAGTGTG CAGACGAATT GGCCCCCAGA AGATGGGGAG TTCTGTCTTG 180
 CCTTCTGTG TCTGCGTGAC CTCACCCAGC CTAGGAGGGA GGTGCATTCA GGGTAGATTT 240
 5 GCCTCTCATT CAAAGTCTG GGGCTTTGGG CGGAAAACAG CCAGCTTTGG CGCTGTGGG 300
 GAGACTCCTC CAGACCAGGA ACCCCAGAAG GAGACAGAGC CTGCCACATC CTCACAGCC 360
 10 AGGCCCTGGG CCAGGGTGAT TGGACTGAGA ATTTGGCCAC AACCAAATG ATGCTGGCTG 420
 GAACCAGAGG CCAGAAAGCC TGGCCTGTG CCCATGTGGG AGCCCTGTCC TCAGCCCTCT 480
 TGTCCCTTG AGCTCAGTGA ATTCCACCA GGTGCCACA GCTCCTGGAC TTCAAATCT 540
 15 ATATATTGAG AGAGTTGGAG AGTATATCAG AGATATTTTT GGAAAGGAGT TGGTCTATGC 600
 AATGTCAGTT TGAATCTTC TTGAAAGTTT AATGTTTTTA TTAGGAGATT TAAAGAAAAT 660
 20 AAAGGTCTAC AATATCAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 720
 AAAAAAAAAA AA 732

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(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 629 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

35 TTAAGGAATT CGGCMCGATC CCGCAAGTA ACATGACTAA AAAGAAGCGG GAGAATCTGG 60
 GCGTCGCTCT AGAGATCGAT GGGCTAGAGG AGAAGCTGTC CCAGTGTCGG AGAGACCTGG 120
 40 AGGCCGTGAA CTCCAGACTC CACAGCCGGG AGCTGAGCCC AGAGGCCAGG AGGTCCCTGG 180
 AGAAGGAGAA AAACAGCCTA ATGAACAAAG CCTCCAATA CGAGAAGGAA CTGAAGTTTC 240
 45 TTCGGCAAGA GAACCGAAG AACATGCTGC TCTCTGTGGC CATCTTTATC CTCCTGACGC 300
 TCGTCTATGC CTA CTGAGACC ATGTGAGCCT GGCACCTCCC CACAACCAGC ACAGGCTTCC 360
 ACTTGGCCCC TTGGTCAGGA TCAAGCAGGC ACTTCAAGCC TCAATAGGAC CAAGGTGCTG 420
 50 GGGTGTTCCT CTCCTAACCT AGTGTTCAG CATGGCTTCC TGGGGGCCA GGCCTTGCCT 480
 CCCTGGCCTG CTGGGGGGTT CCGGGTCTCC AGAAGGACAT GGTGCTGGTC CCTCCCTTAG 540
 55 CCCAAGGGAG AGGCAATAAA GAACACAAAG CTGAAAAAAA AAAAAAAAAA AACTCGTAGG 600
 GGGGGCCCGT ACCCAATCGC CCTNTCGTG 629

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(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1751 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

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CTGCTAGCCG GCCGGCCGAG GCTGCCGAGC GGGTGAGCGC GCAGGCCAGG CCAAAGCCCT 60
 GGTACCCGCG CGGTGCCGGC CTCAGTCTGC GGCCATGGGG GCGTCCGCGC GGCTGCTGCG 120
 AGCGGTGATC ATGGGGGCCC CGGGCTCGGG CAAGGGCACC GTGTGCTGCG GCATCACTAC 180
 ACACTTCGAG CTGAAGCACC TCTCCAGCGG GGACCTGCTC CGGGACAACA TGCTGCGGGG 240
 CACAGAAATT GGCGTGTTAG CCAAGGCTTT CATTGACCAA GGGAACTCA TCCCAGATGA 300
 TGTCACTACT CGGCTGGCCC TTCATGAGCT GAAAAATCTC ACCCAGTATA GCTGGCTGTT 360
 GGATGGTTTT CCAAGGACAC TTCCACAGGC AGAAGCCCTA GATAGAGCTT ATCAGATCGA 420
 CACAGTGATT AACCTGAATG TGCCCTTTGA GGTCACTAAA CAACGCCCTA CTGCTGCTG 480
 GATTCATCCC GCCAGTGGCC GAGTCTATAA CATTGAATTC AACCTCCCA AAACGTGGG 540
 CATTGATGAC CTGACTGGGG AGCCTCTCAT TCAGCGTGAG GATGATAAAC CAGAGAOGGT 600
 TATCAAGAGA CTAAAGGCTT ATGAAGACCA AACAAAGCCA GTCCTGGAAT ATTACCAGAA 660
 AAAAGGGGTG CTGGAACAT TCTCCGAAC AGAAACCAAC AAGATTGGC CCTATGTATA 720
 TGCTTTCCTA CAACTAAAG TTCCACAAAG AAGCCAGAAA GCTTCAGTTA CTCCATGAGG 780
 AGAAATGTGT GTAACATTA ATAGTAAGAT GGGCAAACCT CCTAGTCCTT GCATTTAGAA 840
 GCTGCTTTTC CTAAGACTTC TAGTATGTAT GAATTCCTTG AAAATTATAT TACTTTTATT 900
 TCTACTGATT TTATTTTGA TACTAAGGAT GTGCCAAATG ATTCGGATAC TAAGATGCAT 960
 CGTTTGAAAT CATCTAGTGT GTTGATGCA GTTATCCTCA AAAACATCAG CGATGTCTGA 1020
 ACCTTTAAAA CATCTGTTAG AGCAAAATTA AAAGAGCATT TGGTAGTAAT CTAACTTTTT 1080
 GTTCAGTTAA TAAGTGGTTG ATAAAGTTTC CATATTTTTC TGGAAAAGTT AAAAAAAGTT 1140
 ACATGTCATT TGGAGAAAAT ACGTAATCAG AAATTTGTGC ATAGATTGAT GCCAAAAAG 1200
 ACATTTCCAG CATGTGGAA CATGGTGAGA CACTATATAA AATTCCAGAA AGAAAGCAAC 1260
 TGGATTTACA GATTTATGT GAGACACAAA TTCACTGCTG CCTTTACACT AAGAAATGTA 1320
 TATGTTAACC ATATATGCTG TATTTATTTT GTCGTTAAGC ATACTTTCAG TTTACTCAGA 1380
 ATTTTCAATT TGCTATAAAG ATGTATCAAT TAGCATATAG AAAATATTA CTTTAAGATG 1440
 ACTTGTTTCC TTTGAAAATA CCTGTGTACT GAGGGTTATG ATTTGTGTCA AAAATTGACA 1500

TAAGTGCTTT TACAAGCACC AAAGTTGAAT GAATTTTCAA CAAAATGTAA TTAAAGTCTA 1560
 TGTTTTCAGT TATGACTCAG GTTAAGAAAT GTGTTTTAGG ATCTACTTGC TGGTTTTTCT 1620
 5 TTTTGATCCA AATGTGTGAT CTGCCCTGAT AAATAACAAG TTATNGTACC ATCTCCCCCG 1680
 CCAATAAAAA AAAAAAAAAA AAAAAAAAAAC TCGAGGGGGG GCCCGGTACC CAATTCTCCG 1740
 NAATAGGNAG T 1751
 10

(2) INFORMATION FOR SEQ ID NO: 69:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

GGCACGAGAT TATGTATTAA AATGTTTTTG AATGTGAAA TATTAGAATA TTGTTACTAT 60
 25 TTGACCCAAC TCAAAATCTC CATGGGAAAA TACCTGTCGA TACCCACAGT ATTGTGAAA 120
 ATAATCAGAT GCAGTATCAC AGCTGTGTCA GACTCTAGTA CCAGTTGGGC AATCAAGGCA 180
 30 CAGCTAAAAA TTGAAAACAA AGATCTGGAC AACAAAACAG CCAAAGGTGG GGTCAAGAA 240
 GCTCTGACGT GTACCTAGCT GTAGAATGCT ATGCACACGT GCCAGGTGTA GTGTGCATAT 300
 CCAGGAAAAA CTGCAGAGAG CCCAGTCTT CACCTCTGGT TGACCATGAG CTCTGTGTAA 360
 35 GCAGGAAGTG AAGGCTAAGG CAGATTTAAG CTCTGAAAGC ATTCCACAAC ATACACACAA 420
 ATCGTGCAAA GCATTAAGGA AATCTTGTTA CTGCTAAGTG TTGCTGACCC AGGAACAAC 480
 40 CCTACTCAGC TGGACTTAAA AATAAAAA 508

45 (2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

TACATAGAGC AAAGAGAAAT TTCCAGAATT TCTARAATTC TGGAAAGAGA ATTTTCCTGA 60
 GATTGCAGAT TTGCTTGTGT CCTCAGGTGA TGATGAGGGC TGTMTTCCCC TGTGTCTCTT 120
 60 TCCTCACACT CATGCTTCCT CTCCTAGAGT GTCTGGTTGG CATGATCATG TGCTACCTAG 180

GCATTTCTTT CACTGATACA AGGAAACTG CAGGGTTAAA AAAAAAAAAA AAAAAAAAAA 240
NCNCG 245

5

(2) INFORMATION FOR SEQ ID NO: 71:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 361 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

ATGTTCTCTCA TGAGGATGCA CTTGTGCTTC TGCAAGTATT GCTGCAGCTT CATAGTGACT 60
20 CCCACCAGCA CCAGCAATAC AGCTAGCTAC CTGTGGCCTT GGATCTCAGC CAGCATGGCT 120
GGGAGAGGGA GCAGCTGGGC ATGTACCCTA AATGCTGTTA CCAGGGAAGG ACTCCCAGAG 180
TGAAGACAAG TAGGGACTTC CTGCAGAGGT GGTACATGTG CTCTCTGTAT CCATACTTTT 240
25 TTTTTTTTTT TTTTGAGATA GAGTTTCACC CTTGTTGCCC TGGCTGGAGT GCAATGGTGC 300
GATCTCAGCT CACTGCAACC TCTCTGCTC CCGGGTTCAA GTGATTCTCC TGCTCAGCC 360
30 T 361

35 (2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 713 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

45 AGGATCACAC AATAGAGAAC ACTGTAGTAA CATTTGCGTC TGCTCACAAG ACCCAGAACA 60
TTGATCAGTT TTTGTTGTG GTTTATTATT TTCTGTATAA AAAATTGTGA AAAGTTTGTT 120
TTAGCTAGAT GATATTTTAA TAGCTGCGAG TGCTTTGGAA CTATAAAGAT GTCACTACTT 180
50 AACACACATA CCTTATGTTT TGTTTTGTTT TGTTTTACAC TCAGTATAAA TCAGGAGAAG 240
TTAGCCAACC ATCTAGCATT TAGAATCCTC TTTTTTATTG TCTTCTAAGG ATATGGATGT 300
55 TCCCATAACA GCAACAAAAC AGCAACAAA ACATTTTATA AATATCACTT GATAGACTGT 360
AAGCACTGC TTAACCTTGT GTCCCAAATA TTTAGTGTGT ATATATATAT ATATATATAC 420
ACACACACAC ACATATATAT TCAACAAATA AAGCAAATA TAACATGCAT TTCACATTTT 480
60

GTCTTCCCT GTTACGATTT TAATAGCAGA ACTGTATGAC AAGTTTAGGT GATCCTAGCA 540
TATGTTAAAT TCAAATTAAT GTAAAACAGA TTAACAACAA CAAAGAACT GTCTATTTGA 600
5 GTGAAGTCAT GCTTCTATT ATAATAACTT GGCTTCGGTT ATCCATCAA TGCACACTTA 660
TACTGTTATC TGATTGTTA TAATAAGAA TACTGTACTT ATAAAAAAAA AAA 713

10

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:
15 (A) LENGTH: 862 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

GAAAGTCAGA GCTGTCCAAT CCCTCAGCAC CTTTATGATT TGCTCCAAAT TAGAAACGTG 60
GGGACTATGT GTTCTGGGCA ATCAGAGTC TGGAAATGG CTCTGCAGGC TCTTGATAGT 120
25 GAGACAGTGG TCATCTTACC AGACATGCAT CTGATTTTAA GCCTCAGGCT AATCCACAAT 180
GCTCGCCAT GCCTATGATT AACAAACAAA AGCAAATCT GCTTTATAG TTTAGGAAAC 240
30 CTGGATAGAA CAGTATTTTT CAGCATTCTT GGATAAGCA GTTCTGCATT TTAAATTGG 300
GACTGCAGAA GTGACTGTCT ATAGTTGTGA AATACAAAA ATGGTATGTT TGATCAGAAA 360
AGGAAGCCCG TGCTGGCAC TTGGAAAGAT ACTGAGCATC ATAACCCTAA TGAGAAAATG 420
35 TAGGCTCTGT GAATGTTAAC TACAAATCAG GTTAGGAAAG CATATGACAC CCTTTGTCAA 480
ACTAAGCTTC ACTAGGAGGA CCTGTGCTCA TAGAAGAATA TGCTTTAAAA GTATCAATTT 540
40 TCCACAGTCG ATGATGGAGA AAAGTTCATT TGCACCAGAA TGCTGATAGT CACAATACAC 600
AGCCTGACAT ATATAACAAT ACAGTTTCT GTAAACAGAA GTTCTTCCTC TTCCAATTCA 660
GGAGTCAGTC AGAGCATAAA TATTGCATGT TTCACTTTAG AAAGTATTC ATTTTAGAAA 720
45 GCAGATCTGG ATTATTTTGC AGGGTAGAAA TGAAGGCTAT TTCTGGCATT CTGCTCAA 780
AAGTCAATAT ATGTACATTA AGTATAAAAA AGGGTCTCTT TCACCTCTTT TGTTCGTAG 840
50 CATTGGCTAC ATAACCTGTG CC 862

55 (2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:
60 (A) LENGTH: 4602 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

5	GCGAGGGGGC GKGGGGAGCA GCGCCGARGC CGCCGCCTCC GCCTCCGCGC CCTAGGACTA	60
	GGGGGTGGGG GACGGACAAG CCCCGATGCC GGGGGAKACG GAAGAGCCGA GACCCCCGGA	120
10	GCAGCAGGAC CAGGAAGGGG GAGAGGCGGC CAAGGCGGCT CCGGAGGACC CGCAACAACG	180
	GCCCCCTGAG GCGGTCGCGG CGGCGCCTGC AGGGACCACT AGCAGCCGCG TGCTGAGGGG	240
	AGGTCGGGAC CGAGGCCGGG CCGCTGCGRC CGCCGCGCMG CAGCTGTGTC CCGCCGGAGA	300
15	AGGCCGAGTA TCCCCGCCCG CGAGGAGCAG CCCCAGCGCC AGGCCTCCCG ACGTCCCCGG	360
	GCAGCAGCCC AGGCCGGGAA GTCCCCGTCT CCAGTTCAGG GCAAGAAGAG TCCGCGACTC	420
20	CTATGCATAG AAAAAGTAAC AACTGATAAA GATCCCAAGG AAGAAAAAGA GGAAGAAGAC	480
	GATCTGCCC TCCCTCAGGA AGTTTCCATT GCTGCATCTA GACCTAGCCG GGGCTGGCGT	540
	AGTAGTAGGA CATCTGTTTC TCGCCATCGT GATACAGAGA ACACCCGAAG CTCTCGGTCC	600
25	AAGACCGGTT CATTCGAGCT CATTTGCAAG TCAGAACCAA ATACAGACCA ACTTGATTAT	660
	GATGTTGGAG AAGAGCATCA GTCTCCAGGT GGCATTAGTA GTGAAGAGGA AGAGGAGGAG	720
30	GAAGAAGAGA TGTTAATCAG TGAAGAGGAG ATACCATTC AAGATGATCC AAGAGATGAG	780
	ACCTACAAAC CCCACTTAGA AAGGGAAACC CCAAAGCCAC GGAGAAAATC AGGGAAGGTA	840
	AAAGAAGAGA AGGAGAAGAA GGAAATTAAA GTGGAAGTAG AGGTGGAGGT GAAAGAAGAG	900
35	GAGAATGAAA TTAGAGAGGA TGAGGAACCT CCAAGGAAGA GAGGAAGAAG ACGAAAAGAT	960
	GACAAAAGTC CACGTTTACC CAAAAGGAGA AAAAAGCCTC CAATCCAGTA TGTCCGTGTG	1020
40	GAGATGGAAG GATGTGGAAC TGTCTTGCC CATCTCGCT ATTTGCAGCA CCACATTAAA	1080
	TACCAGCATT TGCTGAAGAA GAAATATGTA TGTCCCCATC OCTCTGTGG ACGACTCTTC	1140
	AGGCTTCAGA AGCAACTTCT GCGACATGCC AAACATCATA CAGATCAAAG GGATTATATC	1200
45	TGTGAATATT GTGCTGGGC CTTCAAGAGT TCCCACAATC TGGCAGTGCA CCGGATGATT	1260
	CACACTGGCG AGAAGCATTA CAATGTGAGA TCTGTGGATT TACTTGTCGA CAAAAGGCAT	1320
50	CTCTTAATTG GCACATGAAG AAACATGATG CAGACTCCTT CTACCAGTTT TCTTGCAATA	1380
	TCTGTGGCAA AAAATTTGAG AAGAAGGACA GCGTAGTGGC ACACAAGGCA AAAAGCCACC	1440
	CTGAGGTGCT GATTGCAGAA GCTCTGGCTG CCAATGCAGG CGCCCTCATC ACCAGCACAG	1500
55	ATATCTTGGG CACTAACCCA GAGTCCCTGA CGCAGCCTTC AGATGGTCAG GGTCTTCCTC	1560
	TTCTTCCTGA GCCCTTGGGA AACTCAACCT CTGGAGAGTG CCTACTGTTA GAAGCTGAAG	1620
60	GGATGTCAAA GTCATACTGC AGTGGGACGG AACGGGTGAG CCTGATGGCT GATGGGAAGA	1680

	TCTTTGTGGG AAGCGGCAGC AGTGGAGGCA CTGAAGGGCT GGTATGAAC TCAGATATAC	1740
	TGGTGCTAC CACAGAGGTT CTGATTGAAG ATTCAGACTC TGCCGGACCT TAGTGGACAG	1800
5	GAAGACTTGG GGCATGGGAC AGCTCAGACT TTGTATTTAA AAGTTAAAAA GGACAAAAA	1860
	AAAATCTAAA GCATTTAAAA TCTAGTGAAA TAACTGAAGG GCCTGCTCTT TCCATTGTGG	1920
10	ATCAGCAGC ACACATACAT ACACCTCCA CCTCCCCATC CCCTGTTCTC CCTCTGTTC	1980
	TCCCCTTATA AAATTGATGT TGTCTTTACC AGAAAGGTAG ACAAAAAAGA AGCAGCAGCA	2040
	GCTCTTAAAG TGAGGGTTAT TCTCATACTC GGTCCAGCC ATCAGCAGAC TTCTGCTCA	2100
15	TGGCAGATC CCCCTTTCCA ACCTGTAACT CTGATGTGCT CTGGATCAGC TTTTAACTTT	2160
	TAATCATATA TTAGTGTCTT CTAAATCCCT TCTCTCTCTC TACTGCTGCC CTATGGTCT	2220
20	GGCTCTTACC CCCTGCGGCA CACTTATCTT CAAATACCAT AGAATTTCTAA TCTCTGAAAT	2280
	CATAGCTCTC CAGTGGCTTT TAAAGAAAGC TGGTCCTCAG CACTAACAAA ATCACTACAA	2340
	TAGCCTAGTG CTTTTTGGGA AGCCTTTTGA GGAAGAATG TTAGGTTTCAT GGTAACTAGT	2400
25	ATGCTCTTTG AGATTTTAC AGTGTGAAA CTTAAGAATT TTGAGAGGGT GAGGAGGGTT	2460
	GTTCAGAATC TAAATTACAG ATAGATGATT GTTCTTGTG AATTGTGTTT TTTTCTTTT	2520
30	TTTTGTGCC TACCATTTC TACATTTCC CTGGGGCCC ATCTCTGGCT CCTGTCTTT	2580
	TGTTTCTTGC TTTGCTTTAT CAGTTCATTC CAGCTCCCTG TTAGTGAAGG ACACTGCTGT	2640
	TAGTGAAGGA ACAAAGTCTA TGAGTCCTAA AATTTTAAAGT CAAAGAAAAC TGCTCTGTTT	2700
35	CCCCTTAGT AACACTTCTG AAGAGGAAAA ACTTCAATAG CCAAAGTTAA TAATCCTATA	2760
	TAATAATTGC TTTGGCTTTC ACCTAAAATT CTGGGCATCA CAATTTCCCTT GGGATAGAGG	2820
40	TTGTGTGGG GAATAGATTG CTTATTGCTG TTTACTGGAG AGAAAAGGTA GTGTTTTTGT	2880
	ACAAGTCAT ACCGCCAGAA GCCCAAATC CTATTTTGGC TCATCTTCAG GTAAAGAGTA	2940
	ATTCCTATCC TGTGTGCTC AGAAGCTAGA ATCGAAGGCT TACCTATTC ATTGTTTATT	3000
45	GTCAGAAATG CATGATGGCT CTGGAAAGA ATGACGTTTT GCTGGAAAAA AAAAAARAA	3060
	CMGTTTGTGT TTCACAAACA TGGCTTATCA ATTTTTTCAA AGAATTTCTT TTTCCAAAA	3120
50	AGAGGAGTAA CAAAATGTCA TTTCTGAAAG AGGCTTACTT TATACCAACT AGTGTACGCA	3180
	TTTGGGATGC CAGGGAACAG AGAGTGAGAC ACCTACAATC ACCAGTCTCA AATGCGCTAT	3240
	TGTTTCTTTT CAGAGTGTG CAGATTTGCC ATTTCTCCAT AATATGGGGA TAGAAAATGG	3300
55	AATAAGATA GAAGGGATGT AGAATATGCT TTCCTGCCAA CATGGTTTGG AGTCGACTTT	3360
	GGTATATTGA CTAGATTTGA AAATACAAGA TTGATTAGAT GAATCTACAA AAAAGTTGTC	3420
60	CTCCTCTCAG GTCCCTTTTA CACTTTTTGA CTAAC TAGCA TCTATATTCC ACACTTAGCT	3480

	TTTTTGTAC ACTTATCCTT TGTCTCCGTA AATTTTCATTT GCAGTGGTGA GTCATCAGAT	3540
	ATTTTAGCCA CCTACACAAA AGCAAACGTC ATTTTAAAA ATCTTCTGA GATGGGAGAA	3600
5	AATGTATTCT CCTTTCCTAT ACCGCTCTCC CAACAAAAA ACAACTAGTT AGTTCTACTA	3660
	ATTAGAACT TGCTGTACTT TTTCTTTTCT TTTAGGGGTC AAGGACCCCTC TTTATAGCTA	3720
10	CCATTGCGCT ACAATAAATT ATTGCAGCAG TTGCAATAC TAAATATTT TTTATAGACT	3780
	TTATATTTTT CCTTTTGATA AAGGGATGCT GCATAGTAGA GTTGGTGTAA TTAACTATC	3840
	TCAGCCGTTT CCTGCTTTC CCTCTGCTC CATATGCCTC ATTGTCTTC CAGGGAGCTC	3900
15	TTTTAATCTT AAAGTTCTAC ATTTCATGCT CTTAGTCAA TTCTGTTACC TTTTAATAA	3960
	CTCTCCAC TGCATATTC CATCTGAAT TGGTGGTTCT AAATTCGAA ACTGTAGTTG	4020
20	AGATACAGCT ATTAAATATT TCTGGGAGAT GTGCATCCCT CTTCTTTGTG GTTGCCCAAG	4080
	GTGTGTTTGC GTAACGAGA CTCCTTGATA TGCTTCAGAG AATTAGGCA AACACTGGCC	4140
	ATGGCCGTGG GAGTACTGGG AGTAAATAA AAATATCGAG GTATAGACTA GCATCCACAT	4200
25	AGAGCACTTG AACCTCCTTT GTACCTGTTT GGGGAAAAAG TATAATGAGT GTACTACCAA	4260
	TCTAATAAG ATTATTATAG TCTGGTTGTT TGAAATACCA TTTTCTCTC CTTTGTGTT	4320
30	TTTCCCACTT TCCAATGTAC TCAAGAAAT TGAACAAATG TAATGGATCA ATTTAAAATA	4380
	TTTTATTCT TAAAGCCTT TTTGCGCTGT TGTAATGTGC AGGACCCTTC TCCTTTCATG	4440
	GGAGAGACAG GTAGTTACCT GAATATAGGT TGAAAAGGTT ATGTAAAAAG AAATTATAAT	4500
35	AAAAGGATA CTTGCTTTT CAAATCTTTG TTTTCTCTTA TTCTAGGTAA GGCATATTAA	4560
	AAATAAATAT GTAAAGAAGA AAAATAAAG TTGTCTTCAT GG	4602

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(2) INFORMATION FOR SEQ ID NO: 75:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

45	CGCGCCCCGG GCCGGGGGTT TCTCTAACA AATAACAGA ACCCGCACTG CCCAGGCGAG	60
	CGTTGCCACT TTCAAAGTGG TCCCTGGGG GAGCTCAGCC TCATCCTGAT GATGCTGCCA	120
55	AGGCCCACTT TTTATTTTA TTTATTTT ATTTTTTTT TAGCATCCTT TTGGGGCTTC	180
	ACTCTCAGAG CCAGTTTTA AGGGACACCA GAGCCGCAGC CTGCTCTGAT TCTATGGCTT	240
60	GGTTGTACT ATAAGAGTAA TTGCCTAACT TGATTMTTCA TCTCTTAAAC CAACTTGTG	300

GCCAAAAGAT ATTTGAOCGT TTCCAAAATT CAGATTCTGC CTCTGCGGAT AAATATTTGC 360
 CACGAATGAG TAACTCCTGT CACCACTCTG AAGGTCCAGA CAGAAGGTTT TGACACATTC 420
 5 TTAGCACTGA ACTCCTCTGT GATCTAGGAT GATCTGTTCC CCCTCTGGAT GAACATCCTC 480
 TGATGATCAA GGCTCCAGC AGGCTACTTT GAAGGGAACA ATCAGATGCA AAAGCTCTTG 540
 10 GGTGTTTATT TAAAATACTA GTGTCACTTT CTGAGTACCC GCGCTTCAC AGGCTGAGTC 600
 CAGGCCTGTG TGCTTTGTAG AGCCAGCTGC TTGCTCACAG CCACATTTC ATTTGCATCA 660
 TTACTGCCTT CACCTGCATA GTCACTCTTT TGATGCTGGG GAACAAAAT GGTGATGATA 720
 15 TATAGACTTT ATGTATAGCC ACAGTTCATC CCCAACCCCTA GTCTTCGAAA TGTTAATATT 780
 TGATAAATCT AGAAAATGCA TTCATACAAT TACAGAATTC AAATATTGCA AAAGGATGTG 840
 20 TGTCTTTCTC CCGAGCTCC CCGTTCCCC TTCATGAAA ACCACCACGG TGCCATCTCT 900
 TGTGTATGCA GGGCTATGCA CCGCAGGCA CGTGTGTATG CACTCCCCGC TTGTGTTTAC 960
 ACAAGCTGTG GGGTGTACG CATGCCTGCT TTTTTCACCT AATAATACAG CTTGGAGAGA 1020
 25 TTTTGTATC ACATTATAAA TCCCACTGC TCTTTTGAT GGCCACATAA TAACTACTGC 1080
 ATAATATGGA TACGCCTTAT TTGATTTAAC TAGTCCCTA ATGATGGACT TTTAAGTTGT 1140
 30 TTCTTTT TTTCTTTTT GCTACTGCAA ACGATGCTAT AATAAATGTC CTTATCAAAA 1200
 AAAAAAAAAA AAAAAAAAAA AAAAAANCCC NGGGGGGGGG CCCC GGGAAC NCAAT 1255

35

(2) INFORMATION FOR SEQ ID NO: 76:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 475 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

GGCACGAGAG AAATGTTTGA TTCTCTTTCC TATTTTAAGG GATCTTCTCT CTTGTTGATG 60
 TTGAAAACCTT ACCTTAGTGA AGATGTGTTT CAACATGCTG TTGTCCTTTA CCTGCATAAT 120
 50 CACAGCTATG CATCTATTCA AAGTGATGAT CTGTGGGATA GTTTTAATGA GGTCAAAAC 180
 CAAACACTAG ATGTAAAGAG AATGATGAAA ACCTGGACCC TGCAGAAAGG ATTTCTTTTA 240
 55 GTGACTGTTC AAAAGAAAGG AAAGGAACTT TTTATACAAC AAGAGAGATT CTTTTTAAAT 300
 ATGAAGCCTG AAATTCAGCC TTCAGATACA AGGTACATGC CCTCTTTCTT TTCATGCCAT 360
 60 CTCTTTTGCA CTCTCAGGTG GAAATATTTT GAAGTGTTTT ATAATCATAA GTTCTTGTGA 420

AACCTAACAA GATTATCCCT TCCTAAGAAT ACITTAACCTT CCTACCAAAT TAAAA

475

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(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

15

TTCTCTCTGC TCTTCGACTG CACCGCACTC GCGCGTGACC CTGACTCCCC CTAGTCAGCT 60
CAGCGGTGCT GCCATGGCGT GCGGCGGCG CGAACCRGCG TCGGGGCTCG CGGCGTGTG 120
GCTCTGGCGT TGCTCGCCCT GGCCCTGTGC GTGCCCGGGG CCCGGGGCCG GGCTCTCGAG 180
TGGTCTCTCG CCGTGGTAAA CATCGAGTAC GTGGACCCGC AGACCAACCT GACGGTGTGG 240
AGCGTCTCGG AGAGTGGCCG CTTCGGGAC AGCTCGCCCA AGGAGGGCGC GCATGGCCTG 300
GTGGGCGTCC CGTGGGCGCC CGGCGGAGAM CTCGARGGCT KCGCGCCCGA CACGCGCTTC 360
TTCGTGCCCG AGCCCGGCGG CCGAGGGGCC GCGCCCTGGG TCGCCCTGGT GGTCTGTTGG 420
GCTGCACCTT TCAAGGACAA AGTGTCTGGT GCGGCGCNGA ANGAA 465

35

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 1907 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

45

ACATGCAGCC CAACTACAGA TTCTTATGGA ATTCTCAAG GTTGCAAGAA GAAATAAGAG 60
AGAGCAACTG GAACAGATCC AGAAGGAGCT AAGTGTTTTG GAAGAGGATA TTAAGAGAGT 120
GGAAGAAATG AGTGGCTTAT ACTCTCCTGT CAGTGAGGAT AGCACAGTGC CTCAATTTGA 180
AGTCTCTTCT CCATCACACA GTAGTATTAT TGATTCCACA GAATACAGCC AACCTCCAGG 240
TTTCAGTGGC AGTTCTCAGA CAAAGAAACA GCCTTGGTAT AATAGCACGT TAGCATCAAG 300
ACGAAAACGA CTTACTGCTC ATTTTGAAGA CTGGAGCAG TGTTACTTTT CTACAAGGAT 360
GTCTCGTATC TCAGATGACA GTCGAACTGC AAGCCAGTTG GATGAATTTT AGGAATGCTT 420
GTCCAAGTTT ACTCGATATA ATTCAGTACG ACCTTTAGCC ACATTGTCAT ATGCTAGTGA 480

60

TCCTATAAT GGTCCAGTA TAGTCTCTAG TATTGAATTT GACCGGGATT GTGACTATTT 540
 TGCGATTGCT GGAGTTACAA AGAAGATTAA AGTCTATGAA TATGACACTG TCATCCAGGA 600
 5 TGCAGTGGAT ATTCATTACC CTGAGAATGA AATGACCTGC AATTOGAAAA TCAGCTGTAT 660
 CAGTTGGAGT AGTTACCATA AGAACCTGTT AGCTAGCAGT GATTATGAAG GCACTGTTAT 720
 10 TTTATGGGAT GGATTACAG GACAGAGGTC AAAGGTCTAT CAGGAGCATG AGAAGAGGTG 780
 TTGGAGTGT GACTTTAATT TGATGGATCC TAAACTCTTG GCTTCAGGTT CTGATGATGC 840
 AAAAGTGAAG CTGTGGTCTA CCAATCTAGA CAACTCAGTG GCAAGCAITG AGGCAAAGGC 900
 15 TAATGTGTGC TGTGTTAAAT TCAGCCCCCTC TTCCAGATAC CATTGGGCTT TCGGCTGTGC 960
 AGATCACTGT GTCCACTACT ATGATCTTCG TAACACTAAA CAGCCAATCA TGGTATTCAA 1020
 AGGACACCGT AAAGCAGTCT CTTATGCAAA GTTGTGAGT GGTGAGGAAA TTGTCTCTGC 1080
 20 CTCAACAGAC AGTCAGCTAA AACTGTGGAA TGTAGGGAAA CCATACTGCC TACGTTCCCTT 1140
 CAAGGGTCAT ATCAATGAAA AAAACTTTGT AGGCCTGGCT TCCAATGGAG ATTATATAGC 1200
 25 TTGTGGAAGT GAAAATAACT CTCTCTACCT GTACTATAAA GGACTTTCTA AGACTTTGCT 1260
 AACTTTTAAG TTTGATACAG TCAAAAGTGT TCTCGACAAA GACCGAAAAG AAGATGATAC 1320
 AAATGAATTT GTTAGTGCTG TGTGCTGGAG GGCACCTACCA GATGGGGAGT CCAATGTGCT 1380
 30 GATTGCTGCT AACAGTCAGG GTACAATTAA GGTGCTAGAA TTGGTATGAA GGGTTAACTC 1440
 AAGTCAAAT GTACTTGATC CTGCTGAAAT ACATCTGCAG CTGACAATGA GAGAAGAAAC 1500
 35 AGAAAATGTC ATGTGATGTC TCTCCCCAAA GTCATCATGG GTTTTGGATT TGTTTTGAAT 1560
 ATTTTTCCTT TTTTTCCTT TCCCTCCTTT ATGACCTTTG GGACATTGGG AATACCCAGC 1620
 CAACTCTCCA CCATCAATGT AACTCCATGG ACATTGCTGC TCTTGGTGGT GTTATCTAAT 1680
 40 TTTTGTGATA GGGAACAAA TTCTTTTGAA TAAAAATAAA TAACAAAACA ATAAAAGTTT 1740
 ATTGAGCCAC AGTTGAGCTT GGAAAGTTT TGTCAAATGC NGCAAGAGAT AACTCTTTT 1800
 45 ANGAAGTAGC ATATGTGAAC TATAATGTAA CAGTGAATAA TTTGTAAAGT TCGTATTTCC 1860
 CAACCTCTTT GGAATTACA CATATCAATA TAAACAAAAT ATAAAGT 1907

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(2) INFORMATION FOR SEQ ID NO: 79:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1168 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

	GCTGGGGTGT CCCCKCSGCC ACCATCGTCA TCGCTTACTT GATGAAGCAC ACTGGGATGA	60
5	CCCATGACTG ATGCTTATAA ATTTGTCAAA GGCAAACGAC CAATTATCTC CCCAAACCTT	120
	AAC TTCATGG GGCAGTTGCT AGAGTTCGAG GAAGACCTAA ACAACGGTGT GACACCGAGA	180
	ATCCTTACAC CAAAGCTGAT GGGCGTGGAG ACGGTTGTGT GACAATGGTC TGGATGGAAA	240
10	GGATTGCTGC TCTCCATTAG GAGACAATGA GGAAGGAGGA TGGATTCTGG TTTT TTTTCT	300
	TTCTTT TTTT TTTGTAGTT GGGAGTAAGT TTGTGAATGG AAACAACTT GTTTAAACAC	360
15	TTTATTTTTA ACAAGTGTAA GAAGACTATA ACTTTTGATG CCATTGAGAT TCACCTCCCA	420
	CAAAC TGACA AATTAAGGAG GTTAAAGAAG TAATTT TTTT AAGCCAACAA TAAAAATATA	480
	ATACAAC TTG TTTCTCCCC TTTTCTTTT AAGCTATTIG TAGAGTTTAT GACTAAATAG	540
20	TCTGTGCAGG TTCATAGACC GAAGATACTA CACACTTTAA ACCAATTAAA AAGAACCAAA	600
	AGTAAATAGA AAAGACATTG AATCACCAAG GCCTGGGATC AACCTGGGCT GTCCACACAG	660
25	AAAACAAAA CCCAACCAAA CCAAGCCCTG TTGTGCTCAC TGGTGCAAAG AGAAGATCAG	720
	GGCAGCTTAA GTGGTCTAAG RATCCTTCAG GCATTCTTTA AGGAGAAAAA GGATACCTTT	780
	GATTTTGTGT GTTTCATGCT CTGGATTTT TTTT TTTT CTCTCTGGG TTTAAGAGAT	840
30	TTTTTTTGAA ATAGTGAGGA ACTGACCATT ATATGCCCTC ACTGGCTTCT TGTGCAATAA	900
	TATGATGTTT TAAGTGTGCA AACAAGTTAG AGCTGGCAGC TGAATGATAG ACAAATAGTG	960
35	CAAATTGCC AGCTTGGAGA TAGAAAGGAA TTCAACAATA TATCAAATAC TTTCCTTCCC	1020
	ACCTTTTTC TTTT TTTT TTTTCTGA TTTGATTCTG GTTACAGTGC CATAAACCTT	1080
	GTTACATATG TATATCAGAA TGTAAAGAAA AAAAATTTAT TTAAAAATAT TTTTCGCAAA	1140
40	AAAAAANNA AAAA ACTCGA GGGGGGCC	1168

45 (2) INFORMATION FOR SEQ ID NO: 80:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1285 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

55	AGAAAATCAC ATCCTAACAA AGAAGTCTGT CTAAGACAGT ACATCTCCTG TTGAACTTGC	60
	ATCTTTCCAC AGGACTTTCT GTTTT TAGGG ATGAGACTAT TCTCTGCTTC ATCAAGGAAA	120
60	GAGAAATGTT CAGGGTTGTA GGGATGGCAC ACTTATTAGT TCTGCCTGTC TGAAAGGTTT	180

	CTGCAGGACA GPTTGGTCAG AGCTGCAATT CTTAGTCCAT GGTCTAATGC TTGAGTATCT	240
	CTTCTTTCCC TTTCCTGTCT CAGGAATCAG CTGAGAATTC ATTCGATTGT CATGCCCTCTA	300
5	GCCCCTTACT GTGATTGTGT GGTGCACTT TCATTTCGCTT TAGTTCCTAGA ATCACCTGTT	360
	GACTCCTCAG ACTTCACCTA ACTTTGAAA CTCTCTTTTG GAGGCTTCTC ATTCCCCCT	420
10	AATTCTGTGC TGCCTGAGCC CTAGAATTTT CCCACCAACG AATTATTCCA GGTAGATCCT	480
	AAGTTGCTGG ATCTAGTTGA TATTTAAACA ATATCTAGTT GATATTCTC ATTCAATTGG	540
	ATCCAGAAAC CAGTATCTCT NAAAAACAAC CTCTCATACC TTGTGGACCT AATTTTGTGT	600
15	GCGTGTGTGT GTGCGGCAT ATGTATATAG ACAGGCACAT CTTTTTACT TTTGTAAAAG	660
	CTTATGCCCTC TTGGTATCT ATATCTGTGA AAGTTTAAAT GATCTGCCAT AATGTCTTGG	720
20	GGACCTTTGT CTCTGTGTA AATGGTACTA GAGAAAACAC CTATATTATG AGTCAATCTA	780
	GTTGGTTTFA TTCGACATGA AGGAAATTC CAGATAACAA CACTAACAAA CTCTCCCTTG	840
	ACTAGGGGA CAAAGAAAAG CAAACTGAC CATAAAAAAC AATTACCTGG TGAGAAGTTG	900
25	CATAAACAGA ATTAGGTAGT ATATTGAAGA CAGCATCATT AAACAGTTAT GTTGTCTCC	960
	TTGCAAAAAA CATGTACTGA CTTCCTGTTG AGTAATGCCA AGTTGTTTTT TTTATTATAA	1020
30	AACTTGCCCT TCATTACATG TTTCAAAGTG GTGTGGTGGG CAAAATATT GAAATGATGG	1080
	AACTGACTGA TAAAGCTGTA CAAATAAGCA GTGTGCCTAA CAAGCAACAC AGTAATGTTG	1140
	ACATGCTTAA TTCACAAATG CTAATTTTCT TATAAATTGT TTTGCTAAAA TACACTTTGA	1200
35	AACTATTTTT CTGTATTCCA AGAGCTGAGA TCTTAGATTT TATGTAGTAT TAAGTGAAAA	1260
	AATACGAAAA TAATAACAT TGAAG	1285

40

(2) INFORMATION FOR SEQ ID NO: 81:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

	TCTCCAGCCC CAATTTCTAC GCGCACOGGA AGACGGAGGT CCTCTTTCCT TGCCTAACGC	60
	AGCCATGGCT CGTGGTCCCA AGAAGCATCT GAAGCGGGTG GCAGCTCCAA AGCATTGGAT	120
55	GCTGATAAA TTGACCGGTG TGTTTGCTCC TCGTCCATCC ACCGGTCCCC ACAAGTTGAG	180
	AGAGTGCTCT CCCCTCATCA TTTTCTGAG GAACAGACTT AAGTATGCCC TGACAGGAGA	240
60	TGAAGTAAAG AAGATTTGCA TGCAGCGGTT CATTAAAATC GATGGCAAGG TCCGAAGTGA	300

	TATAACCTAC CCTGCTGGAT TCATGGATGT CATCAGCATT GACAAGACGG GAGAGAATTT	360
5	CCGTCTGATC TATGACACCA AGGGTCGCTT TGCTGTACAT CGTATTACAC CTGAGGAGGC	420
	CAAGTACAAG TTGTGCAAAG TGAGAAAGAT CTTTGTGGGC ACAAAGGAA TCCCTCATCT	480
	GGTGACTCAT GATGCCCGCA CCATCCGCTA CCCCAGTCCC CTCATCAAGG TGAATGATAC	540
10	CATTCAGATT GATTTAGAGA CTGGCAAGAT TACTGATTTT ATCAAGTTCC ATTACCCAG	600
	CCAGGTGGTC TCGTCACCTC AGAGGCTCCG CAGACTCCTG CCCAGGCCAG GACTGAGGCA	660
	AGCCTCAAGG CACTTCTAGG ACCTGCCTCT TCTACCAAG ATGAACTCAC TGGTTTCTTG	720
15	GCAGCTACTG CTTTTCCTCT GTGCCACCA CTTTGGGAG CCATTAGAAA AGGTGGCCTC	780
	TGTGGGGAAT TCTAGACCA CAGGCCAGCA GCTAGAATCC CTGGGCCTCC TGGCCCCSGG	840
20	GGAGCAGAGC CTGCCGTGCA CCGAGAGGAA GCCAGCTGCT ACTGCCAGGC TGAGCCGTCC	900
	GGGGACCTCG CTGTCCCCG CCCCAGAGAG CTCGGGAGC CCCAGCAGC CGGGCCTGTC	960
	CGCCCCCAC AGCCGCCAGA TCCCGCACC CCAGGGCGCG GTGCTGGTGC AGCGGGAGAA	1020
25	GGACCTGCCG AACTACAAC TGAATCCTT CGGCTGCGC TTCGGCAAGC GGGAGGCGGC	1080
	ACCAGGGAAC CACGGCAGAA GCGCTGGGCG GGGCTGAGG CGCAGGTGCG GGGCAGTGAA	1140
30	CTTCAGACCC CAAAGGAGTC AGAGCATGCG GGGCGGGGCG GGGGGCGGG GACGTAGGGC	1200
	TAAGGGAGGG GGGCTGGAG CTTCCAACCC GAGGCAATAA AAGAAATGTT GCGTAACTCA	1260
35	AAAAAAAAA AAAAAAANC TCGGGGGGGG	1290

(2) INFORMATION FOR SEQ ID NO: 82:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 684 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

45

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

50	TTTATGTAT TCTGTAAC TAAGAACTCT ATTTWATTCT TTTTGGACT TGCTAAGTTG	60
	TCTTTWATGG TTTTWAGTTC CATGCTGAAG TTTTCAGTAT TGACTTATCC CCTTGAACAT	120
	GAGTTGTTTT ATAGACTCTR ATGATTCAAA AATCTTACAT CTTTGGTAG TCTCTTTCAT	180
55	TGTGYCACTG TTTCTGTGA TTCTWACTCA TGGTATTTTA ATTCTTCGTT WTTTTTTTTC	240
	TGTTWAGAWA CATCTTTGA AAAATAATTT GGAGGAATAT TTGATTCTTA TGAACAAGGC	300
60	ATTACTCACC AGAGAAGATT TTTTGTGTYT ACCARGTGCC TARGAATGCT AACAGTCTGG	360

5 GAMCACATAG AMCACCAGGT GATGAGACAA TCCTGGGART CCTGTTTTAC TTTGSSCCAT 420
 CTTTCTCCCC AACCCGTGGG GAATARTCAT YCATATCTTA RCTGCAGGCT ARAAGGTGGT 480
 10 TTATCAGAGC CCAACTTCGA GGGCTCTGGG CTTTAGCTAC TGTACCCCA TCATAACTGA 540
 GCTTCATGGA TTGATTCTCT TTTATCTTT CAGATTCTCT TTTAAAAATC TTTGTTTTTT 600
 TTTTCTTCC GAAAGATTCC CCCAACATTA CCATTCCCA CCTCCGTTG AATTTTTTTG 660
 GCTCTCATTT TGAATTTTTC AAGA 684

15

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2024 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

CTGCAGGAAT TCGGCACAGC TGCCTGGAG GCTTCATCTT TGCCGCGCT GCCGTGCGCT 60
 TCCTGGGATT GGAGTCTCGA GCTTCTCTCG TCGTTCGTC GCGGGGTTG CGCCCTCTCT 120
 30 GCGCCTCGGG GCTGCGAGGC TGGGGAAGGG GTTGAGGGG GCTGTTGATC GCCGCGTTTA 180
 AGTTGCGCTC GGGGCGGCCA TGTGCGCGG CGAGGTCGAG CGCCTAGTGT CGGAGCTGAG 240
 CGGCGGGACC GGAGGGGATG AGGAGGAAGA GTGGCTCTAT GGCGATGAAA ATGAAGTTGA 300
 35 AAGGCCAGAA GAAGAAAATG CCACTGCTAA TCCTCCATCT GGAATTGAAG ATGAAACTGC 360
 TGAAAATGGT GTACCAAAAC CGAAAGTGAC TGAGACCGAA GATGATAGTG ATAGTGACAG 420
 40 CGATGATGAT GAAGATGATG TTCATGTCAC TATAGGAGAC ATTAACCGG GAGCACCACA 480
 GTATGGGAGT TATGGTACAG CACCTGTAAA TCTTAACATC AAGACAGGGG GAAGAGTTTA 540
 TGGAACTACA GGGACAAAAG TCAAAGGAGT AGACCTTGAT GCACCTGGAA GCATTAAATGG 600
 45 AGTTCCACTC TTAGAGGTAG ATTTGGATTG TTTTGAAGAT AAACCATGGC GTAAACCTGG 660
 TGCTGATCTT TCTGATTATT TTAATTATGG GTTTAATGAA GATACCTGGA AAGCTTACTG 720
 50 TGAAAAACAA AAGAGGATAC GAATGGGACT TGAAGTTATA CCAGTAACCT CTAATACAAA 780
 TAAAATTACG GTACAGCAGG GAAGAACTGG AAACCTCAGG AAAGAACTG CCCTTCCATC 840
 55 TACAAAAGCT GAGTTTACTT CTCCTCCTTC TTTGTTCAAG ACTGGGCTTC CACCGAGCAG 900
 GAGATTACCT GGGGCAATTG ATGTTATCGG TCAGACTATA ACTATCAGCC GAGTAGAAGG 960
 CAGCGACGG GCAAATGAGA ACAGCAACAT ACAGTCTCTT TCTGAAAGAT CTGCTACTGA 1020
 60 AGTAGACAAC AATTTTAGCA AACCACCTCC GTTTTCCCT CCAGGAGCTC CTCCCACTCA 1080

CCTTCCACCT CCTCCATTTC TTCCACCTCC TCCGACTGTC AGCACTGCTC CACCTCTGAT 1140
 TCCACCACCG GGTTCCTCCTC CTCCACCAGG CGCTCCACCT CCATCTCTTA TACCAACAAT 1200
 5 AGAAAGTGGA CATTCCTCTG GTTATGATAG TCGTTCCTGCA CGTGCATTTC CATATGGCAA 1260
 TGTTCCTTTT CCCCATCTTC CTGGTCTGTC TCCTTCCTGG CCTAGTCTTG TGGACACCAG 1320
 10 CAAGCAGTGG GACTATTATG CCAGAAGAGA GAAAGACCGA GATAGAGAGA GAGACAGAGA 1380
 CAGAGAGCGA GACCGTGATC GGGACAGAGA AAGAGAACGC ACCAGAGAGA GAGAGAGGGA 1440
 GCGTGATCAC AGTCCTACAC CAAGTGTTTT CAACAGCGAT GAAGAACGAT ACAGATACAG 1500
 15 GGAATATGCA GAAAGAGGTT ATGAGCGTCA CAGAGCAAGT CGAGAAAAAG AAGAACGACA 1560
 TAGAGAAAGA CGACACAGGG AGAAAGAGGA AACCAGACAT AAGTCTTCTC GAAGTAATAG 1620
 20 TAGACGTGCG CATGAAAGTG AAGAAGGAGA TAGTCACAGG AGACACAAAC ACAAAAAATC 1680
 TAAAGAAGC AAAGAAGGAA AAGAAGCGGG CAGTGAGCCT GCCCTGAAC AGGAGAGCAC 1740
 CGAAGCTACA CCTGCAGAAT AGGCATGGTT TTGGCCTTTT GTGTATATTA GTACCAGAAG 1800
 25 TAGATACTAT AAATCTTGTT ATTTTCTGCG ATAATGTTTA AGAAATTTAC CTTAAATCTT 1860
 GTTCTGTTTG TTAGTATGAA AAGTTAACTT TTTTCCAAA ATAAAAGAGT GAATTTTCA 1920
 30 TGTTAAGTTA AAAATCTTTG TCTGTACTA TTTCAAAAAT AAAAAGACAG CAATGACTTT 1980
 ATATCCAAA AAAAAAAAAA AAAAAAAAAA AAAAAAGGCC GGCC 2024

35

(2) INFORMATION FOR SEQ ID NO: 84:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 931 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

CGCGCCMATA GCCGGACGGG GATCTGAGCT GGCAGGATGA ATGTGGGGGT GGCACACAGC 60
 GAAGTAAACC CCAACACCCG AGTGATGAAT AGCCGAGGCA TCTGGCTGGC CTACATCATC 120
 50 TTGGTAGGAT TGCTGCATAT GGTCTACTC AGCATCCCT TCTTCAGCAT TCCTGTTGTC 180
 TGGACCCGTA CCAACGTCAT CCATAACCTG GCTACGTATG TCTTCCTTCA TACGGTGAAA 240
 55 GGGACACCTT TTGAGACTCC TGACCAAGGA AAGGCTCGGC TACTGACACA CTGGGAGCAA 300
 ATGGACTATG GGCTCCAGTT TACCTCTTCC CGCAAGTTCC TCAGCATCTC TCCTATTGTG 360
 CTCTATCTCC TGGCCAGCTT CTATACCAAG TATGATGCTG CGCACTTCCT CATCAACACA 420
 60

GCCTCATTGC TAAGTGTA CTGTCGAAG TTGCCCCAGT TCCATGGGGT TCGTGTCTTT 480
 GGCATCAACA AATACTGAGG GATGGGTTTT GGGACAGCTC CATGGGCATG GGAAGGCAC 540
 5 TGAAACAGAG GACTATAAAA CATCCTTCTC TTATTCTCCA TACTGTCTTC TACACCTTTA 600
 AAGCCTGAGA ACTATACAAC CTTTCCCAGA CTCCCAAGAA GAGAAGAGAT TGGCAAATGG 660
 10 GGCTCCTGGG CCCAGTCCTG CTAGTGCCAA GTTCTTTTGA ATCAGGAAGG CAGGTGAGGT 720
 AAGGGCCAAA TCACTCTCCT CCATAGCAGG AAGCCAATTG GGCAGCTCCT TTGGTGATTA 780
 CATCTTTCCA TATCTTTTAC ACTTACCACC TTCCAGCTCT GTTTTGCTGT GTATTTTCT 840
 15 TACAATAAT TTTTTCAGCT ATAGCTGCAG TTAAATCAGG ATGGGTAGAG AGCTGTCTC 900
 ATAAGGCTGG GGGTGGGAAG ATGGAATACT G 931

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(2) INFORMATION FOR SEQ ID NO: 85:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 825 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

CGGGGCCGGC GGGGTCTTCA GGTACCGGG CTGGTTACAG CAGCTCTACC CCTCAGACG 60
 CAAACATGGC AGCGCAGAAG GACCAGCAGA AAGATGCCGA GCGGAAGGG CTGAGCGGCA 120
 35 CGACCTTGCT GCGAAGCTG ATTCCCTCCG GTGCAGGCCG GGAGTGGCTG GAGCGCGCC 180
 GCGGACCAT CCGGCCCTGG AGCACCTTCG TGGACCAGCA GCGCTTCTCA CGGCCCGCA 240
 40 ACCTGGGAGA GCTGTGCCAG CGCTCGTAC GCAACGTGGA GTACTACCAG AGCAACTATG 300
 TGTTCGTGTT CCTGGGCTC ATCCTGTACT GTGTGGTGAC GTCCCTATG TTGCTGGTGG 360
 CTCTGGCTGT CTTTTTCGGC GCCTGTTACA TTCTCTATCT GCGCACCTTG GAGTCCAAGC 420
 45 TTGTGCTCTT TGGCCGAGAG GTGAGCCAG CGCATCAGTA TGCTCTGGCT GGAGGCATCT 480
 CCTTCCCTT CTCTGGCTG GCTGGTGGG GCTCGGCCGT CTTCTGGGTG CTGGGAGCCA 540
 50 CCCTGGTGGT CATCGGCTCC CACGCTGCCT TCCACCAGAT TGAGGCTGTG GACGGGAGG 600
 AGCTGCAGAT GGAACCGTG TGAGGTGTCT TCTGGGACCT GCGGCCCTCC CGGGCCAGCT 660
 GCCCCACCCC TGCCCATGCC TGTCTGCAC GGCTCTGCTG CTCGGGCCA CAGCGCGTC 720
 55 CCATCACAAG CCCGGGAGG GATCCGCCT TTGAAAATAA AGCTGTTATG GGTGTCATTC 780
 AGGAAAAAAA AAAAAAAGG GGGCCCCCTC TAGGGGTCAA AGTTA 825

60

(2) INFORMATION FOR SEQ ID NO: 86:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1238 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

CATGTAAAG	GATGAAATGT	GACTTCTGGT	GTTTTTTTAT	TTCTATGGAG	GGACTTTCTG	60
GGGACGGTTT	CTGGCTCTCA	GGCTCTGAGA	AGCTGCAGTT	TATGAGTGGC	TCTGTGTGTG	120
CTGCCACCTA	CTGGAGAAGC	CATAAGCTGC	AGCTTTAGGA	AAAGGGAACC	CGGGGCAGAG	180
TGTGGGAAG	TGGATGGCA	GCATGGCAGG	GCTTTGGAAA	ATGAGAGGTG	AGAGTKTKTC	240
CAGGAAGGT	GTAAGGAGAG	GATGGATCCT	GATACATGGA	TTCAGGATCA	TTAGGGTCCT	300
GTCTGGGACA	CTGGCCTTCC	TGCTTACCTG	CTCTTTCCCT	CCTCCTTGGT	CGGAGGAGGG	360
GCTGGCTCAC	TGCTCTGGCT	TCATTTTCCA	GAGCTGCCTG	CTGCAGTCAC	ACTTAGGTCA	420
TCTTCTCTCA	CTTTTCTCCT	TTTGCCGATT	AGTGGACGTG	ACAGAGATGT	GAATGGGGCA	480
GGGATGTCTT	TTGATGGCAT	CAAGACTTTA	GCTTCTGGTG	CGCTGTGTCC	CAGCTCTGAT	540
TTCAAGTTGCA	GCCGTGATGG	AMAGTTNGCA	TGGAAGCTGA	GACTCTCACT	GACAGTGAAA	600
CCCTCAAATG	AACACAATCC	CTGCTTTCCT	GCCAAGGATC	CTTGTAGGGT	NCCCCAGCT	660
TCCCCACTTT	TTTTCTGTGT	CCTGACAAAG	AAACACAGAG	TAACTTGATT	GCCCTGTGAC	720
CTGGCCAGTT	GCATTTCCCC	TGCAGGCTTG	AGCCCAAGCC	AGAGCCTTGA	AAAGGTATTC	780
AGGTGTGTGC	CCAAAACACT	GAAAAAACT	GCCCTGGCCC	TGAACCAAAT	ACCTTGAACC	840
CTCGTAAACT	CCATACCCTG	ACCCCTTGT	TTTGGATATA	CCCAGGTAGA	ACAACTCTCT	900
CTCACTGTCT	GTTGTGAGGA	TACGCTGTAG	CCCACTCATT	AAGTACATTC	TCCTAATAAA	960
TGCTTTGGAC	TGATCACCTT	GCCAGTCTTT	TGTCTTGGGC	AATCTATACT	TTTNTCTAGA	1020
GGTTCCCAAG	GCCTACTGAA	GGGACTTAAC	ATACTCTTAA	TGGCTTTCCT	CTCTCTTGT	1080
TTACCTTATG	CCCTCACTTC	CTGAGTTAAC	CTCCCAAATA	CAGGATTCAC	CTGTACCCAA	1140
GCCCTTAGCT	TCAAGAATAC	AGGATCACCT	GTACCCAAGC	CCTTAGCTCA	AGCTCTGCTT	1200
TGGAAGAACC	CAACTAAGA	CAGTGCTCCT	GGTGCCCT			1238

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(2) INFORMATION FOR SEQ ID NO: 87:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1460 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

	ATTGCCTTCT GGTCCCTGGT GACACTGGGG TCATCCTTCA TCCCCGAGA GCATTTCTGG	60
10	CTGCTCCTCC TGACCCGGGG CCTGGTGGGG GTCCGGGAGG CCAGTTATTC CACCATCGCG	120
	CCCACTCTCA TTGCCGACCT CTTTGTGGCC GACCAGCGCG ACCGGATGCT CAGCATCTTC	180
15	TACTTTGCCA TTCCGGTGGG CAGTGGTCTG GGCTACATTG CAGGCTCCAA AGTGAAGGAT	240
	ATGGCTGGAG ACTGGCACTG GGCTCTGAGG GTGACACCGG GTCTAGGAGT GGTGGCCGTT	300
	CTGCTGCTGT TCCTGGTAGT GCGGGAGCCG CCAAGGGGAG CCGTGGAGCG CCACTCAGAT	360
20	TTGCCACCCC TGAACCCAC CTGCTGGTGG GCAGATCTGA GGGCTCTGGC AAGAAATCCT	420
	AGTTTCGTCC TGTCTTCCCT GGGCTTCACT GCTGTGGCCT TTGTACAGGG CTCCTGGCT	480
25	CTGTGGGCTC CGGCATTCTT GCTGCGTTCC CGCGTGGTCC TTGGGGAGAC CCCACCCTGC	540
	CTTCCCGGAG ACTCCTGCTC TTCTCTGAC AGTCTCATCT TTGGAATCAT CACCTGCCTG	600
	ACCGGAGTCC TGGGTGTGGG CCTGGGTGTG GAGATCAGCC GCCGGCTCCG CCACTCCAAC	660
30	CCCCGGGCTG ATCCCTGGT CTGTGCCACT GGCTTCTGG GCTCTGCACC CTTCCTCTTC	720
	CTGTCCCTTG CCTGCGCCCG TGCTAGCATC GTGGCCACTT ATATTTTCAT CTTTATTGGA	780
35	GAGACCTTCC TGTCCATGAA CTGGGCCATC GTGGCCGACA TTCTGCTGTA CGTGGTGATC	840
	CCTACCCGAC GCTCCACCGC CGAGGCCTTC CAGATCGTGC TGTCCACCT GCTGGGTGAT	900
	GCTGGGAGCC CCTACCTCAT TGCCCTGATC TCTGACCGCC TGCGCCGAA CTGGCCCCC	960
40	TCCTTCTTGT CCGAGTTCCG GGCTCTGCAG TTCTCGCTCA TGCTCTGCGC GTTTGTGGG	1020
	GCACTGGGCG GCGCACTTCC TGGGCACCGC CATCTTCATT GAGGCCGACC GCCGGGGGC	1080
45	ACAGCTGCAC GTGCAGGGCC TGCTGCACGA AGCAGGGTCC ACAGACGACC GGATTGTGGT	1140
	GCCCCAGCGG GGCCGCTCCA CCGCGTGCCT CGTGGCCAGT GTGCTCATCT GGAGAGGCTG	1200
	CCGCTCACCT ACCTGCACAT CTGCCACAGC TGGCCCTGGG CCCACCCAC GAAGGGCCTG	1260
50	GGCCTAAACC CCTTGGCCTG GCCAGCTTC CAGAGGGACC CTGGGCCGTG TGCCAGCTCC	1320
	CAGACACTAC ATGGGTAGCT CAGGGGAGGA GGTGGGGGTC CAGGAGGGG ATCCCTCTCC	1380
55	AACAGGGGCA GCCCCAAGG CTCGGTGCTA TTTGTAAACG GATTAAAATT TGTAGCCAGA	1440
	AAAAAAAAA AAAAAAAAAA	1460

60

(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1395 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

10 CAGGTGCAAA GTGGGAAGTG TGAGTCCTCA GTCTTGGGCT ATTGGGCCAC GTGCCTGCCG 60
GACATGGGAC GCTGGAGGGT CAGCAGCGTG GAGTCCTGGC CTTTTCGTC CACGGGTGGG 120
15 AAATGGCCA TTGCCACGGC GGGAACTGGG ACTCAGGCTG CCCCCCGGCC GTTCTCATC 180
CGTCCACCGG AYTCTGGGC GCTGCACTG GCGCTGATGT AGTTTCCTGA CCTCTGACCC 240
GTATGTCTC CAGATTAAAG GTACGACATT TGGAGGCCCC AGCGAGAAAC GTCACCGGA 300
20 GAAACGTCAC CGGCGAGAG CGGKCCCGCT GTGTGCTCCC CCGGAAGGAC AGCCAGCTTG 360
TAGGGGGGAG TGCCACCTGA AAAAAAATT TCCAGGTCCC CAAAGGGTGA CCGTCTTCG 420
25 GAGACAGCGG ATCGACTACC ATGTGGGTGC CCACAAAAT TYCACCTYTG AGTCTCAAC 480
TGCTGACCCC GGGTCAGTT CCAGAGAGAA GGACTCCCTC CTGCTTGGA GAGACCTCAC 540
ACCGTCATCA CGATGCCAAC GGCTCTGAAG GTGGATGGCA TTCCTGGTG GATTCATCAC 600
30 TCCCGCATCA AAAAGGCCAA CRGAGCCCAA CTAGAAACAT GGTCCCCAG GGCTGGGTCA 660
GGCCCCTTAA AACTGCACCT AAGTTGGGTG AAGCCATTAG ATTAATTCTT TTTCTTAATT 720
35 TTGTAAACA ATGCATAGCT TCTGTCAACT TATGTATCTT AAGACTCAAT ATAACCCCT 780
TGTTATAACT GAGGGAATCA ATGATTTGAT TCCCCAAAA CACAAGTGGG GAATGTAGTG 840
TCCAACCTGG TTTTACTAA CCCTGTTTTT AGACTYTCCC TTTCCTTTAA TCACTCAGCC 900
40 TTGTTCCAC CTGAATTGAC TCTCCCTTAG CTAAGAGCGC CAGATGGACT CCATCTTGGC 960
TCTTTCNACT GGCAGCGCT TCTYCAAGG ACTTAACTTG TGCAAGCTGA CTCCAGCAC 1020
45 ATCCAAGAAT GCAATTAACT GATAAGATAC TGTGGCAAGC TATATCCGA GTTCCAGGA 1080
ATTCTGCTCA TTGATTACAC CCMAGGCC CGGCTCTATC ACCTTGTAAT AATCTTAAAG 1140
CCCCTGACC TGGAATATT AACGTTCTG TAACCATTTA TCCTTTTAA TTTTTCCT 1200
50 ACTTATTTT TGTAATATG TTTTAACTAG ACCCCCCCTC TCCTTTCTAA ACCAAAGTAT 1260
AAAAGCAAAT CTAGCCCTT CTTGAGGCC AGAGAATTTC GAGCGTTAGC CGTCTCTTGG 1320
55 CCACCAGCTA AATAACGGA TTCTTCATGT GTAAAAAAA AAAAAAAA CTCGGAGGG 1380
GGGCCCGTA CCAA 1395

60

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1186 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

10 GGCACGAGCC GGCAAGCCGA GCTAGGGTGA AACTGGGGG CGCACCAGGA TGTNNGACAG 60
AAAAGCAGAA GATGAGACTC TGTTCATTCA CTTTTCCTAG GCCCATCCTG TGGTCATCTT 120
15 TCCCCCTCCC ATCATACCTC CTCCTTCCTG GAGCCTCTGC CGGCTTGGCT GTAATGGTGG 180
CACTTACCTG GATATTTTTCAG TGGGAGGATG AAAGGCGAGA CTCACCTTAC GCGGTGGGAC 240
20 AGATGGGGAG AGGAAAAAGG CAGAGATGGC CAGGAGAGGG GTGCAGGACA AACCAGAGAG 300
GTTGGGTCAG GGGAAAAGGG TGGGGAGAAA GAGGGGTGCA GGCCCTGCAG GCCGGTTAGC 360
CAGCAGCTGC GGCTCCCCG GGCCCTTGGC ATCCAACCTC GCAGACAGGG TACCAGCCTC 420
25 CTGGTGTGTA TCATAGGATT TGTTCACATA GTGTTATGCA TGATCTTCGT AAGGTTAAGA 480
AGCCGTGGTG GTGCACCATG ACATCCAACC CGTATATATA AAGATAAATA TATATATATA 540
30 TGTATGTAAA TTATGGCAG AGAAATTATA GCACTGAGGG CCTGCTGCC CTGCTGGACC 600
AAGCAAACT AAGCCTTTTG GTTTGGGTAT TATGTTTCGT TTTGTTATTT GTTTGTTTTT 660
GTGGCTTGTC TTATGTCGTG ATAGCACAAG TGCCAGTCGG ATTGCTCTGT ATTACAGAAT 720
35 AGTGTTTTTA ATTCATCAAT GTTCTAGTTA ATGCTTACCT CAGCACCTCC TCTTAGCCTA 780
ATTTTAGGAG GTTGCCCAAT TTTGTTTCTT CAATTTTACT GGTACTTTT TTGTACAAAT 840
40 CAATCTCTTT CTCTCTTCT CTCCTCCCCA CCTCTCACC TTGCCCTCTC CATCTCCCTC 900
TCCCGCCCTC CCTCTCTCC TCTGGCTCCC CGTCTCATTT CTGTCCACTC CATTCTCTCT 960
CCTCTCTCC TGCTCTCTGC TGCCCCCTCC CCAGCCCACT TCCCGAGTT GTGCTTGCCG 1020
45 CTCCTTATCT GTTCTAGTTC CGAAGCAGTT TCACTCGAAG TTGTGCAGTC CTGGTTGCAG 1080
CTTCCGCAT CTGCCTTCGT TTCGTGTAGA TTGACGCGTT TCTTTGTAAT TTCAGTGTTT 1140
50 CTGACAAGAT TTAACAAAAA AAAAAGGAAA AAAAAAATA AAAAAA 1186

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 1821 base pairs
60 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

5	AAAACATGCT TTCAGGGCGT COCCTATGTA TTCGGGGGGC CCACGGACAC TCAGGCTGGA	60
	KATCCGTCCT CACTGCGCTC AAGATGGCCT CAGCAGACAC CAGTTACCCA GCTGAAAGTC	120
	ACAATCCCTC CCAGAAGTCT CCCAACACTA GTGCTGACCA GAGGTGGGGC TCTCAGGCTA	180
10	GGAGTTTCAC ACACAATGAC AGGCTGCTGG GGGACATTGC AGGACCCCTT TTCCTYTCTT	240
	CTCCATGCTA GAAGCCAGCC CTAGGMAGCT GCAGTTACTC CCTGTGACTC AGCAGCAGGC	300
15	TGATTCAACA CAGCTGCCCA CACAAAGCCA GTGGTAATAC ATCTGTTTAC CTTTCCCTAT	360
	CACCCAGACA CAAGCCCTT TCCAGGTCA AACACAGGC CGATGCATCT CCAGTTTGAC	420
	AGTCAAATCA CTACTTCCAT TGCTACTTTA GATCAGCCAA AGTGGTGACT GCTGCAGTGT	480
20	GTGGCTATCC CTACAAGGCC CACCAAGGG ATGCCCAAAG CCCAACCTTC TCCAGGGCTG	540
	CAGCAGNAGC AACCCACCA GCTAAGTCC AGCAGAGGAC CTCCCACCCA ATGTCTTGTT	600
25	CTAATTAGAA GGGGAAGTTA GCCACAGAAA ATCAACTTAT CTATAATTAC AAAATTCTCT	660
	TGACTCACCT TAAAGTTCCT ATTGACATCT ACTGCTTTTA AACCTATTTG AAAACTCTGA	720
	TACTAAAACA AATGACACTC TAAGAAAGTT TGGGAGCCCC ATGCTGAGAA CCATTTCTGT	780
30	GCAGTGAGGA TGTTTCCAGA AGCTACTTAC CTACATGTGA ATGTGCCATT TTCTTTCTCT	840
	TTGTAGAGAA AATCCCTTT ACTTTTGGGA ACAGTAATGG CAGCTTCTAG TACAGCCATT	900
35	ACAGTTTCAT ATGAGAAAAA TTAAGAATAA CTATAAAATT GTTAAATAT CCAATAATGG	960
	ATAATGATGG CCAGAAGATT TAACATACAA AGTAATCTC AATGTAAAGC TATTCAGCTC	1020
	TTCCAGGTTG AATGCCCTGT AACCCACCT GACCTTCAC ATCATCTTCA AAAAGCAGTT	1080
40	TCTCTGTCC CCATGATTCT CCTATAAGGT AACTCTTTAG TCCTCCATTT AGCACATTTT	1140
	AAATCCTCCA AAGAATAAGT ATCATGTGAT TATTTTAGCT TTACAAAAAA AAAGTTGAAT	1200
45	GGCGTTTAT TTTTCATGGC TATAAGCAGG TACCTTAGTA GGGCAGATAT AGGAAAAACA	1260
	AATTAGACGA AAACAAATCC TCTACAAATC CAAGGCAGGA AAAGTGGTGG CAGAGTGACT	1320
	CATCTCTCTG TCCCTCCCAT CAGGTCAAAT CAGGAGGCTG CAGTGAATGC CTGTTCTTTG	1380
50	AATGTGTAGC AGTTGTTCCT GTAACCTTT AAAACTTGGC TATAGGCTGT TTAGCACAGT	1440
	ACAGATTAAA GATACAGTTA CGTAAACAGC AAAGTAATTT TATAGTGCTT CATCCATTTA	1500
55	TCATGCTTTG GTTTGCTAAT TTTTTCACAT ACCTTTTCT ATCACAGTCT GTTGCTTTTG	1560
	TACACATTTT TCATATGGG GTTCGACAGG TAAACACAAA CTGCTATTTT AGTAGAAAAA	1620
60	GTTATTGTGA TGAATATTA AACCAATAA ATTGTATAAA GGGTAAAAAA AAAAAAAAAA	1680

AAAAAAAAA AAAAAAAAAA AAAAAAATTC CTGCGGGCCG CANGCTTTT CCCTTTGGGT 1740
GAGGGTTAT TTINGGCTTG GGCAGTGGC CCTTCGTTTT TACAACGTCG TGANGGGGG 1800
5 AACC CGGGG GGGTTCCCC C 1821

10 (2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 862 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

20 TGCCCTTTT CCCACGATT CGGGCINTGG TGAAGGTGG AGATGTGAAC TCCAATTAAG 60
GGACTGGAGA GAGGTGAAGA ATTTGTCAGG TGGGAGATTT GGATTGAAT GTGGACTTGT 120
AAATGACTTG ACCTTGCCAT CTGTGTTCAA GGTACGGTT TGCTGTGGG TTCTGGGAG 180
25 AGCTTACTCA CCCCAGAGTC TTTCTTTCT CTGCTCCAA GAAGAGCCCT GTTGGTGCTT 240
TACCACCGCT TGGAGTCTCC CGAGGACACA AACAGGCAGA GAGGGACGTG TAGGGAGAGT 300
TCTTCTCTGT TTTCTGTGCT TTCTTTTTA CAGGACTCCC GGAAGGCCAC TCATGGCCAT 360
GCCAGGAGCT TTCTCAGAAA CAGTCATAAA CGATCTCTTG AGTCTCTTTC TTGTCTCTCC 420
AGCTGAGCTT TCTTATTCCA CCTTTCTGG TGTCTATAGG AATGCATGAG AAGACCCTGG 480
35 GACGTTTTTC TGCTCTCTTC TGGCCCTCCA TGGAGCCATG GGCCTCGGCC TCGGCGGCTC 540
CTCACCTCA CAATTATTTT CCTCCTCCG TGCCAGCCCT TCTTTTGTGT CTGAAACCGG 600
TTTAAAAATG TGAATCTCCC AGAGAAGAAG CCGCTGGCTG TATGAACTT GACGGCGCTT 660
TTGTAAGGTG CCACCCCAA ACTTTAAGGT AGCTAAACCA ATTTTAAAA GATTCAATGG 720
CTGTTCATC CTCCAGATGT AGCTATTGAT GTACACTTCG CAACGGAGTG TCTGAAATG 780
45 TGGTGGTCTT GATTATAGG ATTCATAAT TAAATGTCT GCTGAATAAA AAAAAAAAAA 840
AAAAACTCGA GGGGGGCCG GT 862

50

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 696 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
60 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

	CTGAGGCGAG TGAAGTGGAC TCTGAGGGCT ACCGCTACCG CCACTGCTGC GGCAGGGGCG	60
5	TGGAGGGCAG AGGGCCCGCG AGGCCGCACT TGCAAACATG GCTCAGAGCA GAGACGGCGG	120
	AAACCCGTTT GCGAGCCCA GCGAGCTTGA CAACCCCTTT CAGGACCCAG CTGTGATCCA	180
10	GCACCGACCC AGCCGGCAGT ATGCCACGCT TGACGTCTAC AACCCCTTTG AGACCCGGGA	240
	GCCACCACCA GCCTATGAGC CTCCAGCCCC TGCCCCATTG CCTCCACCCCT CAGCTCCCTC	300
	CTTGCAGCCC TCGAGAAAGC TCAGCCCCAC AGAACCTAAG AACTATGGCT CATACAGCAC	360
15	TCAGGCCTCA GCTGCAGCAG CCACAGCTGA GCTGCTGAAG AACAGGAGG AGCTCAACCG	420
	GAAGGCAGAG GAGTTGGACC GAAGGAGCGA GAGCTGCAGC ATGCTGCCCT GGGRGGCACA	480
20	GCTACTCGAC AGAACAATTG GCCCCCTCTA CCTTCTTTTT GTCCAGTTCA GCCCTGCTTT	540
	TTCCAGGACA TCTCCATGGA GATCCCCCAA GAATTTTCTA AGACTGTATC CACCATGTAC	600
	TACCTCTGGA TGTGCAGCAC GSTGGNCTT CTCTGAAYT TCMTOGSGTG CCTGGCCAGT	660
25	TCTGTGTGGA AACCAACAAT GCGAGGCTT TGGGTT	696

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 1886 base pairs
35	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

40	CAGGCCACTG ACGCTTCTTT GCGAGGGATG CAGGAGGTCC TACAGAGAAA GCGCTTCTT	60
	GCATKTCAGA GGGCCACAG CCTGTACCC ACAGATCACC AAGCAGCTTT CTACCTGGCT	120
	CTGCAGCTTG CCATCTCCAG ACAGATCCCA GAGGCTCTGG GGTATGTCCG CCAAGCTCTT	180
45	CAGCTTCAAG GTGACGATGC CAACTCCCTG CACCTCCTTG CCTCCTGCT GTGAGCACAG	240
	AAGCATTACC ATGACGCTCT GAACATCATC GACATGGCCC TGAGTGAATA CCCAGAAAAT	300
50	TTTACTACTAC TGTTTTCCTA AGTGAAGTTG CAGTCACTCT GCGAGGCCCC GGACGARGCA	360
	CTGCTGACTT GTAAGCACAT GCTGCAGATA TGGAAATCCT GCTACAACCT CACCAACCCC	420
	AGTGATTCTG GACGTGGGAG CAGCCTCTTA GATAGAACCA TTGCTGACAG ACGACAGCTT	480
55	AATACAATTA CTTTGCCAGA CTTGAGGAT CCCGAGACAG GCTCCGTCCA TGCCACATCG	540
	GTAGCAGCCT CAAGAGTGA GCAGGCACTG TCGGAAGTGG CTTCGTCTCT GCAGAGCATG	600
60	CCCCTAAGCA GGGCCCGCTG CACCCCTGGA TGACGCTGGC ACAGATCTGG CTCCATGCAG	660

	CTGAAGTCTA TATCGGCATC GGAAGCCTG CAGAAGCCAC AGCCTGTACC CAAGAAGCTG	720
5	CCAACCTCTT CCCAATGTCC CACAATGTCC TCTACATGCG CGGCAGATT GCTGAGCTCC	780
	GGGAAGCAT GGACGAGCG CGCGGTGGT ATGAAGAGGC CTTAGCCANT CAGCCCCACC	840
	CACGTGAAGA GCATGCAGCG ACTTGGCCCT GATCCTTCAC CAGYTAGGCC GTACAGTYT	900
10	GGCGGAGAAG ATCCTCCGGG ACGCGGTGCA GGTGAAC TCG ACAGCCCACG AGGCTCGGAA	960
	CGGGCTGGG GAGGTCCTCC AAGCTCAGG CAACGATGCG GCGGCTACG AGTGCTTCCT	1020
15	GACAGCCTTG GAGCTGGAGG CCAGCAGCCC CGCGTGCCC TTCACCATCA TCCCCCGGT	1080
	GCTCTGAGCA GCGCCTGCC AGCCTCACCT GCGCTCAGC CTNCAGAGG CCTGCCGGG	1140
	ACCAGGGCTT GTGCCATCG CCCAAGGGGA TGAATCTGCC GCACTGAGG CAGGGACGAG	1200
20	TGTTTCAGTG GCCACAGTGA ACCAACC AAA CCAACCCGA ATCATCGCTC TCGCCATGTG	1260
	CGTTCTCTT GTTTTTTTTG CCAGCCCAAT GGTAGTTTCT GAACCTATTG ACATTGTTCA	1320
25	AAATGGATCA TGTGCCATAT TTTGTTAGTT GACATCTGAG TTTTCAGTAA AATGATTATG	1380
	GAATTAATCA GCAAATGTAG AAGAATATAT TCAAAGTTAA AATTCAGTGG CAGCACAGAT	1440
	TATTTTATC AGAGCTGTAA AGAAAACAAC TGTCTTTTC TCCCACCAC CCCTCCTGCC	1500
30	CCACTTTGGC CCAGAAACCA AATGTGAAC TCTGTCTCC CACCTCAGCA CTAGTCCATG	1560
	CCAGGACACC AGCTGACAAT TTCTTGGTTT TACTGTCAAT AATGTACCA TGTGATCAAT	1620
35	TACTGTCTC ACTTAGAACA AAGCCTGAGT CCGAGAATAT TTATATTTTA CCAATATATG	1680
	CCTGTTACAA GAGAAGGAAA TATGAGTTAT TTAAGTTTAA CTTTTTTATG TGAATTCAGA	1740
	GTTTTTTTAT CGAGGAAAT ATGTACAAAG AAGCTTCAA TGGAAATATTT ACCGACATTC	1800
40	CTTATACATG ACAGACACTT GGCTACATGG GAAGATGATG TTAATAATAA AATGATTTTT	1860
	AAATGGAAA AAAAAAAAAA AAAAAAN	1886

45

(2) INFORMATION FOR SEQ ID NO: 94:

- 50 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1774 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

	CTCAGCTACC GTATACAGTA GGACATAACC CCATTTACA TGCCTACAC TGAGACTTGC	60
60	CTCCTCTCCC CCCACATTGA AGATGTTCTT TTTTCATAAC TATATACTAT TCCATTGCAT	120

	GAATATTCTG TAATTTATTT AATCCCCTAT GGATTGATAA TTAGGTTTCAT TATAGATAGA	180
	AGTGTAATTA ACATTCCCTGT ACATGTATTT TGCTACTTGT GTGGGTATTT CTGTAGGATG	240
5	AATAACTAGA AATTTATGG ATCAGGTTTC ACATTTGCAG TTTTGAAAAC TACTACCAA	300
	AAGATTTTAC CAATTTACAA CTCCATCATT AGTAAGAATG CCTGTTTGCC TATAGTCTGC	360
10	CAACCCTGAA TCCTTAAAAA TTTTGGCCAA TCTGGTAGGC AAAATTTCTT TCTTTTCTTT	420
	GAATATTAAT GAGGAGGAAC ATCTTTTCAT GTTTCCTGGC CATTTGCATT TCCTATTATG	480
	AATTGCTTTT GCCATTTTC CTTTTTTTAA TTATGAAAGT CTAATGACTA CCTTCTCATT	540
15	GTATAAAAAA CACAGTTCTT TGAATAGAGA GACCCCTTTC TCCAATGCTA CCAATCACAT	600
	TCCACTTACC ACAGTTTAAC ATACATCCCTC TAGTCACCTT TCCGTACGAA TATACATACA	660
20	CATAAAAAA CTTTTTACAT AAATAGGATC TCATATCTG TAGCTTTTAA AAATTTGGT	720
	CTCAAAAAA GATAACAGGT CTTTAAATTT CTTTAATGGT TGAATATGAT TAAATACTAT	780
	GAAAATGCCA TTATTTATTC CCTTAATTTT TTTCTCTCG CTATTACATT GCCAAAGTAA	840
25	ACATCCTATT CAGATGTCTT TGTGCATGTG TGTGAATATT TCTTTAGTCT GGAGTCCAGT	900
	AAGGTGGATT TTTGGATCAA AGGGTTTGT TCTGTCCAC CTTCAGTCTT CCCAAAGGCC	960
30	TTTCATACTG TATTTTCACC AAGTGATGG AGAATGTTCA TTTCCCCATA TAACCATACC	1020
	TACACTTGAT AGTTTTATC TGTGGGCGA AAAAGAACCT TTTCTTATTT TGCAATTCCC	1080
	TGATTATAAA AAAAAATGGT GAGATTGGGG TTATTTTCAT GTTTATTGGC CATTTATAGT	1140
35	TTACTGTGGA TTGTTTGAT CCCTTACCTG CTTTCTATTG GGTATGTGT GGATATATTG	1200
	TTTTTATTTG TTCAGCATCT CCTTCCCCAT CTTCTGGTAA CACAACCTTT ATTTATTTGT	1260
40	GGGGAACCTA TTCCCTGTGG CTTAGGTGAG CATGTGACCA GGCCTGGCCT CCTGAGTCCC	1320
	ACAGCTTCTT AGCCACAGTG ATAAAAGAAT GGGTATATAA CTTAAGCCAG GCTAAGGAAA	1380
	GCCCTTAACA GAACTTCTGC TGGAACACT GGAAAGAAGG CTTTATGGAG ATCCCAGGAA	1440
45	CCAAGGACCA TGTAAGCCTG AATTGTGCC ATGTGGAGAG AGTCTGTCTG AGGAGAACT	1500
	CGGATGCTAG CAGAAATGGA AAGAGAACTA AGTTCTGATG TCATTTTCTT GGAGGCCCTA	1560
50	GATCCAGCTG TGCCTAAAGC CTGCCCTACT CCGGACTTTA AAGTTTGTG AGCCAATAAA	1620
	GTCCCTTTCT TGTTAAGAT AATTGAATTG AGTTTCTGTT CTGATTAATA TAGGTTATTT	1680
	GTATTTTCTT ATTGATTTGT AGAAAACCTT TGTAAATTTA AATCTAGAC TTTATGCACT	1740
55	ATATAAGTTA ATAAAATTAG CATGGCCTTC CATG	1774

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2503 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

10 GGCACGAGCG AAGGCAAGGG GGCACCAGCT CAGGACTGCA TCTGCCTGCC ATTTCCCTTC 60
 CACTCCTCCT TTCTGGAGTC TGACATTAGA AAGCCAGCGA GAAGGAAGAT TCAAACAACC 120
 AACCCTGATT TCCTGCTTCT CCTTTTCATG AGTGTTCCTG TGGTCTCTGC ACCTCCTTTC 180
 15 TGTCCCCCGG CAGAGGGCAG TAGAGATGGC CGGCCCAAGG CCTCRGTGGC GCGACCAGCT 240
 GCTGTTCATG AGCATCATAG TCCTCGTGAT TGTGGTCATC TGCCTGATGT TATACGCTCT 300
 20 TCTCTGGGAG GCTGGCAACC TCACTGACCT GCCCAACCTG AGAATCGGCT TCTATAACTT 360
 CTGCCTGTGG AATGAGGACA CCAGCACCTT ACAGTGTAC CAGTTCCTG AGCTGGAAGC 420
 CCTGGGGGTG CCTCGGGTTG GCCTGGGCTT GGCCAGGCTT GCGGTGTACG GGTCCCTGGT 480
 25 CCTCACCTTC TTGCCCCC AGCCTCTCCT CTTAGCCAG TGCAACAKTG ATGAGAGAGC 540
 GTGGCGSCTG GCAGTGGGCT TCCTGGCTGT KTCCTCTGTG CTGCTGGCAG GCGGCCTGGG 600
 30 CCTCTTCCTC TCCTATGTGT GGAATGGGTC ARGCTCTCCC TCCGGGGGCC TGGGTTTCTA 660
 GCTCTGGGCA GCGCCAGSC CTTACTCATC CTCTTGCTTA TAGCCATGGC TGTGTTCCCT 720
 CTGAGGGCTG AGAGGGCTGA GAGCAAGCTT GAGAGCTGCT AAAGGCTTAC GTGATTGCAA 780
 35 GGGTTCAGTT CCAACCATGG TCAGAGGTGG CACATCTGCT CAGCCATCTC ATTTTACAGC 840
 TAACGCTGAT CTCCAGCTCC AGCGATGGAA CCCACTACAG AGGAGGTGGG GCCCCTGTGT 900
 40 CAAAGAGGCC GAGGGGCAGC AAGGCAGMC AGGGCACCTG TGACTTCTTA GTACAAGATT 960
 GTCTGTCTT CAGGACTTCC AAGGCTCCCA AAGACTCCCT AAACCATGCA GCTCATTGTC 1020
 ACACCAATTC CTGCTTTAAT TAATGGATCT GAGCAAATCT TCCTCTAGCT TCAGGAGGGT 1080
 45 GGGGAGGGAG TGATTGCTGT CATGGGGCCA GACTTCCAGG CTGATTTGCC AAATGCCAAA 1140
 ATGAAACCTA GCAAAGAACT TACGGCAACA AACGAGGACA TTAAAAGAGC GAGCACCTCA 1200
 50 GTGTCTCTGG GGACATGGTT AAGGAGCTTC CACTCAGCCC ACCATAGTGA GTGGGCGGCC 1260
 ATAAGCCATC ACTGGAAGTC CAACCCAGA GGTCCAGGAG TGATCTCTGA GTGACTCAAC 1320
 AAAGACAGGA CACATGGGGT ACAAAGACAA GGCTTGACTG CTTCAAAGCT TCCCTGGACC 1380
 55 TGAAGCCAGA CAGGGCAGAG GGTCCGCTG ACAAATCACT CCCATGATGA GACCCTGGAG 1440
 GACTCCAAAT CCTCGCTGTG AACAGGACTG GACGGTTGCG CACAAACAAA CGCTGCCACC 1500
 60 CTCCACTTCC CAACCCAGAA CTTGGAAAGA CATTAGCACA ACTTACGCAT TGGGGAATTG 1560

5 TGTTGATTTT CTAGCACTTG TGTATTGGAA AACCTGTATG GCAGTGATTT ATTCATATAT 1620
 TCCTGTCCAA AGCCCACTG AAAACAGAGG CAGAGACATG TACTCTGGTG TGATCTCTTG 1680
 TCCTCAGTGT CTCTCTGGG CTCCTGTCCC TCTTGCTTTA TAGCTAGCTG CCCGGGGACC 1740
 AAGGTACAGG TGAAAGCAAG GTAGCAGCTT GCGGGAGGAG GCCTGTCTGG CTTACCAGTC 1800
 10 TATACACTGT GGCCTCAACC TCCAGACAG GGCAGAGAAC TGTGGGCAGC TCGTTTGCTT 1860
 TCTAGCTGG CTGGAGAGGT GGGAGCTCAT TGATAGACTC ATGATGGAAA CTATTTTGA 1920
 AACAGGCTTC CTCCTTCAGG AGAGATCATG CGGACTAAAC TGTAGCAATT CCAGTGCACC 1980
 15 TGGCAGTGAT CCTTTTCTTT GCAAAGTACT GTCTCTTTGG TTCCAGTAAG TTGGACCACC 2040
 ACATGACATY ATTTTCCCTG GAACCTGGTC ACTGACTAAC ACAGACAATT GGGACTCCAG 2100
 20 AGCCTCAAGA GCCAGGAGAG GGCACAGTAC ATACAGAGGG AGTCAAATGG GATCTCATTT 2160
 TGAGTCCTGC CTTCCGCACA CTCAGAACGG CANCCCCAAG GCCCGGAGTG TCCAGGGCTT 2220
 CTGGCCTGAG GTGAATCTGC CAGGCCCAAG AAGGCACAAA GGTAGGAGCA CAGAGAGCCC 2280
 25 CATTCACACA GCGGKCGGC CCAGCAGCAC CAGTGAAGC TCAGCTGTCC TCCAGCTGCT 2340
 CTCGGCAGAC AGTTCAGTGC ACAGTTTATG CCCTAGCTGA AAAAGATCTC CCGGACGTAT 2400
 30 TTCAGCACAT CCTCTCCTC CTCCTCCTCA GGGCTCCTGC TACAGGCAGA GCTGGAACCC 2460
 CCCGGCCTCT GGAAGGGCT GAGGCCTGGA GYCAGTGCCT GTC 2503

35

(2) INFORMATION FOR SEQ ID NO: 96:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2801 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

CTGGAAAGCC GAGGGTAGCC GAGCGGGGCG GCGCTCTGG AGCGCGGGT GCTCGGGCTG 60
 50 CCGTCCGCTC CGCAGAAGC ACCGAGCAGC CGAGCCGGG CCCGCCGCC TCCTCCTCCA 120
 TGAGGCCCGA GTGAGGCGCG GCGGTATAG CCGACCGCG GCGCTTCCC CCGCGTCTT 180
 ATCGCGAGCG CACGACMAGC GGGCCCTGGA GGAGGAGCG GAGGAGGAG AGCATGTGG 240
 55 ACGGTTTCGA TCGGGCCCA GGTGCTGCTC GGGGCCGAR CCGGGGCTG GGCCCGGAG 300
 GGGCGGGCC TRAGGGCGGC GGTTTYCCGA AMGGARCGR CCCTGCTGAG CGGRCGGGC 360
 ACCAGCCGCC GCAACCCAAA GCGCGGGCT TYCTGCARCC AMCGCCGCTG CGCCARCCA 420
 60

	GGACGACCCC GCGCCAGGG GCCCAGTGG AGGTCCCCGC CAGCCCCCAG CGGCCTTCCC	480
	GGCCCCGGGC GCTCCCAGAG CAAACGAGGC CCCTGAGAGC TCCACCTAGT TCACAGGATA	540
5	AAATCCACACA GCAGAACTCG GAGTCAGCAA TGGCTAAGCC CCAGGTGGTT GTAGCTCCTG	600
	TATTAATGTC TAAGCTGTCT GTGAATGCCC CTGAATTTTA CCCTTCAGGT TATTCTTCCA	660
10	GTTACACAGA ATCCTATGAG GATGGTTGTG AGGATTATCC TACTCTATCA GAATATGTTT	720
	AGGATTTTTT GAATCATCTT ACAGAGCAGC CTGGCAGTTT TGAAACTGAA ATTGAACAGT	780
	TTGCAGAGAC CCTGAATGGT TGTGTTACAA CAGATGATGC TTTGCAAGAA CTTGTGGAAC	840
15	TCATCTATCA ACAGGCCACA TCTATCCCAA ATTTCTCTTA TATGGGAGCT CGCCTGTGTA	900
	ATTACCTGTC CCATCATCTG ACAATTAGCC CACAGAGTGG CAACTTCCGC CAATTGCTAC	960
20	TTCAAAGATG TCGACTGAA TATGAAGTTA AAGATCAAGC TGCAAAAGGG GATGAAGTTA	1020
	CTCGAAAACG ATTTTCATGCA TTTGTACTCT TTCTGGGAGA ACTTTATCTT AACCTGGAGA	1080
	TCAAGGGAAC AAATGGACAG GTTACAAGAG CAGATATTCT TCAGGTGGT CTTCGAGAAT	1140
25	TGCTGAATGC CCTGTTTCT AATCCTATGG ATGACAATTT AATTGTGCA GTAAAATTGT	1200
	TAAAGTTGAC AGGATCAGTT TTGGAAGATG CTTGGAAGGA AAAAGGAAAG ATGGATATGG	1260
30	AAGAAATTAT TCAGAGAATT GAAAACGTTG TCCTAGATGC AAATGTCAGT AGAGATGTAA	1320
	AACAGATGCT CTTGAAGCTT GTAGAACTCC GGTCAAGTAA CTGGGGCAGA GTCCATGCAA	1380
	CTTCAACATA TAGAGAAGCA ACACCAGAAA ATGATCCTAA CTACTTTATG AATGAACCAA	1440
35	CATTTTATAC ATCTGATGGT GTTCCTTTCA CTGCAGCTGA TCCAGATTAC CAAGAGAAAT	1500
	ACCAAGAATT ACTTGAAAGA GAGGACTTTT TTCCAGATTA TGAAGAAAAT GGAACAGATT	1560
40	TATCOGGGGC TGGTGATCCA TACTTGGATG ATATTGATGA TGAGATGGAC CCAGAGATAG	1620
	AAGAAGCTTA TGAAAAGTTT TGTTTGGAAT CAGAGCGTAA GCGAAAACAG TAAAGTTAAA	1680
	TTTCAGCATA TCAGTTTAT AAAGCAGTTT AGGTATGGTG ATTTAGCAGA ACACAAGAGA	1740
45	GCAAGAAAAT GTGTCACATC TATACCAAAT TRAGGATGTT GAGTTATGTT ACTAATGTAT	1800
	GCAACTTTAA TTTTGTTTAA CACTATCTGC CAAAATAAAC TTTATTCCCT ATAACTTAAA	1860
50	ATGTGTATAT ATATATAATA GTTTATTATG TACAGTTAAT TCTACTGTTT TGGCTGCAAT	1920
	AAAATCGATT TTGAAATAAA TGAAATGTTG AAAATTTTGC TAGTTGGTTA GATGCTTATC	1980
	CTTTAAATTC TACTTTTCTT GAGGGGAAAA AGTCTTGTGTC TGGAAATACA TATTACTGCA	2040
55	AAAATGTAGC ATCCTTTTTT AGGTAGGAGT ATTATAGCTT YCATTTTAGT TKGACATTTA	2100
	GTGTCCCAAT GAATTGAATT TCAAATATGA ATCATAATCT TGAAAATCTT TAGCACTAAA	2160
60	GTCTTGGGAA TATATCAACA ACTGATTTAC ATATGCAGAT GCTATTTGNA TACCAAGGGC	2220

	TTTTTAAATG TCATGGGGGG GAAAAACCCA ACTTGGTGGA ACTCCAGCT AAACAACCAA	2280
	GACTTCACTG GAAGATTAT TCCAATTCTA GGAATTGTC TTTTATTTT TTATTTTTC	2340
5	AACTGRCTAA CTTCATTACC TTAAAGCCTA GAACATTATT CTGCTTTATT TATATGGCTT	2400
	TCTCACTTTT ATTTTGTAGC AKGGGTGCA TCGACTTTTT TACTAGAGAA TTTTACTAGA	2460
10	TATTGTTCAT TCAAGTTTC ATCTGCTTFA TAATTGATAC ACCTTGAGGG TCACTTTTCT	2520
	AATACTTTFA CTATAATGTG GTACCACCTC AGCCCTAATA AATAATATTT TTACCTAATG	2580
	TCAAATCTTT TTCCAGCTAA CTAAAACTG TGTACAAAAG GATGCTTGT AAATATGCAT	2640
15	GTAATAGTT CTGTTAATAA CCCACTGTTT TACATTGGT ACATCTGTGT CTGCTAATAC	2700
	AGTTAGCTTT CTCACTTTC TGCTGTGTTG TTCAGTCTGA ATTAAATTA GACTTTGAAA	2760
20	ATAAAGCTTA AAAAAAAAAA AAAAAAAAAA AAAAAGCTCGA G	2801

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1631 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

35	ATGGAGCCAA AGACAATCAC TGATGCTTTG GCTTCTAGTA TAATTAAGAG TGTGCTGCCT	60
	AATTTTCTTC CATACAATGT CATGCTCTAC AGTGATGCTC CAGTGAGTGA ACTGTCCCTC	120
	GAGCTGCTTC TGCTTCAGGT TGTCTTGCCA GCATTACTCG AACAGGGACA CACGAGGCAG	180
40	TGGCTGAAGG GGCTGGTGG AGCGTGGACT GTGACCGCG GATACTTGCT GGATCTTCAT	240
	TCTTATTTAT TGGGAGACCA GGAAGAAAAT GAAAACAGTG CAAATCAACA AGTTAACAAT	300
45	AATCAGCATG CTGAAATAA CAACGCTATT CCTGTGGTGG GAGAAGGCCT TCATGCAGCC	360
	CACCAAGCCA TACTCCAGCA GGGAGGGCCT GTTGGYTTTC AGCYTTACCG CCGACCTTTA	420
	AATTTTCAC TCAGGATATT TCTGTTGATT GTCTTCATGT GTATAACATT ACTGATTGCC	480
50	AGCCTCATCT GCCTTACTTT ACCAGTATTT GCTGGCCGTT GGTTAATGTC GTTTTGACG	540
	GGGACTGCCA AAATCCATGA GCTCTACACA GCTGCTTGTG GTCTCTATGT TTGCTGGCTA	600
55	ACCATAAGGG CTGTGACGGT GATGGTGGCA TGGATGCCCTC AGGGACGCAG AGTGATCTTC	660
	CAGAAGGTTA AAGAGTGGTC TCTCATGATC ATGAAGACTT TGATAGTTGC GGTGCTGTTG	720
	GCTGGAGTTG TCCCTCTCCT TCTGGGGCTC CTGTTTGAGC TGGTCATTGT GGCTCCCCTG	780
60	AGGGTTCCCT TGGATCAGAC TCCTCTTTTT TATCCATGGC AGGACTGGGC ACTTGGAGTC	840

CTGCATGCCA AAATCATGTC AGCTATAACA TTGATGGGTC CTCAGTGGTG GTTGAAAAC 900
 5 GTAATTGAAC AGGTTTACGC AAATGGCATC CGGAACATTG ACCTTCACTA TATTGTTGCT 960
 AAATGGCAG CTCCCGTGAT CTCTGTGCTG TTGCTTTCCC TGTGTGTACC TTATGTCATA 1020
 GCCTCTGGTG TTGTTCTTTT ACTAGGTGTT ACTGCGGAAA TGCAAAACTT AGTCCATCGG 1080
 10 CGGATTTATC CATTTTTACT GATGGTCGTG GTATTGATGG CAATTTTGTC CTCCAAGTC 1140
 CGCCAGTTTA AGCGCCTTTA TGAACATATT AAAAATGACA AGTACCTTGT GGGTCAACGA 1200
 CTCGTGAAC ACGAACGGAA ATCTGGCAAA CAAGGCTCAT CTCCACCACC TCCACAGTCA 1260
 15 TCCCAAGAAT AAAGTAGTTG TCTCAACAAC TTGACCTTCC CCTTTACATG TCCTTTTGTG 1320
 TGGACTTCTC TCTTTGGAGA TTTTCCCAG TGATCTCTCA GCGTTGTTTT TAAGTTAAAT 1380
 20 GTATTGACT TGTGTTCTCA GCATTCAGAG AGCAGCGGTG TAAGATTCTG CTGTTCTCCC 1440
 TGGATCTTCT GACATTACTG CTGTCTGAGA TTTGTATATG TGTAAATACA AGTTCCTTGA 1500
 TACCCTAAAA CCTTGGATTA AACAGAATGT GCATTGTACA TCTTTAAACA AAATGTATAT 1560
 25 TAATTTATTA AATCTAGTTG TCACTTTAAA AAAAAAAAAA AAAAAACTCG AGGGGGGCCC 1620
 GGTACCCAAA T 1631

30

(2) INFORMATION FOR SEQ ID NO: 98:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 504 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

CCGAGCTGGG CGAGAAGTAG GGGAGGGCAC GAGCCGCCGC GGTGGCGGTT GCTATCGCTT 60
 45 CGCAGAACCT ACTCAGGCAG CCAGCTGAGA AGAGTTGAGG GAAAGTGCTG CTGCTGGGTC 120
 TGCAGACGCG ATGGATAACG TGCAGCCGAA AATAAAACAT CGCCCTTCTT GCTTCAGTGT 180
 50 GAAAGGCCAC GTGAAGATGC TCGGCTGGA TATTATCAAC TCACTGGTAA CAACAGTATT 240
 CATGCTCATC GTATCTGTGT TGGCACTGAT ACCAGAAACC ACAACATTGA CAGTTGGTGG 300
 AGGGGTGTTT GCACTTGTGA CAGCAGTATG CTGTCTTGCC GACGGGGCCC TTATTTACCG 360
 55 GAAGCTTCTG TTCAATCCCA GCGTCTTCA CCAGAAAAAG CCTGTGCATG AAAAAAAGA 420
 AGTTTGTGTA TTTTATATTA CTTTTFAGTT TGATACTAAG TATTAAACAT ATTTCTGTAT 480
 TCTTCCAAAA AAAAAAAAAA AAAA 504
 60

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1416 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

5	GGCACGAGGG AGGGAGCCCT CTCGGTGGG TGACTCTTGT GTGCCCTTTA GACAGGCTGG	60
10	CCTGCCGGTT CCACAGGGTA CAGTTAGGAC TTGAGTCTTT CTTTTTCTGT TTTGAGTTGG	120
	TGAGTGAGTG ATAGGGTAAC ATGGGCCTTC AGGATGACCC CTTGGAAGTG TGCCGAGTTC	180
15	CTTAAATCTC AGCTGGGATC CTGGACCTGG GAGGCCCTG TGAGGGOCAG CTCTGGAAAA	240
	ACCTGGGAGT TGATGCCGGA GCTGTGGAAG AACTCTGCTC GAGGGCAGGG TGCCCTGGAA	300
20	CACTGGTAGT TCTGGGGCTG GGAGGGAGAG GGGCTCCGGC TTTCTCTGAA ATGAACACTG	360
25	CTCTTCAGCA GTTCAAGTAC TTGTCTCAA AACATTTTCT AATTGATTGG TAGGTTTTCA	420
	TAAGCATTGT TTCTTTAAGG CATGGAAGG GAAGAATGCT CAAGCAAGTC ATGTTTGTGT	480
30	TCAGTGGGAT GGGCCCGGT TCTCACTGCT GGGGCTTCC CCTTCATGTG GCACCTTTGT	540
	GCAGGGGCCA CCAGGCAGAC TCTTCCCACC TTCTCCCACT GAAGCACCAA GGGGCTTGGA	600
35	ACCGTAATTT GGCTAATCAG AGGCATTTT TTTGTCTAG TATCTTTCAC ACTTGCCAA	660
	CCGTCTTATT TTTTAAAAG TTCTGTGCT TGTATTAACA CGAACTAGA GAGAAATAGT	720
40	TTCTGAAGCC AGTTTATTGT GAAGATCCCC AAGGGGAGGT TCGGTAGAGA AAAATAGTAA	780
	GCTGGTTTAG AACTGACGA GGGCAAACAG CCAGGACGCA TTGGAGAGGA ATTTGCCAAA	840
45	GATCTACCTT GAGATAACGC CTGTCCAGTG TCTTCACCAC GTGAATAACC AGCGCTCCAA	900
	AGTGTTTTTC TGCTTTGAAA AAAAAAATTC CACAAGCTTT TAAAGGTGCA TTTAAGAATC	960
50	CATGTGACTT TAGAATGGAA CTGCCGGCCC TGGCAACTGT CACGTGTGCT AGAAGGTTGG	1020
	ATGCCTCTGG AATGCATGTG ATACTCATCT CCATTTTGT TCTTTGATTG CATTTTGTGT	1080
55	CTTTTAGCAG ATCTGTCCCT GTGGGTGGTG TCTAAGAAGT CGGACACCTT GGTTTTGTG	1140
	TTAGATTGAG CTGGGCAGCT GCAATCAGCT TCTTTATATG CAAATTAGGC ACGACCCATC	1200
	TGTGGTTCTT GGTGTGGTGC TAATGAAGTG AGGGGAGGGA GGGATGTCAC CCCAAAAGTA	1260
	GGCCCTCCCA TTGGCTTTGG CCAGGCCAGA CACTTCACAT CGTTTACATG GTTCTGTGTA	1320
	ATTTTAAAGT TTATGTGTAT AAAGCGAAGC TGTTCCTGTG AAAGTGTATA TTTTGTAAAT	1380
60	AAATATATG CTAATTGAAA AAAAAAAAAA AAAAAA	1416

5 (2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 2847 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

15 GGCTAGGACA ATTTTGGTGC TTTACCTATC TCTGCAAAGA CTGGAGAATT TGGCATACCA 60
TTAATTACAA CCACCAATCA TATCCAACAA AAGTACCOCTA AAAGAAGGAC CAGTGGCCAC 120
TCTCGAAAAA ATTAAAGTAT CAGAAGATTA AAAAGATTTT AGGATTTGGA AGCTTGATAT 180
20 GTCTTTCCCC AATAATCATT GTTTGATCTC CAAATAGTAG CCTTATATTA GCAATRGACA 240
GATCATTGGT TCTCCATATC TGATCATATG TTACTACTTT GGAATCAGTA TTTGGGCAAA 300
25 TTCAAGCATT TATGCAGTGG ATATAAATGG AAATATAAAA ATATTTGCCA ACCTGTCTCA 360
GTAACCTATC ATATCTCTGT GNATCCTCAA GGAAAGCACT TTTGCTTTTA CTTAGAAAGC 420
GTTTCAGATT TGCTTTATAG ACTCCTGCTG TCTTCAGTAC CTGATAAAAC TTAAACCAGG 480
30 GAAGCATTAA ACACAGTGCA GCAGCTTTTG CCCAGGCTTC TAAGTTCCCTG CCGGCAGCAT 540
TTATCAATGT AAGAACTAGG ATGCTTCCTG CAGTGGCACT ACCTTCCCCT AGAGCTGGAG 600
35 CATGCTGCTT GGCTTAAGC CCCAGCATGA TGAGGCTTCC CTCCTGCCAG GTCAGTAAAA 660
GTTAGAGAGC TCAGAATGG GTCTTGCCCTG GGTGCAGGTG GCAGGGTTTG CTGAAACCCC 720
TAAAGAGAAG TCACCAAGGG AGGCAGGTAA TGAATGTTTC CAGAATCAGT CKGATACTCA 780
40 TAGCAATTTT TGCTATCTT TCAAAATGTTG AATTTCTGGA TGCTGAGAGG GACTTTGATT 840
TGATATCATT AAATCCAGGA CAGTCCCAAG AAGTGCTTGG AGTCTCGGCT CTGACAGCCC 900
45 AAGAAGGGAA ATAACTTGTA TTAAGGAACA ACTATGAGCC AGGCCCTGAG CTGTCTCTTA 960
GATAATAAAA CAGATGGGGA GTGGAAGAGT CATTTGCTTC AAGTTATACA GCTAGGAAAT 1020
ACTCAAGCCA AATCTTGAAC GCAGTCCCC CTAATTCTGT GGACAGGCAC TTTGTACCAC 1080
50 ACACCATGGT CCACCTAAAA ACAGAAGGAT AAAAAGACTT CAGGTTTTC CACTGTGTGC 1140
TGACCATCCC AATTTATGAA TCTTCTTCAA AATGACATTT CACAGTTATA GTTAGGGCTC 1200
55 AGAAATGGCA TTGAGGTAGC CTTATTTCTC CCCTTTAGCA GATGCTTTAA GTACACATTG 1260
CTGACTTGAG CCCACCCCA GGAGTTAGGA GAACATTTCC TTTTTCATGC CATCTTOCAT 1320
AAATAAGGTG TTTCTTGGCC TTCAAAGATA TAGAACTTTG CAGCAGTAGT AAAAGTGAAG 1380
60

	GGTGTCTGTC TCTCTACTCA ACTTTATTTG AAAATGTCTG CAGCTTCACT CCTGTAGAAA	1440
	AGGAAATCTT CATATTTTAG TAAACTTAGC CGCCAGTGTA CTCTGTGAGG ATGTGGCAAT	1500
5	TCAAAGTCCA GTGAATCTGG CTCTCTTACT GATTCCTGGT TTTAGTGTGT GTGTCGGGGG	1560
	AGTGTGTACC TATATATAAA GGACAAGTGT GATATGTGTG TATATGTATA TACATACATA	1620
10	CATGTCCACA CACACACACA CAATATTTGA GAGCTAAGGA AAACCTCAAAG CAGCCCCCTC	1680
	ATTATCTTGC GTACTACTTC AAAGATTTCT GTCAGCCCTA ATTACAAGTG TCACCATATA	1740
	GTGCGGGCTT AGGFACTTGC TTACAGGAAG AGCAATTCCT TAGCAAAGGT CATTAGCTCC	1800
15	TAAGGCACTG AGTCAAAGTG ACAGCCCTGA AGGAAATTCG ACTCCAGCCC TCCTCCAGGA	1860
	TGCTCTAATA GATGGGAAAC TTGGATGCCC AGCCATTTTG GTGACCTGAG AGTCTAACTA	1920
20	CTCCAGTTAG ACCTAAGGGC ACAAATGCAG AATTCATGAC CTTGTAGTTG TGGCAGGGTC	1980
	TAGGAAGTCC TCTCTCCCA AGTAGAAAAT ATTCTCTTGC CATTCTGAA ATCCACATT	2040
	CATATAATGG CTGTGCAATA CATGCTTCTC AATAAGAAAA TTAAGTGCAT GTTACTGTG	2100
25	TGCTGATCAC ATCAGATTTT TATGTTTAAA AAAATCTCAT TATGGNTTGA GTCCAGCCCA	2160
	GCTCTAAGAG AAAAAGAAGG CCCATATGGG AGACTTCAGT CTCATTATTA TTGCCTTTAT	2220
30	CCAGCAGTGC TTATRAAGCC CCTACCCCTG TCCCATTCOA GAAACCATAA GACTCAGGCA	2280
	GTCTTGATT CTGGAGGCCT GCGTGTAAG ATAAGATAGT ATAATTTGGA ACTGAGAACA	2340
	TACCAGAAAC AGCAGAACGA GGGCCAGAGC AGAAAAATGA AAATAAGTGG AGACACTTAT	2400
35	GGATACATTG GTGCAAAAAA AGCCACGGGS CCCATACTGG GCTTGATATG ACTTTGAGGG	2460
	GACAGCAGAT TAATACTTAA TGAGGGTTAA ACCTGACCAG TCTTCTACA GTGACAGGCC	2520
40	ACACTGCATG AATGGGGAGA ACCAATGAAT CCATTGTCCT CTGCCTATTT TCCTGTGCAC	2580
	AGTCACATTC CCTCCTTAGG AATCTTCCCC TTCCACCCCT TACATTAAC AAGGGAACAC	2640
	TGAATCTTTC AAGGGAATTA CACGTTGGG TTAATGTTTC AGTATATCAT TTTCATACTG	2700
45	TAAATTATTT TGTAAGAGAG ATTTACTGCT ATCCCAGGAT GTTCGGACTT GGTGCCCTG	2760
	TGCATTTGGA AATCAATAAA CTATTACTGG AAATGCCAAA AAAAAAAAAA AAAAAAAAAAN	2820
50	NAAAAAACTC GAGGGGGGCC CGTACCC	2847

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1394 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

5	GAGATTGGTG GAGGAGAGTA AATAATCTAG AGGCAAGAGT TCAGTGAGGG CCAAGGGGGA	60
	CCCCCAGAAA AAGGTATGGA GCTAACTCAT CTC'TTTTACA AGGGGTGGCC ATGACTTACT	120
	GTTGCAAAGT ACTCAGTGTA TATTTAATGT TGATGTGGA ATTTTAGTTA CGAGAGGGAA	180
10	GAACAATTTT ACTTCTGTCC TTATTTCACT TGCTGAAAAG CTGTGGGACA AAATGTATGG	240
	AATAGACAAG GCCACTTTCT TTGTGATTC TGCTTTTCAT GCATATTATT TTATTTACCC	300
15	ATAATTTCCA AGAGGTTTGG CGTCCGCTC TCCTGCTTTT TTCTTTCATC CACCCCTTTC	360
	CTTTTITGG AAGGGGGTGA TATATGAGAG TTCATTGAAG AAGTCCAGTG AGGCTGAAGT	420
	AAAGGGGCAA GATAGGGCAG TTAACATAAG AGCACTTTAT TTCTTTGAAG CCTTCTAAG	480
20	AAAGAAATGG GGGTGCAGT GGCTTGAATC TCCCATGATG TTGGAGGGCA CTTAGTGGGG	540
	TTGAAGTATG ACATAATATT TCCCATGGG GAAAGGAGAA TTCTCTTAG AGGGTGGCAA	600
25	AATGCCITTG CCCAGTGTC CTATTTTAGG CATCTTTTC TTCTTATTC CTTCAGTCA	660
	GGGTGTGTCC TATACAAAAC TTCCCATCAG TTCTCCTCAA TATTCCTCAT TTGTAAATGA	720
	TCACTTCTCT TTTCTAAACC CTMTTCTGT TCAGATCCAT ACAGGATTTG CAAGGGTAGG	780
30	ATCATACATG CAAATGCCCC TTGTTTCTCT GTGTCTTCTG CAACTAGTC TCATGAAGAA	840
	TTCTGGGGTG CAGCAGGGTA GCTGAAGTTT GGGTCTGGGA CTGGAGATTG GCCATTAGGC	900
35	NTCNCIGAGA TTCCAGCTCC CTTCACCAA GCCCAGTCTT GCTACGTGGC ACAGGGCAAA	960
	CCTGACTCCC TTTGGGCTC AGTTTCCCCT CCCCTTCATG AAATGAAAAG AATACTACTT	1020
	TTTCTGTGTG GTCTAGCATT GCTGGACACA AAGTGTAGTC ATTATTGTG TATTGGGTGA	1080
40	TGTGTGCAAA ACTGCAGAAG CTCACTGCCT ATAAGAGGAA ATAAGAGAGA AAGTGGAGGA	1140
	GAGGGACAAA AGGAGTAATT ATTGGTATA GATCCACCCA TCCCAACCTT TCTCTCCTCA	1200
45	GTCCCTGCTC CTCATGTTTC TGGTTTGGTG AGTCCTTTGT GCCACCACCC ATAATGCTTT	1260
	GCATGTCTGC ATCCTGGGAA GGGGTATAT GGTCTCACAA GTTGTGTCA TTGTTTTTTT	1320
	GCATGCTTTC TTAATAAAAA AAAAAAAAAA ATGTTTANAG TTTTATCTTA AAAAAAAAAA	1380
50	AAAAAAAAA ACCC	1394

55 (2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 794 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

5	GGMRCGAGGC GGAGTAAAGG GACTTGAGCG AGCCAGTTGC OGGATTATTC TATTTCCCTT	60
	CCCTCTCTCC CGCCCCGTAT CTCTTTTCAC CCTTCTCCCA CCCTCGCTCG CGTACCATGG	120
	CGGAGCGTCG GCGGCCACTC AGTCCCATTC CATCTCCTCG TCGTCCTTCG GAGCCGAGCC	180
10	GTCCGCGCCC GGCGGCGGCG GGAGCCCAGG AGCCTGCCCC GCCCTGGGGA CGAAGAGCTG	240
	CAGCTCCTCC TGTGCGGTGC ACGATCTGAT TTTCTGGAGA GATGTGAAGA AGACTGGGTT	300
15	TGTCTTTGGA CACGCTGATC ATGCTGCTTT CCCTGGCAGC TTTCAGTGTG ATCARTGTGG	360
	GTTTCTTAMC TCATCCTGGC TCTTCTCTCT GTACCATCA RCTTCAGGAT CTACAAGTCC	420
	GTCATCCAAG CTGTWCAGAA RTCAGAARAA GGCCATCCAW TCCAAAGCCT ACCTGGACGT	480
20	AGACATTACT CTGTCTCAG AAGCTTTCCA TAATTACATG AATGCTGCCA TGGTGACAT	540
	CAACAGGGCC CTGAACTCA TTATTGCTCT CTTTCTGGTA GAAGATCTGG TTGACTCCTT	600
25	GAAGCTGGCT GTCTTCATGT GGCTGATGAC CTATGTGGT GCTGTTTTTA ACGGAATCAC	660
	CCTTCTAATT CTTGCTGAAC TGCTCATTTT CAGTGTCCCG ATTGTCTATG AGAAGTACAA	720
	GACCCAGATT GATCACTATG TTGGCATCGC CCGAGATCAG ACCAAGTCAA TTGTTGAAAA	780
30	GATCCCAAGC AAAA	794

35

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:

- | | |
|----|-----------------------------|
| 40 | (A) LENGTH: 1544 base pairs |
| | (B) TYPE: nucleic acid |
| | (C) STRANDEDNESS: double |
| | (D) TOPOLOGY: linear |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

45	TTTGCTTGCT AGTCTGAACC AAAGAGTTGT TTGGGCATTT GCTGTGTGG CCATTTCTGG	60
	AGCAAGAGGG TCTTCTTCCT CCTTCCCCCA GCCAGCCAGC TGTCTGGGG CCAGGCTTTC	120
50	CTGGGTGGAA AGAAGTATAC CTTTCCCTGG GGCCCTAGGA TAGCAAAGTG AGCCATAGTG	180
	GGCCAGGCTG CCTCCATGC TGGGCCCCAG CCCAGGTC TG CACTCGCCTG GATCACCTTC	240
	TTTGAGCCTT AGCCATCTCC TGTGAGGTAG GAATGAACTT GCCAGCCTTC AGGYTCGTTT	300
55	AGCTATGACC ATCTGTGCGG TCAGGGTACA CTCAGCTCTC CTCCCCAACT CCAGCAGCCT	360
	TTAAGAAGTG TCCCTTTGGC GCCCCCTGGA GGCAGAGCAC TGAGCTGGAC CCTGGGTAGA	420
60	CTCCACAGG GAGGACGGAG CTGGCCTCAG GAGTGGGACA CCCAGACTTG GCAGGGCCTT	480

	CAAGAGGCCT GTGTGGGGC CCCAGGAATC CTTAGCTGAA GCGGGGAGAC TCACTCTCCA	540
	TCTCAGGAAA TTCTAGCCCT TGCCCTCAGG GAGCCACGGT TGAGGGTGAG GCCCAACACC	600
5	TGCCTTAGGG CCCTGGGTGG GCAAGTCTGG GCCCTGGGGT AGGGAGGGAG ACTCAGGCC	660
	ACACTTGGGT ATTTTCTAAT TTCAGACAAA CACACACTCA GCGGCACTC ACTGATTCTT	720
10	ACACATTGCC AAGATTTTAC ACATGTGACC AGGGGCCACC AAAGTCCCTG TGACCTTTGT	780
	GACTAGGATC CTAATTTCTC TATTTTCTCC TGGGTGCCTG GGTCTGTGTC ACCTGGGGCA	840
	GTGTGGATAA TGTTTAGTTC TGTGACACTG TTTTTTGGGG GTGGCACCTG GTTCTCCGAT	900
15	GCCTGGGCTG GTGTCAGGCC CAGGACTGTA GTGCTGGGAG CAGTAAAGCT CAGCTCTGTG	960
	TAATGAGTGA TGCTATGGCT TGCTCGTGTC TTATGATCCA ATCCTTTTCT ACATCAGCCC	1020
20	TTGTTTGTGTT TTATGGCTAG TCTTATCTGG CCTGGTTATT TCCTTGCGGG GAGGAGAGGG	1080
	TTTGCTAATC TGCTCCAGC CCAACCTATT ACCACCCAC CTCGCTGGGA CTTACTGCTC	1140
	GGGAGGCAGC AGACAGGGAG CCACCAGCAG TGGCTTCCTG GCCCTGTGCT GGGGGTGGG	1200
25	GGAAGCTGGG GGCACATGTG GCCCTTGCCT TCTGAGCAGC TCCAGTGCC AGGGCTTTGA	1260
	GACTTTCCCA CATGATAAAA GAAAAGGGAG GTACAGAAGT TCCAATTCCC TTTTATTTT	1320
30	GCTGGTGGT ATCTGTAAAT GTTTAATAAA TATCTGAGCA TGTATCTATC AACGCCAAGA	1380
	ATTTCAAAGT CTCCTTCAAC AATATGAGGC TTTTAGGATG TTTATATTCC TTCATCCCTC	1440
	TTGTTTCCCA GGTTTTGAG GGAATAAAG TCTGGAATTA TAGATACAGC TTATTATTAA	1500
35	ATTTGTCTT GCATAAAAAA AAAAAAAAAA AACNCNNGG GGGG	1544

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(2) INFORMATION FOR SEQ ID NO: 104:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 871 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

50

	ACCCACGCGT CGNCTTGTC CACCCGGGGG CGTGGGAGTG AGGTACCAGA TTCAGCCCAT	60
	TTGGCCCCGA CGCCTCTGTT CTCGGAATCC GGGTGCTGCG GATTGAGGTC CCGGTTCTTA	120
55	AGGTGGGTG CTGTCCACCC GGGGGCGTGG GAGTGAGGTA CCAGATTGAG CCCATTTGGC	180
	CCCAGCGCT CTGTTCTCGG AATCCGGGTG CTGCGGATTG AGGTCCCGGT TCCTAACGGA	240
60	CTGCAAGATG GAGGAAGGCG GGAACCTAGG AGGCCTGATT AAGATGGTCC ATCTACTGGT	300

CTTGTCAGGT GCCTGGGGCA TGCAAATGTG GGTGACCTTC GTCTCAGGCT TTCTTGCTTT 360
TCCGAAGCCT TCCCCGACAT ACCTTCGGAC TAGTGACAGAG CAAACTCTTC CCCTTCTACT 420
5 TCCACATCTC CATGGGCTGT GCCTTCATCA ACCTCTGCAT CTTGGCTTCA CAGCATGCTT 480
GGGCTCAGCT CACATTCTGG GAGGCCAGCC AGCTTTACCT GCTGTTCTCG AGCCTTACGC 540
10 TGGCCACTGT CAACGCCCGC TGGCTGGAAC CC CGCACCCAC AGCTGCCATG TGGGCCCTGC 600
AAACCGTGGG AGAAGGAGCG AGGCCTGGGT GGGGAGGTAC CAGGCAGCCA ACAGGTTCCT 660
GATCCTTAAC GCCAGNTGCG AGAGAAGGAC CCCAAGTACA GTGCTCTCCG CCAGAATTTT 720
15 TTCCGCTACC ATGGGCTGTC CTCTCTTTGC AATCTGGGCT GCGTCCTGAG CAATGGGCTC 780
TGTCTGCTG GCCTTGCCCT GGAAATAAGG AGCCTCTAGC ATGGGCCCTG CATGCTAATA 840
AATGCTTCTT CAGAAAAAAA AAAAAAAAAA A 871
20

25 (2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 404 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

GGCACGAGTT ATAGCATGGC ATTCATACTT TTGTTTATT GCCTCATGAC TTTTGTGAGT 60
35 TTAGAACAAA ACAGTGCAAC CGTAGAGCCT TCTTCCCATG AAATTTTGCA TCTGCTCCAA 120
AACTGCTTTG AGTTACTCAG AACTTCAACC TCCCAATGCA CTGAAGGCAT TCCTTGTCAA 180
40 AGATAACCAGA ATGGGTTACA CATTTAACCT GGCAAACATT GAAGAACTCT TAATGTTTTC 240
TTTTTAATAA GAATGACGCC CCACCTTGGG GACTAAAATT GTGCTATTGC CGAGAAGCAG 300
TCTAAAATTT ATTTTITTA AAAGAGAAAC TGCCCCATTA TTTTGGTGGG GTTGGTTTTT 360
45 AATTNTAAT NTGAAAAAT TTTTGGGGT TTTTGGGCC ATGG 404

50 (2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1542 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

60

	GTCAGACAGG TGGAGCCGCC GGGGCAGGAG TCTCAAAGAG CCAGGCTCCA GGAGAGGAAG	60
	GGCTCTFCGA GAGGAGAGAG GAGAGCGCTG GAGAGGAGAG GCTGGAGAGT CCTTAGCCAG	120
5	GATGGAGGCT GTTGTGAACT TGTACCAAGA GGTGATGAAG CACGCAGATC CCCGGATCCA	180
	GGGCTACCCCT CTGATGGGGT CCCCCTTGCT AATGACCTCC ATTCTCCTGA CCTACGIGTA	240
10	CTTCGTTCTC TCACTTGGGC CTCGCATCAT GGCTAATCGG AAGCCCTTCC AGCTCCGTGG	300
	CTTCATGATT GTCTACAAC TCTCACTGGT GGCACCTCTCC CTCTACATG TCTATGAGTT	360
	CCTGATGTCG GGCTGGCTGA GCACCTATAC CTGGCGCTGT GACCTGTGG ACTATTCCAA	420
15	CAGCCCTGAG GCACTTAGGA TGGTTCGGGT GGCTGGCTC TTCCTCTTCT CCAAGTTCAT	480
	TGAGCTGATG GACACAGTGA TCTTTATTCT CCGAAAGAAA GACGGGCAGG TGACCTTCCT	540
20	ACATGTCTTC CATCACTCTG TGCTTCCCTG GAGCTGGTGG TGGGGGGTAA AGATTGCCCC	600
	GGGAGGAATG GGCTCTTTCC ATGCCATGAT AACTCTTCC GTGCATGTCA TAATGTACCT	660
	GTACTACGGA TTATCTGCCT TTGGCCCTGT GGCACAACCC TACCTTTGGT GGAAAAAGCA	720
25	CATGACAGCC ATTCACTGA TCCAGTTTGT CTTGGTCTCA CTGCACATCT CCCAGTACTA	780
	CTTTATGTCC AGCTGTAAC ACCAGTACCC AGTCATTATT CACCTCATCT GGATGTATGG	840
30	CACCATCTTC TTATGTCTGT TCTCCAACCT CTGGTATCAC TCTTATACCA AGGGCAAGCG	900
	GCTGCCCCGT GCACTTCAGC AAAATGGAGC TCCAGGTATT GCCAAGGTCA AGGCCAACTG	960
	AGAAGCATGG CCTAGATAGG CGCCACCTA AGTGCCCTCAG GACTGCACCT TAGGGCAGTG	1020
35	TCCGTCAGTG CCTCTCCAC CTACACCTGT GACCAAGGCT TATGTGGTCA GGAAGTACCA	1080
	GGGACTGGC CCTCCCCCTC CCACAGCTGC TCTACAGGA CCACGGCTTT GTTCTCTCAC	1140
40	CCACTTCCCC CGGGCAGCTC CAGGGATGTG GCCTCATTCG TGTCTGCCAC TCCAGAGCTG	1200
	GGGGCTAAAA GGGCTGTACA GTTATTTCCC CCTCCCTGCC TTAAACTTG GGAGAGGAGC	1260
	ACTCAGGGCT GGGCCACAA AGGGTCTCGT GGCCTTTTTC CTCACACAGA AGAGGTCAGC	1320
45	AATAATGTCA CTGTGGACCC AGTCTCACTC CTCACCCCA CACACTGAAG CAGTAGCTTC	1380
	TGGGCCAAAG GTCAGGGTGG GCGGGGCCT GGAATACAG CCTGTGGAGG CTGCTTACTC	1440
50	AACTTGTGTC TTAATTAAAA GTGACAGAGG AAACCANAAA AAAAAAAAAA AAAAACTCGA	1500
	GGGGGCCCCG TACCCAAATC GCCGTATGA TCGTAAACAA TC	1542

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(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2327 base pairs

(B) TYPE: nucleic acid

60

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

5	GGTAGCTCAN TGCAGTGAAG TAGTCTTACT GGAAACAAAG CCCTTTATCA AGAATAATTA	60
	ACTCTTCCCT TTTCTTTTGT GAGAGGTGCT TTGTTTCTGA TCGGACCATT TCACTGCAGC	120
10	AAGCAACACA GTATTCTRAG CAGAAGATCG GGACTTGAGG CCATGTTGCG GAGGGCCAGT	180
	RACATTATCT GGACTCTGGA GTGTGAGGAA TATGGACTCC ACTCTTCACT ATATTACAR	240
15	CGATTACAGC TTGAGCAACA ATAGCAGTTT TAGCCCTGAT GAGGAAAGGA GAACTAAAGT	300
	ACAAGATGTT GTACCTCAGG CGTTGTTAGA TCAGTATTTA TCTATGACTG ACCCTTCTCG	360
	TGCACAGACG GTTGACACTG AAATTGCTAA GCACTGTGCA TATAGCCTCC CTGGTGTGGC	420
20	CTTGACACTC GGAAGACAGA ATTGGCACTG CCTGAGAGAG ACGTATGRGA CTYTGGCCTC	480
	AGACATGCAG TGGAAAGTTC GACGGAACTC TAGCATTCTC CATCCACGRG CTGTCAGTTA	540
	TTCTTGAGA TCAATTGACA GCTGCAGATC TGGTTCCAAT TTTTAATGGA TTTTAAAAG	600
25	ACCTCGATGA AGTCAGGATA GGTGTCTCTA AACACTTGCA TGATTTTCTG AAGCTTCTTC	660
	ATATTGACAA AAGAAGAGAA TATCTTTATC AACCTCAGGA GTTTTGGTG ACAGATAATA	720
30	GTAGAAATTG GCGGTTTCGA GCTGAAGTGG CTGAACAGCT GATTTTACTT CTAGAGTTAT	780
	ATAGTCCCAG AGATGTTTAT GACTATTTAC GTCCCATGTC TCTGAATCTG TGTGCAGACA	840
	AAGTTTCTTC TGTTCGTTGG ATTTCCTACA AGTTGGTCAG CGAGATGGTG AAGAAGCTGC	900
35	ACGCGGCAAC ACCACCAACG TTCGGAGTGG ACCTCATCAA TGAGCTTGTG GAGAACTTTG	960
	GCAGATGTCC CAAGTGGTCT GGTGCGCAAG CCTTTGTCTT TGTCTGCCAG ACTGTCATTG	1020
40	AGGATGACTG CCTTCCCATG GACCAAGTTG CTGTGCATCT CATGCCGCAT CTGCTAACCT	1080
	TAGCAAATGA CAGGTTTCCT AACGTGCGAG TGCTGCTTGC AAAGACATTA AGACAACTC	1140
	TACTAGAAAA AGACTATTTC TTGGCCTCTG CCAGCTGCCA CCAGGAGGCT GTGGAGCAGA	1200
45	CCATCATGGC TCTTCAGATG GACCGTGACA GCGATGTCAA GTATTTTGCA AGCATCCACC	1260
	CTGCCAGTAC CAAATCTCC GAAGATGCCA TGAGCACAGC GTCCTCAACC TACTAGAAGG	1320
50	CTTGAATCTC GGTGTCTTTC CTGCTTCCAT GAGAGCGAG GTTCAGTGGG CATTCGCCAC	1380
	GCATGTGACC TGGGATAGCT TTGGGGGAG GAGAGACCTT CCTCTCTGCG GAACTTCATT	1440
	GCAGGTGCAA GTTGCTTACA CCAATACCA GGGATTTCAG GAGTCAAGAG AAAGTACAGT	1500
55	AAACACTATT ATCTTATCTT GACTTTAAKG KKWAWKMMWW KCTCAGMSRA TTATAMTTSW	1560
	CWMMRARGSM WYMAAWSCTK SWGCTCYWCC KSRSTGRMKG MMRCTCTAGA AYTRGYRGAK	1620
60	CMYYKSGCT KMWGGAARKS GGCASGAGCC AGAGACCTGC ATTGCTTTCT CCTGGTTTTA	1680

5 TTTAACAATC GACAAATGAA ATTCTTACAG CCTGAAGGCA GACGTGTGCC CAGATGTGAA 1740
 AGAGACCTTC AGTATCAGCC CTAACCTCTC TCTCCCAGGA AGGACTTGCT GGGCTCTGTG 1800
 GCCAGCTGTC CAGCCCAGCC CTGTGTGTGA ATCGTTTGTG ACGTGTGCAA ATGGGAAAGG 1860
 AGGGGTTTTT ACATCTCCTA AAGGACCTGA TGCCAACACA AGTAGGATTG ACTTAAACTC 1920
 10 TTAAGCGCAG CATATTGCTG TACACATTTA CAGAATGGTT GCTGAGTGTC TGTGTCTGAT 1980
 TTTTTCATGC TGGTCATGAC CTGAAGGAAA TTTATTAGAC GTATAATGTA TGTCTGGTGT 2040
 TTTTAACTTG ATCATGATCA GCTCTGAGGT GCAACTTCTT CACATACTGT ACATACCTGT 2100
 15 GACCACTCTT GGGAGTGCTG CAGTCTTTAA TCATGCTGTT TAAACTGTG TGGCACAAGT 2160
 TCTCTGTGCC AAATAAAATT TATTAATAAG ATCTATAGAG AGAGATATAT ACACTTTGA 2220
 20 TTGTTTTCTA GATGTCTACC AATAAATGCA ATTTGTGACC TGTAAAAAAA AAATAAAAAA 2280
 ACTCGAGGGG GGCCCGGTAC CCAAATCGCC GATATGATCT AANCATC 2327

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(2) INFORMATION FOR SEQ ID NO: 108:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1062 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

GGCCGCGAG GCGCAACAGC CGTTCTGTCA GCTCTGGGTC CAACCGGACT AGCGAANATC 60
 40 TTCTCATCC TCATCATCGT CTTCCTCATC CCGATCTCGG TCCAGGTCCC TCTCCCCCCC 120
 ACACAAGAGG TGGCGAAGGT CCAGCTGTAG TTCTCTGGA CGTTCTCGAA GATGCTCTTC 180
 CTCTCTTCG TCATCATCTT CCTCTTGTG TTCTCATCC TCATCATCCA GTTCTCGAAG 240
 45 CCGCTCACGA ATCCCCATCC CCCCGCCGGA GRAAGTGACA GGAGGCGGCG GTACAGCTCT 300
 TATCGTTTAC ATGACCATT CAAAGGCAA AGAGTGCTAC AAAAGGAGCG TGCAATAGAA 360
 50 GAAAGAAGGG TGGTCTTCAT TGGAAAGATA CCTGGCCGCA TGAATCGATC AGAGCTGAAA 420
 CAGAGGTTCT CCGTTTGTG AGAGATTGAG GAGTGCACCA TCCACTTCCG TGTCCAAGGG 480
 GACAACTACG GCTTCGTAC TTATCGCTAT GCTGAGGAGG CATTTGCAGC CATTGAGAGT 540
 55 GGCCACAAGC TGCGGCAGGC AGATGAGCAG CCCTTTGATC TCTGCTTTGG GGGCCGAAGG 600
 SWGTNCTGCA AGAGGAGCTA TTCTGATCTT GACTCCAACC GGAAGACTT TGACCCAGCA 660
 60 CCTGTAAAGA GCAAATTGA TTCTCTTGAC TTTGACACAT TGTTGAAACA GGCCGAGAAG 720

AACCTCAGGA GGTAACCTTG GGCCCTTCCC TGCTATCCTT TTTCTCCTTT GGAGGTGCCC 780
 AACCTCCTCC ACCCCCTTCC CCTACTCTAG GGGAGAGAGC TGCTAGTGAG ATGACTGTTT 840
 5 TATAAAGAAA TGGAAAAAAG TGAAATAAAA AATATGTTGA ATCAGATTTT TTAAAAGGGG 900
 TATTTGTTTT TTTATAACAG GTATTGAAAC AAGTTAACTT GCATTCTAT GTAAGATAGG 960
 AGGGGCTGAG GGGATCCCCA GTGTTTGGA CATAAGTCAC TATGCAGACT AATAAACATC 1020
 10 AACTAGAGAG NAAAAAAAAA AAAAAAAAAA ATTTAAAAAA CT 1062

15

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 2539 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

GAGAGACTCA CACTTCTTTT CCATTATCAC TGACGATGTA GTGGACATAG CAGGGGAAGA 60
 GCACCTACCT GTGTGGTGA GGTGTTGTTGA TGAATCTCAT AACCTAAGAG AGGAATTTAT 120
 30 AGGCTTCCTG CCTTATGAAG CGATGCAGA AATTTTGGCT GTGAAATTTC AACTATGAT 180
 AACTGAGAAG TGGGGATTAA ATATGGAGTA TTGTCGTGGC CAGGCTTACA TTGWCTCTAG 240
 TGGATTTTCT TCCAAAATGA AAGTTGTTGC TTCTAGACTT TYAAGMKMRA TWKCCCCMAK 300
 35 YWAWCKGAAC AMAMKCTGSW CYTCCWSYGC SKTRRMKRYC GYKSTATRRC WARWKSAYYM 360
 CCYGKKMTGS RRGTAWYTSK TGCAYKAGGG AACAAATTGAG GAAGTTTGTT CTTTTTTCCA 420
 40 TCGATCACCA CAACTGCTTT TAGAACTTGA CAACGTAATT TCTGTCTTTT TTCAGAACAG 480
 TAAAGAAAGG GGTAAGAAGC TGAAGGAAAT CTGCCATTCT CAGTGGACAG GCAGGCATGA 540
 TGCTTTTGAA ATTTTAGTGG AACTCCTGCA AGCACTTGTT TTATGTTTAG ATGGTATAAA 600
 45 TAGTGACACA AATATTAGAT GGAATAACTA TATAGCTGGC CGAGCATTG TACTCTGAGT 660
 GCAGTGTGAG ATTTTGATTT CATGTGTACT ATTGTTGTTT TAAAAATGT CCTATCTTTT 720
 50 ACAAGAGCCT TTGGGAAAAA CYCMAGGGG CAAACCTCTG ATGCTCTCTT TGCKKMSRT 780
 ARMTTTTGAY ATRMARYACT RMTKSAYTY AAYGRWGTGA CWSGAWAATA TTRAASTYA 840
 TACAATKAAT YWTRRYTSM KRMAGMYAAT CCGAAAYGT GGMAAMYAAA CTTGATATTC 900
 55 AAATGAAACT CCTGGGAAA TTCCGCAGAG CTCACCAGG TAACTTGGAA TCTCAGCTAA 960
 CCTCTGAGAG TTACTATAAA GAAACCTAA GTGTCCCAAC AGTGGAGCAC ATTATTCAGG 1020
 60 AACTTAAAGA TATATTCTCA GAACAGCACC TCAAAGCTCT TAAATGCTTA TCTCTGGTAC 1080

	CCTCAGTCAT GGGACAACCTC AAATTCAATA CGTCGGAGGA ACACCATGCT GACATGTATA	1140
5	GAAGTGACTT ACCCAATCCT GACACGCTGT CAGCTGAGCT TCATTGTTGG AGAATCAAAT	1200
	GGAAACACAG GGGGAAAGAT ATAGAGCTTC CGTCCACCAT CTATGAAGCC CTCCACCTGC	1260
	CTGACATCAA GTTTTTTCCT AATGTGTATG CATTGCTGAA GGTCTGTGT ATTCTTCTCTG	1320
10	TGATGAAGGT TGAGAATGAG CGGTATGAAA ATGGACGAAA GCGTCTTAAA GCATATTTGA	1380
	GGAACACTTT GACAGACCAA AGGTCAAGTA ACTTGGCTTT GCTTAACATA AATTTTGATA	1440
15	TAAAACACGA CCTGGATTTA ATGGTGGACA CATATATTAA ACTCTATACR AKTAMGTCAG	1500
	MGCTYYCTAC AKAYRAYTCM SWAWMGTGG AAARYWSSTA MGMSWGCWKK TAMMRRIMCG	1560
	GMWWTYYMK RKTYGAYMYW YCGGWMCGAG AAAAAGCCGT AAGGTGTATG TAGACCACTT	1620
20	AATCACTAAA TATCTTTGCC TATAGGACTC CATTTGAATAC ATTAGCCATT GATAATCTAC	1680
	CTGTTTAAAT GGGCCCTGTT TGAAGTCTCA AGCTTTGAAG ACCTACCTGT TCTTCCAGAA	1740
25	GAGAACGTTG AAAGTGCCAT GTTTCCTTTT GCGTGATCTC TGTTGATGGC ACTCTGGAAT	1800
	TGTTTCCAGT TTAAKTCATT TTAGACATAG CATTTATTAT CACTGTGGAT CTCTACTTGT	1860
	TGGGTGTTAT GAATTCCTTG AAGAATATAT TTTGAAGAGG TGTGGGAGGA AGGAATACAT	1920
30	TTTATAAAAT GTTGTAGTGA AGCCCAACAAT TGACCTTKGA CTAATAGGAG TTTTAAGTAT	1980
	GTAAAAATC TATACTGGAC AGTTACAAGA AATTACCGGA GAAAAGCTTG TGAGCTCACC	2040
35	AAACAAGGAT TTCAGTGTAG ATTTTGTCTT TCTTGAACCT AAAGAAACAA ATGACAAAGT	2100
	TTGAATGGAA AAGCCTGCTG TTGTTCCACA TCTCGTGTCT GTTTACATTC CTTTGTGGAG	2160
	CCTACATCTT CCTAAGCTTT TTAGCAGGTA TATGTTGAAC ACTTCTGTTT CATGGTTGAG	2220
40	ACAGAATCAG AGGCCATGGA TACTGACAAC TGATTGTGCT GTTTTTTTTC TCTGTCTTTT	2280
	TCCATGACTC TTATATACTG CCTCATCTTG ATTTATAAGC AAAACCTGGA AAACCTACAA	2340
45	AATAAGTGTT GTGGTTTATC TAGAAAAATA TGGAAAATAT TGCTGTTATT TTTGGTGAAG	2400
	AAAATCAATT TTGTATAGTT TATTTCAATC TAAATAAAAT GTGAATTTTG TTWATTAAA	2460
	AATTWGSAC AAABTBGHGG GGGDTCCAAA CHTWVTCGHG KAAMTCTCT WAARMATYTK	2520
50	ATAAACMSCT TCACAATTC	2539

55 (2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1751 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

5	AGCATGAAGC CGATGGCCGT GGTGGCCAGT ACCGTCTTGG GCCTGGTGCA AAACATGCGT	60
	GCGTTTGGCG GGATCCTGGT GGTGGTCTAC TACGTATTGG CCATCATTGG GATCAACTTG	120
10	TTTAGAGGCG TCATTGTGGC TCTTCCTGGA AACAGCAGCC TGGCCCTGCG CAATGGCTCG	180
	GCGCCCTGTG GGAGCTTCGA GCAGCTGGAG TACTGGGCCA ACAACTTCGA TGACTTTGCG	240
	GCTGCCCTGG TCACTCTGTG GAACTTGATG GTGGTGAACA ACTGGCAGGT GTTCTGGAT	300
15	GCATATCGGC GCTACTCAGG CCGTGGTCC AAGATCTATT TTGTATTGTG GTGGCTGGTG	360
	TGCTCTGTCA TCTGGGTCAA CCTGTTCTG GCCCTGATTC TGGAGAACTT CCTTCACAAG	420
20	TGGGACCCCC GCAGCCACCT GCAGCCCTT GCTGGGACCC CAGAGGCCAC CTACCAGATG	480
	ACTGTGGAGC TCCTGTTTCTG GGATATTCTG GAGGAGCCCG GGGAGGATGA GCTCACAGAG	540
	AGGCTGAGCC AGCAGCCGCA CCTGTGGCTG TGCAGGTGAC GTCGGGGCTG CCATCCAGC	600
25	AGGGGCGGCA GGAGAGAGAG GCTGGCCTAA CACAGGTGCC CATCATGGAA GAGGCGGCCA	660
	TGCTGTGGCC AGCCAGGCAG GAAGAGACCT TTCTCTGAC GGACCACTAA GCTGGGGACA	720
30	GGAACCAAGT CCTTTGCGTG TGGCCCAACA ACCATCTACA GAACAGCTGC TGGTGCTTCA	780
	GGGAGCGGCC GTGCCCTCCG CTTCTTTTTA TAGCTGCTTC AGTGAGAATT CCTCGTCGA	840
	CTCCACAGGG ACCTTTCAGA CAAAAATGCA AGAAGCAGCG GCCTCCCCTG TCCCCGTCAG	900
35	CTTCGGTGGT GCCTTTGCTG CCGGCAGCCC TTGGGGACCA CAGGCTGAC CAGGGCCTGC	960
	ACAGGTAAAC CGTGAGTCTG TCTCATCTAT TCACAGCTGG GAATGATACT AATACCTCCG	1020
40	ATTTTAGCCC AGCACCACAG GGTACGTTCC AGTTTTTCTC TCTTTCCATA GCTGTAAGGC	1080
	CCTTCTGGG AATGGTTCTC ATTCTCCTTA ATCTATTATT GGGTCAGTTT TCCTGCATGT	1140
	CCCCAGCCTC CCATCACTGC CACCCACTCC CCACAGAGAT GCCCTGCTCA TCCGACTGGG	1200
45	GCTTTGACTC CCACACTGTG TACCCCTCTT GTGTGGACGC CCTGCTGCCA AAACCTTCAG	1260
	CAAACAGCTT TCCAAATGGA AGTTGTCACT GTCAGGCTT TACAATCAGC AACAGCAAAA	1320
50	TCTACATGCT GCTGAGGGTC CTGCCTCATT AAGATGCAAT AAATATGTAA GTACATAAAA	1380
	ACAGCAATAG AAGAAACGTA ATGCTTTATT CTCAAATATG ATGTCTACAT AGAAAAGCCA	1440
	AAATTATTAA GAATAGTAAG AATTCACCCA GCACCTTGGG AGGCCGAGGC GGGTGGATCA	1500
55	TGAGGTCAGG AGATCGAGAC CATCCTGGCT AACAGGGTGA AACCCCGTCT CTAATAAAAA	1560
	TACAAAAAAT TGGCCGGGCG CAGTGGCGGG CGCCTGTGGT CCCAGCTACT GGGGAGGCTG	1620
60	AGGCAGGAGA ATGGCGTGAA CCCGGAAGC GGAGCTTGCA GTGAGCCGAG ATTGCGCCAC	1680

TGCAGTCCGC AGTCCAGCCT GGGCGACAGA GCGAGACTCC GTCTCAAAAA AAAAAAAAAA 1740
AAAAAAAAA A 1751

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(2) INFORMATION FOR SEQ ID NO: 111:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1117 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

AATGTTGTGG TGGTAGCATT TGGGTTAATT CTRATTATAG AGTCTCTTGG AGAGCAATGT 60
20 CCATAAACTA ATCCCAAACA ACATTGTCTT TTTRATGTTG TAGTGAACAG CAGAGAATTT 120
CAAAGGACCT TGCTAATATC TGTAAGACGG CAGCTACAGC AGGCATCATT GGCTGGGTGT 180
ATGGGGGAAT ACCAGCTTTT ATTCATGCTA AACAACAATA CATTGAGCAG AGCCAGGCAG 240
25 AAATTTATCA TAACCGGTTT GATGCTGTGC AATCTGCACA TCGTGTGCC ACACGAGGCT 300
TCATTCGTTA TGGCTGGCGC TGGGTTGGA GAACTGCAGT GTTTGTGACT ATATTCAACA 360
30 CACTGAACAC TAGTCTGAAT GTATACCGAA ATAAAGATGC CTTAAGCCAT TTTGTAATTG 420
CAGGAGCTGT CACGGAAGT CTTTTAGGA TAAACGTAGG CCTGCGTGGC CTGGTGGCTG 480
GTGGCATAAT TGGAGCCTTG CTGGGCACTC CTGTAGGAGG CCTGCTGATG GCATTTTACA 540
35 AGTACTCTGG TGAGACTGTT CAGGAAAGAA AACAGAAGGA TCGAAAGGCA CTCCATGAGC 600
TAAAACTGGA AGAGTGGAAA GGCAGACTAC AAGTTACTGA GCACCTCCCT GAGAAAATTG 660
40 AAAGTAGTTT ACAGGAAGAT GAACCTGAGA ATGATGCTAA GAAAATTGAA GCACTGCTAA 720
ACCTTCCTAG AAACCTTCA GTAANTAGATA AACAAGACAA GGAAGTGAAG TGCTCTGAAC 780
TTGAAACTCA CTGGAGAGCT GAAGGAGCT GCCATGTCCG ATGAATGCCA ACAGACAGGC 840
45 CACTCTTTGG TCAGCCTGCT GACAAATTTA AGTGCTGGTA CCTGTGGTGG CAGTGGCTTG 900
CTCTGTCTT TTTCTTTTCT TTTTAACTAA GAATGGGGCT GTTGTTACTCT CACTTTACTT 960
50 ATCCTTAAAT TTAAATACAT ACTTATGTTT GTATTAATCT ATCAATATAT GCATACATGA 1020
ATATATCCAC CCACCTAGAT TTAAAGCAGT AAATAAACA TTTCGCAAAA GATTAAAGTT 1080
GAATTTTACA GTTAAAAAAA AAAAAAAAAA AAAAAA 1117

55

(2) INFORMATION FOR SEQ ID NO: 112:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1313 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

10	GGCAGAGGTT TTCTTATATT TTAAGTAAAT TTAAAGTGGC TATCAGAATA TTTATTCTTG	60
	TTTGAGACTA CCAACATAAC TACGTGTTGA AGGTGCTTCA CAGAGAATAT ATTGCCCTTTA	120
	ATGTGAAATA ATTTTCACCA ATGTGCTAA CTTAATAAAA GTATAAAATT TGTAGAATAT	180
15	TCAGTTAAGT AGTTGGTAAC CCTTTTCTAT TTTAGTAAAA CTTAATGCAT GTTACTTTT	240
	TTTTGAAAGA TGCAGACAAT CTCTTTGAAC ATGAATTGGG GGCTCTCAAT ATGGCTGCAT	300
20	TACTACGAAA AGAAGAAAGA GCAAGTCTTC TTAGTAATCT TGGCCCATGT TGTAAAGCGT	360
	TGTGCTTCAG ACGGGATTCT GCAATTCGAA AGCAGCTTGT TAAAAATGAG AAGGGCACCA	420
	TAAAACAAGC TTACACGAGT GCTCCAATGG TAGACAATGA ATTACTTOGA TTGAGTCTTC	480
25	GGTTATTTAA GCGGAAGACT ACTTGCCATG CTCCAGGACA TGAAAAGACT GAAGATAATA	540
	AACCTTCACA GTCCAGTATC CAACAGGAAC TGTGTGTGTC TTAAGACCGA AGTTACAATA	600
30	TGGTATTTTT GGTACTGTCT TCCTTCAGCA GTGCATATTC TTTTGCAAAG TTCTTTGGTT	660
	TGACAAGCAT TAGTGACAAA GGCAGAAAAG ATTTATCAGC CATGCTAAAA GAGTGAAGAA	720
	TTTTGATCTT TAGAGACACT AGTTTGGGCC AACTTAAGAT TTTACGTAA TTTTACATA	780
35	GTATTTGACA CTCATGCAAA ATAATGTGAA AACATCTAGA TTTAGTAGTT TATTCGCGC	840
	CTTTGTAA AACTGAAGAT TTTGGAAAT GGTGTCACT GCTCTCCAG CCTATGAATA	900
40	TTTTTGTGAA ATGGAACCAT GGATTTATGT CTGGATCATC CATAAGAAC CAACAATTTT	960
	ATTCAAAAAC AATGTGTCA TCAAAGTAAT TGCTCACATT GTGCAGTACT ATGTTGTACA	1020
	GACCACGTGA AAGGGAATGC TGGTCTAGCT GCGTGGTAT GTTTATAGGC GAATTCAGC	1080
45	AGAAGGAAGC CAAATAGTT TTTTCTTTT GAAAGTTTTT TAAAAATTAT TTCATGGGT	1140
	TTTTTTTTAA TTAATATGTG TGCATTGTTA CAATGTATGT TGGGATGTCT TTTGACCCTA	1200
50	AATGCTTTTT TTGTTATCAG AGATTGTGTA CTATTTTTAT TTTAATAAAA TGTATCTTCC	1260
	CTTTTMAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA	1313

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(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1654 base pairs
 (B) TYPE: nucleic acid

60

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

5	ACAGGGACAG AATACTTTCT TTCCTTCCTT CAAGTACAAG AAGGCTTTCT CTACCATTTG	60
	CGTCTACACT TTATTTTAAA AGCTATCCCTT TTCTAGTAGT ATTTTATCAT GGCAATGGCA	120
10	TGATGACAAC AACAGTCTTT CATTACAGAC TGAAGGGAAG CATGTCCTTA CTTAAAATAG	180
	TTCTGCTACT TTCCCTCCTA TTATAAGGAA ATTTTACAGA TTCTAAAAAT ACCTTAATTT	240
15	TTCTTTGATT TTTATTTTAC CAAGTCACAA ATGTCITTTT GATGTTTTGA GAATTGTTCT	300
	CATAGAATCA CAAATACTGA CATTTCATTA GATGATTATT TTCCTAGAAT CCCCAAAGAG	360
	CAGTGGCAGT CCATGGCTTG GTTGAAGCTA GAAATTTTCC TGCCCCCTGGT GACCTGGTAA	420
20	GCCTCCTGCT CGGAACCGTG TGAGTGGGTG AGGAAGATGA GAGATGGTCA GATGGAAGAG	480
	AGRAATACAT GAACTGCTCT GGCCTCTCTG GTTCTGTTCT TGGCCCAGAG TTTTGA AAA	540
25	GCAGCGGANA TNGACTGACT TCACATGCTC AGCTTTCTCA GCCTTTTGTT TATTTGTTG	600
	TCCTTAGATT TCCCTGTTGT AAAAGGGGCA AGAAAAGTAA CTCATCATCT CTAACACACC	660
	ATGGCAGCTT AGCCAGGTAG TCTTAGTGGT GGTGTTTAGG CATAAGATAT GCTGATCATC	720
30	AGTCTCAGGC CACAGTTTCC TTCACTAATC GTCCAGCTTG AGTGTCTGT TCTCTTCCTG	780
	CCCATTTCCT TGAACCTCCT GCTCTAGCCT TGGCGGAGGG AGAGTGCTAT TTGCTTTTGT	840
35	TCTCCCTCTG TCTTAGGAAA AGCCATCTTT AATATAGTTC TTCACCACTG TTGGGGTTGT	900
	TTTGTGATTT TTTTTCCTT CCGAAGAACT CCTGGTTGTT ATTGGAATTT GTATTTAAT	960
	ACAAATTATT GAATTTTATA AGCTTGTA CAATATTTAA TTAGTGTGAA AGGAAACAAA	1020
40	GAATGCAGGA AAAATAATTT AATATCAACC TCAGTTGACA AGGTGCTCAG ATTATTCAAT	1080
	TCGGGATCCT CCTTTTGTTA GGTTTTGTAG ACAACCCTAG ACCTAAACTG TGTACAGAC	1140
45	TTCTGAATGT TTAGGCAGTG CTAGTAATTT CCTCGTAATG ATTCTGTTAT TACTTTCCTA	1200
	TTCTTTATTC CTCTTCTTC TGAAGATTAA TGAAGTTGAA AATTGAGGTG GATAAATACA	1260
	AAAAGGTAGT GTGATAGTAT AAGTATCTAA GTGCAGATGA AAGTGTGTTA TATACATCCA	1320
50	TTCAAAATTA TGCAAGTTAG TAATTACTCA GGGTTAACTA AATTACTTTA ATATGCTGTT	1380
	GAAYCTACTC TGTTCCTTGG CTAGAAAAA TTATAAACAG GACTTTGTAG TTTGGGAAGC	1440
55	CAAATTGATA ATATTCTATG TTCTAAAAGT TGGGCTATAC ATAAATTATT AAGAAATATG	1500
	GATTTTTATT CCCAGGATAT GGTGTTTATT TTATGATATT ACGCAGGATG ATGTATTGAG	1560
	TAAAATCAGT TTTGTAAATA TGAAATATG TCATAAATAA ACAATGCTTT GACTTATTTT	1620
60	CAAAAAA AAAAATAA NTTCGAGGGG GGGC	1654

5 (2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1171 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

15 GGCAAACTTT CCCCAANGC TTCGAACTT GCAAGCOGAA ACCTTGAATC GTTAAAAGTT 60
GGGTTCGCNC GCGCCCTGG CCCGAAGAAG CGCAATTGGC GTTCCGCGAA CGTTGGCCCT 120
CAACGGCTCG GCAGCCAGCC ATGTCTTGCA CCCAGGACAG CGGCCCTGGG CTACAAGGAC 180
20 CTGMCCTCA TCTTCTGCG CCGACCTGCG CGGGTAAGG GGWAGTTTCA GACTGTGAAG 240
GACGTCGTGC TGGACTGCCT GTTGGACTTC TTACCCGAGG GGGTGAACAA AGAGAAGATC 300
25 ACACCACTCA CGCTCAAGGA AGCTTATGTG CAGAAAATGG TTAAAGTGTG CAATGACTCT 360
GACCGATGGA GTCTTATATC CCTGTCAAAC AACAGTGGCA AAAATGTGGA ACTGAAATTT 420
GTGGATTCCC TCCGAGGCA GTTTGAATTC AGTGTAGATT CTTTCAAAT CAAATTAGAC 480
30 TCTCTTCTGC TCTTTTATGA ATGTTCAAG AATCCCAATGA CTGAGACATT TCACCCACAA 540
ATAATCGGG AGAGCGTCTA TGGCGATTTC CAGGAAGCCT TTGATCACCT TTGTAACAAG 600
35 ATCATGCGCA CCAGGAACCC AGAGGAAATC CGAGGGGAG GCCTGCTTAA GTAGTCAAC 660
CTCTTGGTGA GGGGCTTTAG GCGCCCTCT GATGAAATCA AGACCCCTCA AAGGTATATG 720
TGTTCAGGT TTTTCATCGA CTTCTCAGAC ATTGGAGAGC AGCAGAGAAA ACTGGAGTCC 780
40 TATTTGCAGA ACCACTTTGT GGAATTGGA AGACCGCAAG TATGAGTATC TCATGACCTT 840
TCATGGAGTG GTAAATGAGA GCACAGTGTG CCTGATGGA CATGAAAGAA GACAGACTTT 900
45 AAACCTTATC ACCATGCTGG CTATCCGGGT GTTAGCTGAC CAAAATGTCA TTCCTAATGT 960
GGCTAATGTC ACTTGCTATT ACCAGCCAGC CCCCTATGTA GCAGATGCCA ACTTTAGCAA 1020
TTACTACATT GCACAGGTTT AGCCAGTATT CACGTGCCAG CAACAGACCT ACTCCACTTG 1080
50 GCTACCTGTC AATTAAGAAT CATTTAAAAA TGCTCTGTGG GGAAGCCATT TCAGACAAGA 1140
CAGGAGAGAA AAAAAAAAAA AAAAAAAAAA A 1171

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(2) INFORMATION FOR SEQ ID NO: 115:

- 60 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 842 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

GGTCTGCGCC GGAAGTGCAT GAGCTGCCGA TGTGGTGCTT AGTGATTGCG GTTTCGGTCC	60
10 CTCTCCCGTG TTTCCCGGGC TGGGTATTGT CCTCGCACCA TGGCGCCCAA GGGCAAAGTG	120
GGCACGAGAG GGAAGAAGCA GATATTTGAA GAGAACAGAG AGACTCTGAA GTTCTACCTG	180
CGGATCATAC TGGGGGCCAA TGCCATTTAC TGCTTTGTGA CGTTGGTCTT CTTTACTCA	240
15 TCTGCCTCAT TTTGGGCTG GTTGGCCCTG GGCTTTAGTC TGGCAGTGTA TGGGGCCAGC	300
TACCACTCTA TGAGCTCGAT GGCACGAGCA GCGTTCTCTG AGGATGGGGC CCTGATGGAT	360
20 GGTGGCATGG ACCTCAACAT GGAGCAGGGC ATGGCAGAGC ACCTTAAGGA TGTGATCCTA	420
CTGACAGCCA TCGTGCAGGT GCTCAGCTGC TTCTCTCTCT ATGTCTGGTC CTTCTGGCTT	480
CTGGCTCCAG GCGGGGCCCT TTACCTCCTG TGGGTGAATG TGCTGGGGCC CTGGTTCACT	540
25 GCAGACAGTG GCACCCGAGC ACCAGAGCAC AATGAGAAAC GGCAGCGCCG ACAGGAGCGG	600
CGGCAGATGA AGCGGTTATA GCCATTGACA TTGTGGCCAC AGGCCACTGG CCCTGGGTGG	660
30 CTCTGTGAGG GTGCACAGCC CCTCATGCCT GGAGCAATGA GGGTCTAGTC CAGGGGCCAA	720
AAGCAGTCTG AGGTATTGGG TATACTTATA CTCTATAGGG TCGTTGAATA AATGGCTTAG	780
AATGTGAAAA AAAAAAAAAA AAAAACTCG AGGGGGGCCC GGTACCCAAT TTCNCCTANA	840
35 AT	842

40

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 1640 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

50

GGCACGAGGC GCGGCAGCG GTGGCGGCGG CGCCCCCGG CGGGAGCCGT TCCCTTTCCC	60
GTCGGGGAGC GCGGGGYCGG GGCCAGGGG ACCCGGGCC ACGGAGAGCG GGAAGAGGAT	120
55 GGATTGCCCC GCCCTCCCC CCGGATGGAA GAAGGAGGAA GTGATCCGAA AATCTGGGCT	180
AAGTGCTGGC AAGAGCGATG TCTACTACTT CAGTCCAAGT GGTAAGAAGT TCAGAAGCAA	240
GCCTCAGTTG GCAAGGTACC TGGGAAATAC TGTGATCTC AGCAGTTTTC ACTTCAGAAC	300
60	

	TGGAAAGATG ATGCCTAGTA AATTACAGAA GAACAAACAG AGACTGCGAA ACGATCCTCT	360
	CAATCAAAAT AAGGGTAAAC CAGACTTGAA ATACAACATT GCCAATTAGA CAAACAGCAT	420
5	CAATTTTCAA ACAACCGGTA ACCCAAAGTC ACAATCATC CTAGTAATAA AGTGAAATCA	480
	GACCCACAAC GAATGAATGA ACAGCCACGT CAGCTTTTCT GGGAGAAGAG GCTACAAGGA	540
10	CTTTAGTGCA TCAGATGTAA CAGAACAAAT TATAAAAACC ATGGAAC TAC CCAAAGGTCT	600
	TCAAGGAGTT GGTCCAGTAG CAATGATGAG ACCCTTTTAT CTGCTGTTGC CAGTGCTTTG	660
	CACACAAGCT CTGCGCCAAT CACAGGGCAA GTCTCCGCTG CTGTGGAAAA GAACCTGCTG	720
15	TTTGGCTTAA CACATCTCAA CCCTCTGCA AAGCTTTTAT TGTACAGAT GAAGACTCAG	780
	GAAACAGAAG AGCGAGTACA GCAAGTACGC AAGAAATTGG AAGAAGCACT GATGGCAGAC	840
20	ATCTTGTCGC GAGCTGCTGA TACAGAAGAG ATGGATATTG AAATGGACAG TGGAGATGAA	900
	GCCTAAGAAT ATGATCAGGT AACTTTTGAC CGACTTTCCC CAAGAGAAAA TTCCTAGGAA	960
	ATTGAACAAA AATGTTTCCA CTGGCTTTTG CCTGTAAGAA AAAAAATGTA CCCGAGCACA	1020
25	TAGAGCTTTT TAATAGCACT AACCAATGCC TTTTITAGATG TATTTTIGAT GTATATATCT	1080
	ATTATTCAAA AAATCATGTT TATTTTGAGT CCTAGGACTT AAAATTAGTC TTTTGTAATA	1140
30	TCAAGCAGGA CCCTAAGATG AAGCTGAGCT TTTGATGCCA GGTGCAATCT ACTGGAAATG	1200
	TAGCACTTAC GTAAAACATT TGTTTCCCCC ACAGTTTAA TAAGAACAGA TCAGGAATTC	1260
	TAAATAAATT TCCCAGTTAA AGATTATGTT GACTTCAC TG TATATAAACA TATTTTATA	1320
35	CTTTATMGAA AGGGGACACC TGTACATTCT TCCATCGTCA CTGTAAAGAC AAATAAATGA	1380
	TTATATTCCA CAGAAAAAAA AAAAAAAAW MWSTYGARRR GSRGCMCRSW AYMMARWCC	1440
40	CCWMRIWRGS MKTCSTMTKA YTTACATTCA ACTCTGATCC CGGGGCTTA GGTTTGACAT	1500
	GGGAGGTGGG AGGAAGATAG CGCATATATT TGCAGTATGA ACTATTGCCT CTGGGACGTT	1560
	GTGAGGAATT GTGCTTTCAC CAGAATTCT AAGGATTCT GGCTTAAATA TCACCTAGCC	1620
45	TGTGGTAATT TTTTTCCT	1640

50 (2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 952 base pairs

(B) TYPE: nucleic acid

55 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

60 TGAATTTAGN AAACACTTTG GAAAACATCAT AACCTCATCA GAAACTGCCT TTAGCCACAC 60

	TCCTGACCTT CTAGATGAGT AACAAAAAA TGAAATAAGT TCTTGAAAT TAAGCCATTT	120
5	ATTTTAATTT GCTATTTTTT TCAATGTTCT AGGTATCTTT AAATTTGTTA TTGTGGAATC	180
	ATTTTCCTGC CAGATACCTT TATCAAAAT ATGGCCTCA TGAGAGCTGA AGTAAGTCAG	240
	CTTTTGGTG AACTTTAGTG GACTTCTGTG AGATTGTAGT TGTACTTTGT ATCTCTAAAT	300
10	CTAAAGATAG TTTTTTAAAA CTCCCAAAGA AAATCTGCTC TCCTTTCTGA TCTAAAACT	360
	CATCTTTGGG GTAAAGAGTT AAGTGTCCAA AGGTTGTAC AGTTCATGAG GTCAGAGGGA	420
15	GCTAGCCTGG CACCTGGACT CTGCCATCC ACAGCTGACA GATTCCAACA GAAGTGATT	480
	TAAATCTCC AGTAGACAAT GCTGGGTAAG GGAGGGGTA GGGCTGGGT ATTAAGATAC	540
	AGGCTGCTGT ATTTTACATT GGTGTGGGG GAAGGGGAGC CTGGAGAAAA CAAAGTCACT	600
20	ATTCCCTTTT TTGAAACAGG AAAAAAAT ATTTTTTGT CAGTAAAAAT GGTAGAGAAT	660
	TCCAATGTCC CTAGCCACAA GGGACCAGT CCACTGAGAA GTGAACAGTG GGAATCAAA	720
25	ATTTCAGAAA CATTGGGGGA AGGGAAAAT GGCTTTCTCT TAATTGGCAG ATGTTCCAGT	780
	GGGSGGGG GGCTCTGTTT TTGTGGGAT GTGTTATGTT GTATGTACGC ATATATGGAC	840
	CGGAGTCTGC TGAGTTTATA AGGTTCCAAA AATATGGTAA AATCTTGGTT TTTGTTAAT	900
30	TATCTCAATA AAAGCCCACT GGRACCTCAA AAAAAAAAAA AAAAAAAGA NN	952

35 (2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1256 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

45	GACGTCATAG GTAAACAGGC TCTGTATCCG TGGCAGCGGC CGTGGCAGGC TGGCTGGGTA	60
	CCGGCTGTGC CTGACCCAGG AGAAGCTGCC TGTCTACATC AGCCTGGGCT GCAGCGCGCT	120
50	GCCGCCGCGG GGCCGCGAGC TGAAGTATGT GCTCTTCAGG GCGGGCACCG TGTTCATTC	180
	ATCTTTGTAC CCCAGCATC TAGCAGTGTT GGCATGTAGT AGGCACTCAA GAAATGTGTG	240
	TTGAATGAAC GATGCCTGTG ACAAGCAAGC GGACTTTTATT CTTTCTGAC CCTTGCTCCT	300
55	ATGACACACC TCCTCTGAC TGCCACTGTC ACTCCTTCAG AGCAGAACTC CTCTAGGGAA	360
	CCTGGATGGG AAACAGCCAT GGCCAAGGAC ATCCTGGGTG AAGCAGGGCT ACACTTTGAT	420
60	GAAGTGAACA AGCTGAGGGT GTTGGACCCA GAGGTTACCC AGCAGACCAT AGAGCTGAAG	480

	GAAGAGTGCA AAGACTTTGT GGACAAAATT GGCCAGTTTC AGAAAATAGT TGGTGGTTTA	540
	ATTGAGCTTG TTGATCAACT TGCAAAAGAA GCAGAAAATG AAAAGATGAA GGCCATCGGT	600
5	GCTCGGAACT TGCTCAAATC TATAGCAAAG CAGAGAGAAG CTCACAGCA GCAACTTCAA	660
	GCCCTAATAG CAGAAAAGAA AATGCAGCTA GAAAGGTATC GGGTTGAATA TGAAGCTTTG	720
10	TGTAAAGTAG AAGCAGAACA AAATGAATTT ATTGACCAAT TTAATTTTCA GAAATGAACT	780
	GAAAATTTTCG CTTTATAGT AGGAAGGCAA AACAAAAAAA AGCCTCTCAA AACCAAAAAA	840
	ACCTCTGTAG CATTCACGCG GCTTGACCAA TGACCTATGT CACAAGAGGT GCGGTGTAAG	900
15	GAATGCAGCC CCCTGAAGAC AGCACTACAA GTCTGGGGGA GCCAGTTTTA ACATCAGTGC	960
	ACAGCTGCTG CTGGTGGCCC TGCAGTGAC GTTCTCACCT CTTATGCTTA GTTGGAACCTA	1020
	AGCAGTTTGT AAACCTTTCAT CCTTTTTCAT GTAAATTCAC AAAGCTTTGG AAGGAGAAGC	1080
20	AATAAATTTT TGTMTTCAA TGGCTTGATG TACCTTTTTC CCTGTTGCTC TTGAAATATG	1140
	TTTAACCTCT CATGAGAGAA CCCTGGATTC TCTATCCCTC AGTCCACAAA ACAAAACCAGG	1200
25	CAGTGGTCAG CAGCTACCTT TNATTGGAT CACACACGTG AGTCAGACAG TACCAC	1256

30 (2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1143 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

40	GGCCGTAGCA GCCGGGCTGG TCCTGCTGCG AGCCGGCGGC CCGGAGTGGG GCGGCGGCAT	60
	GTACCTTCCA CATTGAGTAT TCAGAAAGAA GTGATCTGAA CTCTGACCAT TCTTTATGGA	120
45	TACATTAAGT CAAATATAAG AGTCTGACTA CTTGACACAC TGGCTCGAGC AAACATGAAC	180
	GTTGGAGTTG CCCACAGTGA AGTGAATCCA AATACCGTG TCATGAACAG CCGGGGTATG	240
	TGGCTGACAT ATGCATTGGG AGTTGGCTTG CTTTCATATG TCTTACTCAG CATTCCTTC	300
50	TTTCTGTTT CTGTTGCTTG GACTTTAACA AATATTATAC ATAATCTGGG GATGTACGTA	360
	TTTTTGATG CAGTGAAAGG AACACCTTTC GAACTCCTG ACCAGGGTAA AGCAAGGCTC	420
55	CTAACTCATT GGAACAACCT GGACTATGGA GTACAGTTTA CATCTTCACG GAAGTTTTC	480
	ACAATTTCTC CAATAATTCT ATATTTTCTG GCAAGTTTCT ATACGAAGTA TGATCCAAC	540
	CACCTTCATC TAAACACAGC TTCTCTCTG AGTGTACTAA TTCCCAAAAT GCCACAAC	600
60	CATGGTGTTC GGATCTTTGG AATTAATAAG TATTGAAATG TTTTGAACT GAAAAAAAT	660

TTTACAGCTA CTGAATTTCT TATAAGGAAG GAGTGGTTAG TAAACTGCAC TGTTCCTSTG 720
 5 ATAATGTGAA ATGAGAAGTA TTTACATTGG AGGGCCCAATG GCTGGTCCTT CAAGTGCTGT 780
 TTGAAGTGC AGATTTCCAT TAAATGATGC CTCGTGTTAA TACACCTGGT ACATTTCTGA 840
 AGAGGGGCTT TATAAGCAGG CTGGGCAGGC CCAGCTTATA AGTTAAAGGG CATCACAGTG 900
 10 AGGGTGTAGT AGATAAATTC AAGGAAATAA GAGATTTGTA AGAACTAGG ACCAGCTTAA 960
 CTTATAATGA ATGGGCATTG TGTTAAGAAA AGAACATTTT CAGTCATTCA GCTGTGGTTA 1020
 15 TTAAAGCAG ACTTACATGT AAACCGGAAT CCTCTCTATA CAAGTTTATT AAAGATTATT 1080
 TTTATTACCG TAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1140
 GAN 1143

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(2) INFORMATION FOR SEQ ID NO: 120:

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- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1782 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

CAGGCCCCGG CCCCCACCC ACGTCTGCGT TGCTGCCCCG CCTGGGCCRG GCCCCAAAGG 60
 35 CAAGGACAAA GCAGCTGTCA GGAACCTCC GCCGGAGTCG AATTACGTG CAGCTGCCGG 120
 CAACCACAGG TTCCAAGATG GTTTGCGGGG GCTTCGCGTG TTCCAAGAAC TGCCTGTGCG 180
 40 CCCTCAACCT GCTTTACACC TTGGTTAGTC TGCTGCTAAT TGGAATTGCT GCGTGGGGCA 240
 TTGGCTTCGG GCTGATTTC AGTCTCCGAG TGGTCGGCGT GGTCAATTGCA GTGGGCATCT 300
 TCTTGTTCTT GATTGCTTTA GTGGGTCTGA TTGGAGCTGT AAAACATCAT CAGGTGTTGC 360
 45 TATTTTITTA TATGATTATT CTGTACTTGT TATTTATTGT TCAGTTTTCCT GTATCTTGCG 420
 CTTGTTTAGC CCTGAACCAG GAGCAACAGG GTCAGCTTCT GGAGGTTGGT TGAACAATA 480
 50 CGGCAAGTGC TCGAAATGAC ATCCAGAGAA ATCTAACTG CTGTGGGTTT CGAAGTGTTA 540
 ACCCAAATGA CACCTGTCTG GCTAGCTGTG TTAAAAGTGA CCACTCGTGC TCGCCATGTG 600
 CTCCAATCAT AGGAGAATAT GCTGGAGAGG TTTTGAGATT TGTGTTGGC ATTGGCCTGT 660
 55 TCTTCAGTTT TACAGAGATC CTGGGTGTTT GGCTGACCTA CAGATACAGG AACCAGAAAG 720
 ACCCCCGCGC RAATCCTAGT GCATTCCTTT GATGAGAAAA CAAGGAAGAT TTCCTTTCGT 780
 60 ATTATGATCT TGTTCACTTT CTGTAATTTT CTGTTAAGCT CCATTTGCCA GTTTAAGGAA 840

	GGAAACACTA TCTGGAAAAG TACCTTATTG ATAGTGGAAT TATATATTTT TACTCTATGT	900
	TTCTCTACAT GTTTTTTCT TCCGTTGCT GAAAAATATT TGAAACTTGT GGTCTCTGAA	960
5	GCTGGTGGC ACCTGGGAAT TTACTGTATT CATGTGCGG CACTGTCCAC TGTGGCCTTT	1020
	CTTAGCATTT TTACCTGCAG AAAAAGTTG TATGGTACCA CTGTGTGGT TATATGGTGA	1080
10	ATCTGAACGT ACATCTCACT GGTATAATTA TATGTAGCAC TGTGCTGTGT AGATAGTTCC	1140
	TACTGGAAAA AGAGTGGRAA TTTATTAAAA TCAGAAAGTA TGAGATCCTG TTATGTTAAG	1200
	GGAAATCCAA ATTCCCAATT TTTTGTGTC TTTTTAGGAA AGATGTGTG TGGTAAAAAG	1260
15	TGTTAGTATA AAAATGATAA TTWACTKGTA GTCTTTTATG ATWACACCAA TGTATTCTAG	1320
	AAATAGTTAT GYCTAGGAA ATTGTGGTTT AATTTTGTGAC TTTTACAGGT AAGTGCAAAG	1380
20	GAGAAGTGGT TTCATGAAAT GTTCTAATGT ATAATAACAT TTACCTTCAG CCTCCATCAG	1440
	AATGGAACGA GTTTTGAGTA ATCAGGAAGT ATATCTATAT GATCTTGATA TTGTTTTATA	1500
	ATAATTGAA GTCTAAAAGA CTGCATTTT AAACAAGTTA GTATTAATGC GTTGGCCAC	1560
25	GTAGCAAAAA GATATTGAT TATCTTAAAA ATTGTTAAAT ACCGTTTCA TGAAAGTCT	1620
	CAGTATTGTA ACAGCAACTT GTYAAACCTA AGCATATTG AATATGATCT CCCATAATTT	1680
30	GAAATTGAAA TCGTATTGTG TGGCTCTGTA TATCTGTGA AAAAATTAAA GGACAGAAAC	1740
	CTTCTTTGT GTATGCATGT TTGAATTAAA AGAAAGTAAT GG	1782

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(2) INFORMATION FOR SEQ ID NO: 121:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 610 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

45	GTGGCTGCA GATTGTGGT GCGTCTGAG CCGTCTGCC TCGCCAAGA TGCTCAAAG	60
	TATTATTAAA AACATATGGA TCCCCATGAA GCCCTACTAC ACCAAAGTTT ACCAGGAGAT	120
50	TTGGATAGGA ATGGGGCTGA TGGGCTTCAT CGTTTATAAA ATCCGGGCTG CTGATAAAAG	180
	AAGTAAGGCT TTGAAAGCTT CAGCGCCTGC TCCTGGTCAT CACAACCAGA TTTACTTGGA	240
55	GTACATGTGA AAGAAAACGT CAGTCTGCCT GTAAATTTC GCAAGCCGTG TTAGATGGGG	300
	AGCGTGAAC GTCACGTGAC ACTGTATATA GTACCGTTTA CTTCATGGCA TGAATAAATG	360
	GATCTGTGAG ATGCACTGCT ACCTGGTACT GCTTTCAGTG TGTCCCCCT CAGCCCTCCG	420
60	CGGTGTCAGG CATACTCTGA GTAGATAATT TGTATGCGAG CGCATGCAAT CAGAATCTCA	480

CTGAGCCACC CATCATTTGTG AAATAATTAC CTCAGTTGTA CAGGACTTGG TGATCAGGAT 540
 5 CCAGGCACTC ACTTGTATTTC TACTGCTCAA TAAACGTTTA TTAAACTTGA AAAAAAAAAA 600
 AAAAAAAAAA 610

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(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 526 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

20 GGTACGCCCTG CAGGTACCGG TCCGGAATTC CGGGTCGCCC ACGGCTCNGG CCACGCGTCC 60
 ACCCAGCGGT CCGSCCAGC GTCCGAGCCG AGCCGGACTG GTCAGGATGA TCACGGACGT 120
 25 GCAGCTCGCC ATCTTCGCCA ACATGCTGGG CGTGTGCTC TTCTTGCTTG TCGTTCTCTA 180
 TCACTACGTG GCCGTCAACA ATCCAAGAA GCAGGAATGA AAGTGGCGCT TTCTCCGCC 240
 30 CAGGGTTCCA GGACATAGTC TGAGGCAAGA TGGAGGGTAT GAGGGGCCCT CACTTTCAC 300
 TTCATCCCTT CTACCCATCA CAACATACAA AGCAACTACA CCTGGATTTT TCCAAACAAC 360
 TTTTATTTCC TCAGAGTCTT CCTTAATCCT ATGGAACAAG AAGCTGCCAC TGAATAGGGC 420
 35 CCAGTATAGG GGCTTGCTTT TCTACTCCCT CCCCCAATA TAAAAATATA GACTTTTTAA 480
 AAAAAAAAAA AAAAANTCG NGGGGGGSCC GGTACCCATC CCCCTA 526

40

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:
 45 (A) LENGTH: 2081 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

TGTACCGGTC CGGAAATTCC CGGGTCGACC CACGTCGTCS GGGGAACATG GCGGCTKCGG 60
 AGCCGCGGGT CCTTGCCTC CCCAACAGCG GCGCCGGGGG CGCGGGGGCG CCGTCGGGCA 120
 55 CAGTCCCGGT GCTCTTCTGT TTCTCAGTCT TCGCGCGACC CTCGTCGGTG CCACACGGGG 180
 CGGGCTACGA GCTGCTCATC CAGAAGTTCC TCAGCCTGTA CGGCGACCAG ATCGACATGC 240
 60 ACCGCAAATT CGTGGTGCAG CTGTCGCGG AGGAGTGGGG CCAGTACGTG GACTTGCCCA 300

	AGGGCTTCGC GGTRAGCGAG CGCTGCAAGG TCGCCTCGT GCGYTGACAG ATCCAGCTCA	360
	CTACCCCTGGG AAATCTTACA CCTTCAAGCA CTGTGTTTTT CTGCTGTGAT ATGCAGGAAA	420
5	GGTTCAGACC AGCCATCAAG TATTTTGGGG ATATTATTAG CGTGGGACAG AGATTGTTGC	480
	AAGGGCCCG GATTTTAGGA ATTCTGTGA TTGTAACAGA ACAATACCCT AAAGGTCTTG	540
10	GGAGCACGGT TCAAGAAATT GATTTAACAG GTGTAAACT GGTACTTCCA AAGACCAAGT	600
	TTTCAATGTT ATTACCAGAA GTAGAAGCGG CATTAGCAGA GATTCCCGGA GTCAGGAGTG	660
	TTGTATTATT TGGAGTAGAA ACTCATGTGT GCATCCAACA AACTGCCCTG GAGCTAGTTG	720
15	GCCGAGGAGT CGAGGTTTAC ATTGTTGCTG ATGCCACCTC ATCAAGAAGC ATGATGGACA	780
	GGATGTTTGC CCTCGAGCGT CTCGCTCRAR CCGGGATCAT AGTGACCACG AGTGAGGCTG	840
20	TTCTGCTTCA GCTGGTAGCT GATAAGGACC ATCCAAAATT CAAGGAAATT CAGAATCTAA	900
	TTAAGGCGAG TGCTCCAGAG TCGGGTCTGC TTTCCAAAGT ATAGGACATT TGAAGAACTG	960
	GTATGCTACT CACTGGTGAA GGACAGTCAG GTGAAGGACT GTAAGCCCAC ACAAGCTCTT	1020
25	CTTATCTCTA CTAGAATTAA AATGTTAAGT CAAAAACGGC TCCTTTTTTG CGCCTCCTAG	1080
	TGAAACTTAA CCAGCTAGAC CATTTGAGTA CCAGCATTTA GTTACAAACG TCAAAGGCTT	1140
30	CCGGTGCTGC TTACCTTCCT TTTTGTGTTA TGTGCTTTTA TTTATTAAAA AAAATTACAA	1200
	TGAAGATGCC TGTTTTGTCT CTACTGTGTA CTCTGATCGT ATCTTTCCAA AGTGCAGACT	1260
	CTTGTGAAGT TTTCTTAAAT TGTTCACTTT AAAGAAAATG ACGTACCAAC AATGATTG	1320
35	CTTTTATATT ACTGTAAGAT GTTATAATGT TAATGTGGAT GTAGTGCTTT TACTTTACAG	1380
	ATTGATTGGA ATAAGATTAT TGCATATGAA TTTACCCACA GGA CTCTGAA TCATGTTACC	1440
40	CACTCCCCCT ACAATGTTGT CCACTTAGTG AGTTGCATTG ATCTATCCGT ACCAAATGAT	1500
	GTGAATAAT TACATATCTT TCTTGACTAT ACTGATTCTT TATTTTGGTC ACTATTACTA	1560
	AATCTCTGTT AATATTCTCT CTTTAACTG AAAAGGGATG GGATAGAAGG GTTTGCAATG	1620
45	CCATATTATT GGTGGAGGGC TGTTTTAAACA TCTTTGAAGT ATGGCTTGCT GAATATCTTT	1680
	ACCAACATCT TGAATATATA TTCTAGTGTC CACAAGATTT AGCAAAAAGA TAAAGCTTGG	1740
50	GTGGAATATC ATTTTAAAT GTTCATGTTT TGTCTATAT TTTCTTCACC TACTCTCCAA	1800
	ATATTGTAAT GCAAAAAGTC TCAGTAATGA TTTGGTAGTA TTAATTTTGT GGTCAATGTT	1860
	TCTCTTCGAT AAATTTATTT TCATTAAATA CTTRITAGAG GGTTTTGAAA TGTTTTTC	1920
55	ATATGTGAAA TGTGAACTG CTGTCTTTTA TATTAAAGTA ATTAAAGAAA ATGTATTGTG	1980
	ATTGAAATTA TTTTGNCTC CACAAGATGG CTCTATGAGT ATTCTTCCAG GGATTCTAAT	2040
60	ATTTATTTAA GGTNATAAAA TCTTGACATT TATAATCTTT C	2081

5 (2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1717 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

15 CCCCCGCGGA GCTGGACCCG CGGTGGGCTA GGGGCAGGGC CGGAGCCCGG GCGGCGGAGC 60
 TGTGGATCCT TCATGATGAG AGATTTGGGG ACACCTTCTCT CTCTGTGTG TAGTTGATAG 120
 TTTGGTGGTG AAGAGATGGC TGACAGTGTC AAAACCTTTC TCCAGGACCT TGCCAGAGGA 180
 20 ATCAAAGACT CCATCTGGGG TATTTGTACC ATCTCAAAGC TAGATGCTCG AATCCAGCAA 240
 AAGAGAGAGG AGCAGCGTCG AAGAAGGGCA AGTAGTGTCT TGGCACAGAG AAGAGCCAG 300
 25 AGTATAGAGC GGAAGCAAGA GAGTGAGCCA CGTATGTGTA GTAGAATTTT CCAGTGTGT 360
 GCTTGAATG GTGGAGTGT CTGGTTCAGT CTCTCTTGT TTTATCGAGT ATTTATTCCT 420
 GTGCTTCAGT CGTAACAGC CCGAATTATC GGTGACCCAT CACTACATGG AGATGTTTGG 480
 30 TCGTGGCTGG AATTCTTCCT CACGTCAATT TTCAGTGCTC TTTGGGTGCT CCCCTTGTFT 540
 GTGCTTAGCA AAGTGGTGAA TGCCATTGG TTTCAAGATA TAGCTGACCT GGCATTTGAG 600
 35 GTATCAGGGA GGAAGCCTCA CCCATTCCCT AGTGTGAGCA AAATAATTGC TGACATGCTC 660
 TTCAACCTTT TGCTGCAGGC TCTTTTCCTC ATTCAGGGAA TGTGTGTGAG TCTCTTTCCC 720
 ATCCATCTTG TCGGTGAGCT GGTAGTCTC CTGCATATGT CCCTTCTCTA CTCAGTGTAC 780
 40 TGCTTTGAAT ATCGTTGGTT CAATAAAGGA ATTGAAATGC ACCAGCGGTT GTCTAACATA 840
 GAAAGGAATT GGCCTTACTA CTTTGGGTTT GGTTTGCCCT TGGCTTTTCT CACAGCAATG 900
 45 CAGTCTCAT ATATTATCAG TGGCTGCCTT TTCTCTATCC TCTTTCCTTT ATTCAATATC 960
 AGCGCCAATG AAGCAAAGAC CCCTGGCAA GCTATCTCT TCCAGTTGCG CCTCTTCTCC 1020
 TTTGGTGGTCT TCTTAAGCAA CAGACTCTTC CACAAGACAG TCTACCTGCA GTCGGCCCTG 1080
 50 AGCAGCTCTA CTCTGCAGA GAAGTTCCT TCACCGCATC CGTGCCTGC CAACTGAAG 1140
 GCTACTGCAG GTCAGTGTG TGCCGCCAT CCAAAGGGGA TGGCGGGAT TGAAGAAGC 1200
 55 TGTGGCAGCT CTTTTCCTG TTCACTCCC GCCTGCCAGG GAAGGCAGGA CCCGCTCTGC 1260
 CAAGGCCCT CTGCGTATTC CCTTCTCTCT GAGGAATTGA AATTTTGTG TCTGGTGAC 1320
 60 GTAAGCAGA ATGTTCCCTG ACACAGTGT GTGGATTTT AACATCACCG TGAGTCTGAA 1380

AGGACCACAG GTTTTCTGCG AGCTATTTTC TAGCATTTGC CAGTCCCTGT GCCTGGACTG 1440
ATTGGAACAC TTGTGTTTTC TCCCTGTGCC ATTTACCCCTT CCACCTTTCC ATCCTGCCTT 1500
5 CTACCACCCT TGGATGAATG GATTTTGTA TTTCTAGCTGT TGTATTTTGT GAATTTGTTA 1560
ATTTTGTGTG TTTCTGTGA AACACATACA TTGGATATGG GAGGTAAAGG AGTGTCCAG 1620
TTGCTCCTGG TCACTCCCTT TATAGCCATT ACTGTCTGT TTTCTGTAAC TCAGGTAGG 1680
10 TTTTGGTCTC TCTGTCTCCA CTGCAAAAAA AAAAAA 1717

15

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 804 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

CCACGCGTCC GGTCACATG TAGTGGAGGG GCAGACACCC TCCCGCAAAT TCTGGAAGGT 60
TCTTAGTCTC GACTAGGGCA GTAGCCCCAG GACTCCTAGT CGCGGGCTTC AGGTCACTGC 120
30 CGGCTGAACG GAGCTGCCGT CGCCATGTTT GGCTGCTTGG TGGCGGGGAG GCTGGTGCAA 180
ACAGCTGCAC AGCAAGTGGC AGAGGATAAA TTGTGTTTGG ACTTACCTGA TTATGAAAGT 240
ATCAACCATG TTGTGGTTT TATGCTGGGA ACAATCCCAT TTCCTGAGGG AATGGGAGGA 300
35 TCTGTCTACT TTTCTTATCC TGATTCAAAT GGAATGCCAG TATGGCAACT CCTAGGATTT 360
GTCACGAATG GGAAGCCAAG TGCCATCTTC AAAATTTCAG GTCTTAAATC TGGAGAAGGA 420
40 AGCCAACATC CTTTGGAGC CATGAATATT GTCCGAATC CATCTGTGC TCAGATTGGA 480
ATTTCACTGG AATTATTAGA CAGTATGGCT CAGCAGACTC CTGTAGGTAA TGCTGCTGTA 540
TCCTCAGTTG ACTCATTCAC TCAGTTCACA CAAAAGATGT TGGACAATTT CTACAATTTT 600
45 GCTTCATCAT TTGCTGTCTC TCAGGCCAG ATGACACCAA GCCCATCTGA AATGTTTCATT 660
COGGCAAATG TGGTCTGAA ATGGTATGAA AACTTTCAA GACGACTAGC ACAGAACCCT 720
50 NTNTTTTGGN AAACATAATT TGAATAAAT AATTTTAAT GGATTNTGNA AAAAAAAAAA 780
AAAAAAAAA AAAAAAAAAA AAAA 804

55

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 431 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

	GGCACAGCCC AGGCCTTGA AGCCAGCTGG CCTGGAGAG GGGCTGCTGT GCCAGCTTGG	60
	GGAGGGTCTG GGATGGGGCT GCCCCTGATG GCCCTGATGT GGAGTACCTT GCCAGCATCT	120
10	GCTGGGGTGA ACTTTATTTT AGCCCTTCCC TTGTTGCTCT TATGGAAGAA CAGAGGAGGG	180
	GTGGGCAGGT CAGTGATGTC AGCAGTGGAG TGATTCCAG CACAGCGGCT TCTGGGAAGA	240
15	GGGCATGGAG GCATTTCTTT CAGGAAATG GTCCATNATT TCAGCCAGAA GGCATTGCAT	300
	TAAGTTAAGT CCNGGACTTT TGTGGCCAG CTCTGTGTTA TTAAGGGCCC TTGGCGAAGA	360
	CTTCAAGGAG GGGGCAAAAN GACCTTTAAG TTTTATAGTT TAACACAGGG AACCCNCAA	420
20	GGGTATTTT G	431

25

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

30	(A) LENGTH: 3752 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

	NGGCACGAGG AGAGTCACCT GGACTCAGAA CTAGAGATAT CCAATGACCC AGACAAAAT	60
	AAACTTCAGC TTTCTAAGCA TAAGGAGTTT CAGAAGACTC TTGGTGGCAA GCAGCCTGTG	120
40	TATGATACCA CAATTAGAAC TGGCAGAGCA CTGAAAGAAA AGACTTTGCT TCCCGAAGAT	180
	ASTCAGAAAC TTGACAATTT CCTAGGAGAA GTCAGAGACA AATGGGATAC TGTTTGTGGC	240
	AAGTCGTGG AGCGGCAGCA CAAGTTGGAG GAAGCCCTGC TCTTTTCGGG TCAGTTCATG	300
45	GATGCTTTGC AGGCATTGGT TGA CTGTTA TACAAGGTGG AGCCACAGCT GGCTGAGGAC	360
	CAGCCCGTGC ACGGGGACC TTGACCTCGT CATGAACCTC ATGGATGCAC ACAAGTTTTT	420
50	CCAGAAGGAA CTGNGAAAG CGAACAGGAA CCGTTCAGGT CCTGAAGCGG TCAGGCCGAG	480
	AGCTGATTGA GAATAGTCGA GATGACACCA CTGGGTAAA AGGACAGCTC CAGGAACTGA	540
	GCACTCGCTG GGACACTGTC TGTA AACTCT CTGTTTCCAA ACAAAGCCGG CTTGAGCAGG	600
55	CCTTAAACA AGCGGAAGTG TTTCGAGACA CAGTCCACAT GCTGTGGAG TGGCTTCTG	660
	AAGCAGAGCA AACGCTTCGC TTTCGGGGAG CACTTCCTGG ATGACACAGA GGCCCTGCAG	720
60	TCTCTCATTG ACACCCATAA GGAATTCATG AAGAAAGTAG AAGAAAAGCG AGTGGACGTT	780

	AACTCAGCAG TAGCCATGGG AGAAGTCATC CTGGCTGTCT GCCACCCCGA TTGCATCACA	840
5	ACCATCAAAC ACTGGATCAC CATCATCCGA GCTCGCTTCG AGGAGGTCCT GACATGGGCT	900
	AAGCAGCACC AGCAGCGTCT TGAAACGGCC TTGTCAGAAC TGGTGGCTAA TGCTGAGCTC	960
	CTGGAAGAAC TTCTGGCATG GATCCAGTGG GCTGAGACCA CCCTCATTCA GCGGGATCAG	1020
10	GAGCCAATCC CGCAGAACAT TGACCGAGTT AAAGCCCTTA TCGCTGAGCA TCAGACATTT	1080
	ATGGAGGAGA TGA CTCGCAA ACAGCCTGAC GTGGACCGGG TCACCAAGAC ATACAAAAGG	1140
15	AAAAACATAG AGCCTACTCA CGCGCCTTTC ATAGAGAAAT CCCGCAGCGG AGGCAGGAAA	1200
	TCCCTAAGTC AGCCAACCCC TCCTCCCATG CCAATCCTTT CACAGTCTGA AGCAAAAAAC	1260
	CCACGGATCA ACCAGCTTTC TGCCCGCTGG CAGCAGGTGT GGCTGTTAGC ACTGGAGCGG	1320
20	CAAAGGAAAC TGAATGATGC CTTGGATCGG CTGGAGGAGT TGAAAGAATT TGCCAACTTT	1380
	GACTTTGATG TCTGGAGGAA AAAGTATATG CGTTGGATGA ATCACA AAAA GTCTCGAGTG	1440
25	ATGGATTTCT TCCGGCGCAT TGATAAGGAC CAGGATGGGA AGATAACAAG TCAGGAGTTT	1500
	ATCGATGGCA TTTTAGCATC CAAGTCCCC ACCACCAAGT TAGAGATGAC TGCTGTGGCT	1560
	GACATTTTCG ACCGAGATGG GGATGGTTAC ATTGATTATT ATGAATTGT GGCTGCTCTT	1620
30	CATCCCAACA AGGATGCGTA TCGACCAACA ACCGATGCAG ATAAAATCGA AGATGAGGTT	1680
	ACAAGACAAG TGGCTCAGT CAAATGTGA AAAAGTTTC AGGTGGAGCA GATCGGAGAG	1740
35	AATAAATACC GGTTCCTCCT CGGCAATCAG TTTGGGATT CTCAGCAGTT GCGGCTGGTC	1800
	CGTATTCTGC GCAACCGTGA TGGTTCGGT TGGTGGAGGA TGGATGGCCT TGGATGAATT	1860
	TTTAGTGAAA AATGATCCCT GCCGAGCAG AGGTAGAACT AACATTGAAC TTAGAGAGAA	1920
40	ATTTCATCCTA CCAGAGGGAG CATCCAGGG AATGACCCCC TTCCGCTCAC GGGGTCGAAG	1980
	GTCCAAACCA TCTTCCGGG CAGCTTCCCC TACTCGTTCC AGCTCCAGTG CTAGTCAGAG	2040
45	TAACCACAGC TGTACATCCA TGCCATCTTC TCCAGCCACC CCAGCCAGTG GAACCAAGGT	2100
	TATCCCATCA TCAGGTAGCA AGTTGAAACG ACCAACACCA ACTTTTCATT CTAGTCGGAC	2160
	ATCCCTTGCT GGTGATACCA GCAATNAGTT CTTCCCGGC CTCACAGGT GCCAAACTA	2220
50	ATCGGGCAGA CCTAAAAAG TCTGCCAGTC GCCCTGGGAG TCGGGCTGGG AGTCGAGCCG	2280
	GGAGTCGAGC CAGCAGCCGG CGAGGAAGTG ACGCTTCTGA CTTTGACCTC TTAGAGACGC	2340
55	ATTGCTTGTT CGGACACTTC AGAAAGCAGC GCTGCAGGGG GCCAAGGCAA CTCCAGGAGA	2400
	GGGCTAAACA AACCTTCCAA AATCCCAACC ATGTCTAAGA AGACCACCAC TGCCCTCCCC	2460
	AGGACTCCAG GTCCCAAGCG ATAACACTGT CTAAGCACCC CCAAGCCACT ATCCACTTTG	2520
60	AATCTGCTC CATACATTTG GTGTATATTT ATTCTGAACG GGAGAAGTTA TATTGTTAAA	2580

	AGTGTAAAAG AATAATTGTG TTATGAAGCT GCCTTATTTT TTTCTTTTTT GTAAGTTACT	2640
5	ATTTTCATGT GAATATTTAT GTAGATAAAA TTTGCCCTCT GGTAACCCCTG TAATGGATGG	2700
	GGCCCAGAAA TGAAATATTT GAGAAAAACA AGTGAAAAGG TCAAGATACA AATGTGTATT	2760
	AAAAAAAAA AAGCCTATTA ATAGGGTTTC TCGCGGGTGC AGGGTTGTAA ACCTGCTTTA	2820
10	TCTTTTAGGA TTATTCCTAA ATGCATCTTC TTTATAAACT TGACTTGCTA TCTCAGCAAG	2880
	ATAAATTATA TTAAAAAAT AAGAATCCTG CAGTGTTTAA GGAACCTCTT TTTGTAAAT	2940
15	CACGGACACC TCAATTAGCA AGAACTGAGG GGAGGGCTTT TTCCATTGTT TAATGTTTTG	3000
	TGATTTTtag CTAAAGAGAG GGAACCTCAT CTAAGTAACA TTTGCACATG ATACAGCAAA	3060
	AGGAGTTCAT TGCAATACTG TCTTTGGATA TTGTTTCAGT ACTGGGTGTT TAAAGGACAA	3120
20	ATAGCTGCTA GAATTCAGGG GTAAATGTAA GTGTTTCAGAA AACGTCAGAA CATTTGGGGT	3180
	TTTAACTGA TTTGTTGCTC CCTATCCAGC CTAGACACCA GTAACCTCTG TGTTCACCAG	3240
25	GACCCAGACC CTTGGCAAGG GATAGGCTCG TTGGTGACAT TGTGAATTTC AGATTGTGTT	3300
	TATCCACTTT TTTTGCTATT TATTTAAATG GTCGATCAAC TTCCCACAAA CTGAGGAATG	3360
	AATTCCACGA GCCTGTTCTG AAAATGTGGA CGTAAGACAA ACACGTGCTC GTCCTTTAAT	3420
30	GGAGTTCACC AGCACACTTG TTAACCAGTC CTGTTTGCTT TCGTCTTTTT TTGTGCGTAA	3480
	TAAAGTCAAC TGACCAAGTG ACCATGAAAA GGGGCTGTCT GGGGCTCCTG TTTTITAGCT	3540
35	GCTGTCTTTC AGCTCCGACC ATGTGCTGT GTGATTATCT CAATTGGTTT TAATTGAGGC	3600
	AGAACTGAA GCTCTACCAA TGAACGTGTT AGAAACAAGA CACACTTTTG TATTAAAAAT	3660
	GCTTGCACTA ACAAAAAA AAAAAA AAAAAA AAACTCGAGG GGGGCCCGGT	3720
40	ACCCAATTCG CCGTATATGA TCGTAAACAA TC	3752

45 (2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1144 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

55	TGACCTCTG CCTGCCGGGC TCAGTGCTGG ACGCTTCTG TTTTGTGCA GTGGTCTCTC	60
	GGTAACACCA GGGCCTGTG GTCCACCACT CCATTGAGCA GCTCCATTTG GTCCAGCAAC	120
60	CTTAGCAGCG CCTTCCCTTC ACCACTCCAG CAAACACGCT GGCAAGCATC GGCCTCATGG	180

	GCACAGAAAA CTCCCCTGCT CCTCACGCTC CCTCCACCTC CAGTCCAGCT GACGACTTGG	240
	GACAGACCTA CAACCCGTGG CGGATATGGA GCCCCACGAT TGAAGAAGA AGCTCGGACC	300
5	CTTGGTCTAA TTCGCACTTT CCTCACGAGA ATTAAATTAA GCAAAAAACA AACAAACATA	360
	GTGGGCCCTC GTCTAGATCA TGATGTGCCA GTTCTGAGA CATCTTTTTA AGGCTCTTAC	420
10	TGCAGCTCCC CTCCCCACCC TCCTCTTCTT TGCAAAACAG ACCCAAGCAG GGCAGGCTCA	480
	GACCACTCGC TTCTTTCAGA TCTTCTTGC AATTATGATA ACATGAGATT TGCTGTGTG	540
	CTTTTAGAGA AAAGTCTGGA CTCAGCCACA AACTCTAATA AGACCTGTAC ATCTGAGAAC	600
15	CTTCCCGTT ACTGCGTTT CACCACCTGT CTCCCATG CTTTATTTAT CTGTATGAAC	660
	ACAGATTTGA CATTACAGCT AAGGAAATAA TTTGAGTTGA TTCAGAAATC CTGGCATGTG	720
20	ACAATTTTGT TAAATTACCA AGTTTGGTTT TTAATAATTT CTCAATATTA TGCGCCAAGA	780
	TCTAATTTTA AAAGTGTATG AGGACTTTGT GCTGAAAATA GAGTATTTT TTAAGTAAG	840
	GCTGTCTTGG TTTAAAAGCA GATTACAGAA ATGTAAGTCA ACTTAAGAAC RGTGAATGAA	900
25	TGTAAAAACA TTCAGTYGAG ACCATATGCA TTTCTGTGC TGTGTGTACT TGAGGTATGT	960
	AACATTTGTA TACCTGAACT TATTTTAAAG ATGAACTGAA ATGCACATAG CCAAGTCTTG	1020
30	AGATACAAGA TTGAATGTGT ATTTCTTAAA AATACAACCT TGTGTGTAC TTTGAAATAA	1080
	ATGATGCTTT TTTCAAAAAA AAAAAAAAAA AAAAAAAAC TCGAGGGGGG GCCCGGTACC	1140
	CAAT	1144

35

(2) INFORMATION FOR SEQ ID NO: 129:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1830 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

	GCATGCAGAG GAGCACCTG AGCGTGTGCC TGGAGCAGGC GGCCATSTTG GCACGGAGCC	60
50	ACGGGTGCT GCCCAAGTGC ATCATGCAGG CCACGGACAT CATGCGGAAC AGGGCCCAAG	120
	GGTGGAGATT CTGGCCAAAA ACCTGCGAGT CAAGGACCAG ATGCCCCAGG GTGCTCCGCG	180
55	CCTCTACCGC CTCTGCCAGC CGCCGGTGA TGGGGACCTC TGAACACCCA AATGCCCCAC	240
	GCTGGGCCGC GGCTCTGGA GCTGGGATT GGGAGGACAC AGCAGGCAGC GCTGGCTTC	300
	TCCAGGGATG GCCCAANGCT TCCGCARCCG CCCGTTCCGG GACCTGCCCA GCGTCTCCCC	360
60	TGCTCTCTC CGGACAAGC CTGGCCACCC TCGCTGTGAT GACGAGCTGG CTGATGGCC	420

	CTGGGCCGGC CCATTCTTCA CACGCCTGCC AGAAGCTGGA GGGGTGCTGG AGACCCATAG	480
5	AGCTGATGGG AGCAGCTGGT GCCTGGCCTT CGGCTCCTGC GTCCCCAGAA CCCAAGGGAA	540
	CGTCATGGAG GCCACATGGG GCCACCCGGC TCCTCGGGA TGGCTCCGCT GCACTTTTGA	600
	AACCCCGGTT TCCTTCAACG TCCACATTCC AGGTGACCAC ACGTGTCTCC TCCTCCTCAT	660
10	CTTAGCTTCC AGGTTCACCC TAACCTGTGA CTAACCTGCT TGGTGGACTT GGAAAAGACT	720
	TGGCTCTGTC GGGAAAGGAG AGACGGGGCC TCCATCACGC CTGTTACCAG AGGATCCCCG	780
15	AGAGCCACAC CAGCTCTGGA CATCACCGCC CCTGGAAC TG GGGCCACCAG CCCTGGGCAC	840
	GAGATTGCT CTGACTTTAT TTATATGGCA TGAAATCTCT GGTTTATTTT GGGATTTTTT	900
	GTGTGTGGTG TTGTCAAAGT TTGTTTTTC TAAAGTTGTG TGATTATATA TTTGACATTT	960
20	TACATTTCAA AGAAAGGTAT GTTGTCTAAC AGGGGACCAA CAGAAGGTAG TATTGACAAC	1020
	TGTTCTGCT TCTACTAAAA AAAAAAGAGC ACAAAGAAA AACTAAATTA TTGAAAAATT	1080
25	AAAAAATGTC ATTGTTTCCT GTTGTTAAT ATTAGGTTG TAAGGTGTCG TTTTGAGGTA	1140
	TCGACTGTGA TTCCTTCCCC CACCTCCAT TCTCCAGCGG TTGGCCGGTG TTAGAACTCG	1200
	CTCTCTTTGA GTGACTGGCT ACAAGGGCCT GAGAGGTGGC CAGCCAGGCT TGGAGCTGGA	1260
30	GGGATGGAG CCCACCTGA GGTGCCGTGT CACACGGGTT AGAGGGTCAC TGGGAAACAC	1320
	CGGGCGGTGG CTCTGTGAT TTATTTTCTT GATGGTAACT TCTCAGAGCA GGGCRATTGG	1380
35	GACATCACCA GCCAGGCAC AGGAAGCCAC CCTGCCTGCT GGGGAGGAGG GACCCACACA	1440
	AGCCCCCTCG GCAGTTTGTG CCCCCAGCTT CGGTATGCCT TCAGGGAAAG GTCACAGCTG	1500
	GGGAGGAAGC GGGGGGACGC CTGTACCCCC TGGCAGGTGG TGAGTTTCAGG TGGGGGCTCC	1560
40	CTGCTKCCCC CAGGCCTGGG AGCTTGAAGC CCTCCCGCA TCTGGCATCC GAGCCTCCCG	1620
	CCCTCCAGGG TCGCTTCCC TCTCTTGCCG CAGCATACAC GAGGGCAGGC AGTGGCCTTG	1680
45	TCACTGTATC TTGCATCAGA GACAAAGGAG GACCCGCTTT AGCCCTGCTG CGGGAAATGG	1740
	GGGATGGCCC AGGGCCAGCG CATGTGCAC TGGTTTACTT TAAAATGTAC AGATTCTTCT	1800
	CGTTAAATTC TTGATAGATT TTTTATTATT	1830
50		

(2) INFORMATION FOR SEQ ID NO: 130:

- 55 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1864 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- 60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

	GGCCGCCCGG ATGGCGACCC CAGCCTCGGC CCCAGACACA CGGGCTCTGG TGGCAGACTT	60
5	TGTAGGTTAT AAGCTGAGGC AGAAGGGTTA TGTCTGTGGA GCTGGCCCCG GGGAGGGCCC	120
	AGCAGCTGAC CCGCTGCACC AAGCCATGCG GGCAGCKGGA GATGAGTTGG AGACCCGCTT	180
10	CCGGCGCACC TTCTCTGATC TGGCGGCTCA GCTGCATGTG ACCCCAGGCT CAGCCCAACA	240
	ACGCTTCACC CAGGTCTCCG ATGAACCTTT TCAAGGGGGC CCCAACTGGG GCCGCCTTGT	300
	AGCCTTCTTT GTCTTTGGGG CTGCACTGTG TGCTGAGAGT GTCAACAAGG AGATGGAACC	360
15	ACTGGTGGGA CAAGTGCAGG AGTGGATGGT GGCCTACCTG GAGACGCGGC TGGCTGACTG	420
	GATCCACAGC AGTGGGGGCT GGTATATCCA GATCACTGAA GCTGAGATGG CTGATGAAGT	480
20	AATTTGCAGT GAAATTTTAA GCGACTGTGA CTCTGCTGCA AGTTCCCCAG ATCTTGAGGA	540
	GCTGGAAGCT ATCAAAGCTC GAGTCAGGGA GATGGAGGAA GAAGCTGAGA AGCTAAAGGA	600
	GCTACAGAAC GAGGTAGAGA AGCAGATGAA TATGAGTCCA CCTCCAGGCA ATGCTGGCCC	660
25	GGTGATCATG TCCATTGAGG AGAAGATGGA GGCTGATGCC CGTCCATCT ATGTTGGCAA	720
	TGTGGACTAT GGTGCAACAG CAGAAGAGCT GGAAGCTCAC TTTTCATGGCT GTGGTTCAGT	780
30	CAACCGTGTT ACCATACTGT GTGACAAATT TAGTGGCCAT CCCAAAGGGT TTGCGTATAT	840
	AGAGTTCTCA GACAAAGAGT CAGTGAGGAC TTCCCTGGCC TTAGATGAGT CCCTATTTAG	900
	AGGAAGGCAA ATCAAGGTGA TCCCAAAACG AACCAACAGA CCAGGCATCA GCACAACAGA	960
35	CCGGGGTTTT CCACGAGCCC GCTACCGCGC CCGGACCACC AACTACAACA GCTCCCGCTC	1020
	TCGATTCTAC AGTGGTTTTA ACAGCAGGCC CCGGGGTGCG GTCTACAGGG GCCGGGCTAG	1080
40	AGCGACATCA TGGTATTCCC CTACTAAAA AAAGTGTGTA TTAGGAGGAG AGAGAGGAAA	1140
	AAAAGAGGAA AGAAGGAAAA AAAAAAGAA TAAAAAATA AAAAAAATA ACAGAAGWTG	1200
	MCCTTGATGG AAAAAAATA TTTTAAAAA AAAAGATATA CTGTGGAAGG GGGGAGAATC	1260
45	CCATAACTAA CTGCTGAGGA GGGACCTGCT TTGGGGAGTA GGGGAAGGCC CAGGGARTGG	1320
	GGCAGGGGGC TGCTTATTCA CTCTGGGGAT TCGCCATGGA CACGTCTCAA CTGCGCAACT	1380
50	GCTTGCCCAT GTTCCCTGC CCCACCCAC CCCTCTCTC CGGCTCCCTG CCCCTCCAGA	1440
	TGCCCTGGT ATCTATTTTG TTCTCTTTG TGTCTCTTT TCTGTTTGA GTGTCTTTCT	1500
	TTCAGGTTT CTGTAGCCGG AAGATCTCCG TTCCGCTCCC AGCGGCTCCA GTGTAAATTC	1560
55	CCCTTCCCC TGGGGAATG CACTACCTTG TTTTGGGGG TTTAGGGTG TTTTGTTTT	1620
	TCAGTGTGTT TGTPTTTTGG TTTTPTTNT TTTCTTTGC CTTPTTTCCC TTTTATTTGG	1680
60	AGGGAATGGG AGGAAGTGG AACAGGAGG TGGGAGGTGG ATTTGTGTTA TTTTPTTAGC	1740

TCATTTCCAG GGGTGGGAAT TTTTITTAA TATGTGTCAT GAATAAAGTT GTTTTGAAA 1800
 AKAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1860
 5 AAAA 1864

10 (2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2041 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

20 GGCACGAGCG CGCGGCAGGG CCTTGGACCC GCGCGGCTCC CGGGGATGGT GAGCAAGGCG 60
 CTGCTGCGCC TCGTGTCTGC CGTCAACCGC AGGAGGATGA AGCTGTGCT GGGCATCGCC 120
 TTGCTGGCCT ACGTCGCCTC TGTTGGGGC AACTTCGTTA ATATGAGGTC TATCCAGGAA 180
 25 AATGGTGAAC TAAAAATTGA AAGCAAGATT GAAGAGATGG TTGAACCACT AAGAGAGAAA 240
 ATCAGAGATT TAGAAAAAG CTTTACCCAG AAATACCCAC CAGTAAAGTT TTTATCAGAA 300
 30 AAGGATCGGA AAAGAATTTT GATAACAGGA GGCGCAGGGT TCGTGGGCTC CCATCTAACT 360
 GACAACTCA TGATGGACGG CCACGAGGTG ACCGTGGTGG ACAATTCTTT CACGGGCAGG 420
 AAGAGAAACG TGGAGCACTG GATCGGACAT GAGAACTTCG AGTTGATTAA CCACGACGTG 480
 35 TGGAGCCCTT CTACATCGAG GTTGACCAGA TATACCATCT GGCATCTCCA GCCTCCCTC 540
 CAACTACAT GTATAATCCT ATCAAGACAT TAAAGACCAA TACGATTGGG ACATTAAACA 600
 40 TGTTGGGGCT GGCAAAACGA GTCGGTGCCC GTCTGCTCCT GGCTCCACA TCGGAGGTGT 660
 ATGGAGATCC TGAAGTCCAC CCTCAAAGTG AGGATTACTG GGGCCACGTG AATCCAATAG 720
 GACCTCGGGC CTGCTACGAT GAAGGCAAAC GTGTTCAGA GACCATGTGC TATGCCTACA 780
 45 TGAAGCAGGA AGCGTGGAA GTGCGAGTGG CCAGAATCTT CAACACCTTT GGGCCACGCA 840
 TGCACATGAA CGATGGGCGA GTAGTCAGCA ACTTCATCCT GCAGGCGCTC CAGGGGGAGC 900
 50 CACTCACGGT ATACGGATCC GGTCTCAGA CAAGGGCGTT CCAGTACGTC AGCGATCTAG 960
 TGAATGGCCT CGTGGCTCTC ATGAACAGCA ACGTCAGCAG CCCGTCAAC CTGGGGAACC 1020
 CAGAAGAACA CACAATCCTA GAATTTGCTC AGTTAATTAA AAACCTTGTT GGTAGCGGAA 1080
 55 GTGAAATCA GTTTCTCTCC GAAGCCAGG ATGACCCACA GAAAAGAAA CCAGACATCA 1140
 AAAAGCAA GCTGATGCTG GGTGGGAGC CCGTGGTCCC GCTGGAGGAA GGTTTAAACA 1200
 60 AAGCAATCA CTAATCCGT AAAGAACTCG AGTACCAGGC AAATAATCAG TACATCCCCA 1260

	AACCAAAGCC TGCCAGAATA AAGAAAGGAC GGACTCGCCA CAGCTGAACT CCTCACTTTT	1320
5	AGGACACAAG ACTACCATTG TACACTTGAT GGGATGTATT TTGGCTTTT TTTTGTGTC	1380
	GTTTAAAGAA AGACTTTAAC AGGTGTCATG AAGAACAAC TGAATTTCA TTCTGAAGCT	1440
	TGCTTTAATG AAATGGATGT GCCTAAAAGC TCCCTCAAA AACTGCAGA TTTTGCCTTG	1500
10	CACTTTTGA ATCTCTCTTT TTATGTAAAA TAGCGTAGAT GCATCTCTGC GTATTTTCAA	1560
	GTTTTTTTAT CTGCTGTGA GAGCATATGT TGTGACTGTC GTTGACAGTT TTATTTACTG	1620
15	GTCTCTTGT GAAGCTGAAA AGGAACATTA AGCGGACAA AAAATGCCGA TTTTATTTAT	1680
	AAAAGTGGT ACTTAATAAA TGAGTCGTTA TACTATGCAT AAAGAAAAAT CCTAGCAGTA	1740
	TTGTCAGGTG GTGGTGCGCC GGCATTGATT TTAGGGCAGA TAAAGAATT CTGTGTGAGA	1800
20	GCCTTATGTT TCTCTTTTAA TTCAGAGTTT TTCCAAGTC TACTTTTGAG TTGCAAACTT	1860
	GACTTTGAAA TATTCCTGTT GGTCAATGATC AAGGATATTT GAAATCACTA CTGTGTTTGT	1920
25	CTGCGTATCT GGGCGGGGG CAGGTGGGG GGCACAAAGT TAACATATTC TTGGTTAACC	1980
	ATGGTTAAAT ATGCTATTTT AATAAAATAT TGAACTCAC CAAAAAAA AAAAAAAA	2040
	A	2041

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(2) INFORMATION FOR SEQ ID NO: 132:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2012 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

	TACCAAGCTG CAAGAATCTA CTATATCATG GCAGAAGAAG TAGAGTGGGA CTATTGCCCT	60
45	GACCGGAGCT GGAACGGGA ATGGCACAAC CAGTCTGAGA AGGACAGTTA TGGTTACATT	120
	TTCTGAGCA ACAAGGATGG GTCCTGGGT TCCAGATACA AGAAGCTGT ATTCAGGGAA	180
50	TACACTGATG GTACATTCAG GNTCCCTCGG CCAAGGACTG GACCAGAAGA ACACTTGGGA	240
	ATCTTGGGTC CACTTATCAA AGGTGAAGTT GGTGATATCC TGACTGTGGT ATTCAAGAAT	300
	AATGCCAGCC GCCCTACTC TGTGCATGCT CATGGAGTGC TAGAATCTAC TACTGTCTGG	360
55	CCACTGGCTG CTGAGCCTGG TGAGGTGGTC ACTTATCAST GGAACATCCC AGAGAGGTCT	420
	GGCCCTGGGC CAATGACTCT GCTTGTGTTT CCTGGATCTA TTATTCTGCA GTGGATCCCA	480
60	TCAAGGACAT GTATAGTGGC CTGGTGGGC CCTTGGCTAT CTGCCAAAAG GGCATCCTGG	540

	NAGCCCCATG GAGGACGGAN TGACATGGAT CGGGAATTG CATTGTTGTT CTGATTTTT	600
	GATGAAAATA AGTCTTGGA TTTGGAGGAA AATGTGGCAA CCCATGGGTC CCAGGATCCA	660
5	GGCAGTATTA ACCTACAGGA TGAAACTTTC TTGGAGAGCA ATAAAATGCA TGCAATCAAT	720
	GGGAACTCT ATGCCAACCT TAGGGGTCTT ACCATGTACC AAGGAGAACG AGTGGCCTGG	780
10	TACATGCTGG CCATGGGCCA AGATGTGGAT CTACACACCA TCCACTTTCA TGCAGAGAGC	840
	TTCTCTATC GGAATGGCGA GAACTACCGG GCAGATGTGG TGGATCTGTT CCCAGGGACT	900
	TTTGAGGTTG TGGAGATGGT GGCCAGCAAC CCTGGGACAT GGCTGATGCA CTGCCATGTG	960
15	ACTGACCATG TCCATGCTGG CATGGAGACC CTCCTCACTG TTTTTTCTCG AACAGAACAC	1020
	TTAAGCCCTC TCACCGTCAT CACCAAAGAG ACTGAAAAAG CAGTGCCCCC CAGAGACATT	1080
	GAAGAAGGCA ATGTGAAGAT GCTGGGCATG CAGATCCCCA TAAAGAATGT TGAGATGCTG	1140
20	GCCTCTGTTT TGGTTGCCAT TAGTGTACC CTCTGCTCG TTGTTCTGGC TCTTGGTGGA	1200
	GTGGTTTGGT ACCAACATCG ACAGAGAAAG CTACGACGCA ATAGGAGGTC CATCCTGGAT	1260
25	GACAGCTTCA AGCTTCTGTC TTTCAAACAG TAACATCTGG AGCCTGGAGA TATCCTCAGG	1320
	AAGCACATCT GTAGTCACT CCCAGCAGGC CATGGACTAG TCACTAACCC CACACTCAAA	1380
	GGGGCATGGG TGGTGGAGAA GCAGAAAGGAG CAATCAAGCT TATCTGGATA TTTCTTTCTT	1440
30	TATTTATTTT ACATGGAAAT AATATGATT CACTTTTCT TTAGTTTCTT TGCTCTACGT	1500
	GGGCACCTGG CACTAAGGGA GTACCTTATT ATCCTACATC GCAAATTTCA ACAGCTACAT	1560
35	TATATTTCTT TCTGACACTT GGAAGGTATT GAAATTTCTA GAAATGTATC CTCTCACAA	1620
	AGTAGAGACC AAGAGAAAAA CTCATTGATT GGGTTTCTAC TTCTTTCAAG GACTCAGGAA	1680
	ATTTCACTTT GAACTGAGGC CAAGTGAGCT GTTAAGATAA CCCCACTTA AACTAAAGGC	1740
40	TAAGAATATA GGCTTGATGG GAAATTGAAG GTAGGCTGAG TATTGGGAAT CCAAATTGAA	1800
	TTTTGATTCT CCTTGGCAGT GAACTACTTT GAAGAAGTGG TCAATGGGTT GTTGCTGCCA	1860
45	TGAGCATGTA CAACCTCTGG AGCTAGAAGC TCCTCAGGAA AGCCAGTTCT CCAAGTTCTT	1920
	AACCTGTGGC ACTGAAAGGA ATGTTGAGTT ACCTCTTCAT GTTTTAGACA GCAAACCTTA	1980
50	TCCATTAAAG TACTTGTTAG AACACTGAAA AA	2012

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1669 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

5	GAGCAGTATT TTAACCAACT TGTATTACAG ATGTTACAGT TCATGTTAGG AAGTCAGAAA	60
	AGACTTTGTT TGCTTTGTT CTGCTGATGT GAGTCATGTT TTGTGGGGTC TTCCATGGCA	120
	CATTTACCTG TTGCTCCGTC CAGATGTTGA GGCCAGTCT AGGCTGACAC ATCCTACCCG	180
10	AGGACAAGCC TGTCTCCAT TTCTTCACTC TCCCTCCCC ATATAGCAAC TCTCCCAGGT	240
	TTAGATTACC GTTTTCGACG ACAGATTAAAC CAAAAATGCC CCACACAGGT TTTATTACTG	300
15	TTATATACTA TACTTTTAAAC AGTACAGACC CTAAATTTTA TTATTTGTTG CTCCCCAAT	360
	CTGATACCAA ATGTTTAAAG TTGTTTGAAA TCCAAACATG GTAGTGTTC TGGGTAAATA	420
	TTTTCTAGGC TATGTAAGAG TTAGCAGCCC ATAGCATAGA AGTAATCAAG TAGCATCTGA	480
20	GACTGTTGGA GGCACTAGGG CCTCTCTGGG CCTAACAGCC TCACTTCCCC AGCCTCACCT	540
	TGCTGTCTCT TGACACTGCC ATCAGGGCTG TTAGTGGCAC CTGTATGAGG CCAAGTGTGC	600
25	GTCCAGGGGA ACAGCACAGG TTAATGCGTC TCCCTAGAAC TCATGAAGTC AGTTTAAATC	660
	ATGCATGAAC ATGAGTTCAT TTTATGTTTT ATATAGCTTT CTTAGACATA CCAAACCATC	720
	ATTCTATAAT CAGATAAATT ATTCAGTTTT TGTGTTTAGA AAGCTAAGTA TGTGTAGCTG	780
30	GAAACAAAA TGAGCGTGT TTCTCTCCTG TTAATCTAGA GTGTGCAGTT ACACATGTGT	840
	GGATAATTTT ATGTTCCAGG GGCGCTTGGC ATCTCCCATG GACTGATTCC CAGGAAGAAA	900
35	AGCCCAAAGG GAAACCCAGC ATTCTTTTCG AGTAGATGTG GGAAAGAGCC CATTGGAGGA	960
	TATGAGGTCC TGTGAAATTC AGTTGTGTGT GTGGCTCCTT GTTAGCAGTC ATGTTGACAT	1020
	GGTGTAGGA GGCTCCCAT CCACCTTTA CATGATGTAG GGACCAGTGT CTTGTGAGAT	1080
40	TAACCTTGGG ACACAGTGGG TTAGCCTGGA GAAAATGAGA GGCCCTGCCT GGACCCAGGG	1140
	AGAGGAGCCA GTGACACAGG CAGAGCGGTG CAGCCCTCCT TCCCTTCCAT TTGGAGGAGG	1200
45	TGGTGCCAGG AGCCTGCCCG CTTACCTCTG CTGAAGCATA AGTGGACTTT GCTTTTGGGG	1260
	CTTATCTCTG ATACATGCTG GAGCCCTGCC TCTCCACTGC TAGATGGAAC CTGGAATCTC	1320
	TCATCTACCT CTTAGTCTGT CAGTTTCTAC GTGTGAGAAG CAAGCTTGTG GGCCAGTGTG	1380
50	CTGTACATG CTGTAGCACT TAAAAATAA TTCCAGGGTT CCCTGGAAAA CCAGTCCCAG	1440
	GGTTCTATG ATCTGTAGTT TCTACCTGGA TTATAACTGG TTTTGGGTAC CTGAATTTTG	1500
55	ATTGGTTAGC CTTAATTATA GTCTGGGTG ATCATGTAGA ATCTTTTCTG GTGAACAGAT	1560
	CATAAAGTTC TATCAAGGAG TTCTATCAAG GCATCCATGT CAGTGGTGCT ATGCTGGTTA	1620
	CAACTTGAGA TTTTGAAT AAAAATTG TCATAAAAA AAAAAAAA	1669
60		

(2) INFORMATION FOR SEQ ID NO: 134:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1565 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

	CACTTTGTCT ATATAACCTA AGTGATAACC CTCTTTTAGT TACCTGCCAA ACTCTGGNCT	60
15	TGGTTTATAT TGCAGTTAAC ACAGTTACAA AGCTGTAATG GTGTCTTTTT TTCCTTTGTA	120
	ACGGAATGTG TAAATCAAAG TATATACATT GTGTGGTGTG CCGTTTCTG GAGTTTCATG	180
20	AGGATTTACA CATGGCATTG AGTGTCTGT ATAGATCTGC CTACCTTGT GAATTCATCT	240
	GTTAACCCCT CTCCTTTGA GAGAGCACCG GCGATGGTGG TTAACCTCT GTGTTTCTC	300
	TCTCTCTAC TGGTTATTCT TGAATTAAGC ACAGACTCGT CAGCTCGGTT GCTTTATCAT	360
25	GAATAATGTG TGTGACCTTG CAGTTCTTCC ACAGTTCAGC AAACAAGTGC TAGCTTCACT	420
	GACCAAAAAT TAAGGAAGGA AAACACAGTT TTAAAAACGA TCCATCTTTT AACAGCOGAA	480
30	ACCGATGTGT CTATGGTGCT GCACCTTGCT GTTGTACTTC TGAAATCAGA CGTGTGTGAA	540
	CGATCATTTT TGACTTAACC GTGAGATGCT CACGAGTACC CTCCTGTTG TTTTGTAGC	600
	ATTGAAATCG AGACTATTTA TTTGGAATAT ATACAACAGT GTTTTTCCAC TGTATTTTAT	660
35	TTGCAAAAGT TGAGAACTGC TTTCTCTACC TTTTGCAAAA TAATTGATAT TCCATATTGG	720
	ATTCTCAAAG ACTTCGATAT GGTGAACCTA TTAAACCTAG AAATTGTATT CATCCTTTCA	780
	TGACTGTGGC CTGAGTTCCC CAGCCCCCTC CTCCTTTTTT TTTAGATGAG ATTTAGCACA	840
40	CTCTCAGTTA TTAAACATG CAACATTCTT TGAGTATGTA TGTGAGGCC ATCTGAGCTC	900
	ATAGCTGATT CAGTAACCAG TTTCATGCTG TGTCAATCAC ACTCACTACT TAATACTGCC	960
45	ATGGTGAAAA TGTGGAGGAA AAATGTATCC ATGTGTGTCT GGAAGCATA TAACTTTGTA	1020
	CATTTTTTAA TACTCTGATT CTGTAACATT TCTGAGTTT GTTTGTGTTT ACAGNAAAAA	1080
	AAAAAAAAGT GATAAGCAA TCAGAAGACC AAGAGGTTTA CTATTGATGC TTAGGGTCGT	1140
50	CTGACCTTGG CTGGCCAATA GACCTACACG GCCAAATTAA TTTACGAGAG TAATAATTTT	1200
	TCAAAAGCCA ATTTTTTTTC TGTATTTTCT GTATGAAACT GCCAATATCA TGAATAGAAA	1260
55	GGGAGAACCA TAAAGGAGAA AGAACGTGAT GTTCTGTTAT GTTCATGTAA ACCTAAAGAA	1320
	ACAGTGTGGA GGCAGGCGC ATCAGCCGAA CTCTAGGGAC TTGGTGTGTC TTGGAAGGCA	1380
60	TCCATACCTG CATTTTGCAT TCTTCGTATG TAATCATATT GCCAAAGACA AACTATTTCA	1440

	TCATTTATTG TAAATAACAC TTTTCCCCAG ACCTACCATA AAGTTTCTGT GATGTATTGT	1500
	CTTCCAGTTG CAATAAAAAT TACTGAGTTG CATCAATGA AGAAAAAAAA AAAAAAAAAA	1560
5	CTCGA	1565
10	(2) INFORMATION FOR SEQ ID NO: 135:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 2007 base pairs	
	(B) TYPE: nucleic acid	
15	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:	
20	TCTAAAAGCC CCCTTATACC CCACTTTGTG CAGCAAAGAT CCCCGTGCAG GTCACAGCCT	60
	GATTTGTGGC CAGGCTGGAC AAATTCCTGA GGCACAACTT GGCTTCAGTT CAGATTTCAA	120
25	GCTGTGTGG TGTGGGACC AGCAGAAGGC AAACGTCCAG CCAACACACA GGAAGTGAAG	180
	AGGACTCTGA GCTACGTGCC CTGTGAAGAC CCCAGGCTT TGTTCATAGGA GGTCTGTTG	240
	CTTCCCCAAA GTCAGAGGTG ATTTGATTTG GGAAGACTG AATATTCACA CCTAAGTCGT	300
30	GAGCATATCC TGAGTTTAC TTCCTTATGG CTGCCCCTCC AAGTTCTCTC TCTCATACAC	360
	ACACACACCC TTGCTCCAGA ATCACCAGAC ACCTCCATGG CTCCAGCTAT GGAACAGCT	420
35	GCATTGGGGC TGCCTTTCTG TTTGGCTTAG GAACCTCTGT GCTTCTGTG GCTCCACTCG	480
	CGAGGCAGCT CGGAGGTGTG GACTCCGATT GGGCTGCAGG CAGCTCTGGG ACGGCACAGG	540
	GCGGGCGCTC TGATCAGCTC GTGTAAAACA CACCGTCTTC TTGGCCTCCT GGCAGTTCTT	600
40	TCTGCGAATA GTCTCTCCC TGGCCAGTTG AATGGGGGAA GCTGCTGGCA CAGGAAGGAG	660
	AGGCGATCCC GGCTGAGGCT TAGGAAATTG CTGGAGCCGG CTCCAAGCAG ATAATTCAT	720
45	GGGGAGGTTT TCAGAGTCAA ACATCATTTCT GCCTGTTTGG GGGGCCAGGT GTGTACACA	780
	AGCATCTCAA AGTCAAAAGC CATCTGGGGC TGCTGCTTCT CTCTCTCAGG CTCTGGGAA	840
	AGGAATCTCC CTCTCTCTC ACTTGATTCC AAGTGTGGTT GAATTGTCTG GAGCACTGGG	900
50	ACTTTTTTTC TCTTTTCTT GATGGACCAA CAGTGCAAAT GCAATCTCGC CATTTAAGTT	960
	TCAGGTGAT TTCTTTCTT GATCAGACAT CTTTGTGCCC CCTTTAGGAA GGAAAAGAAT	1020
55	ACACCTACGA TGTGCCAGGC ACTGTGTTAG GCGCTTTTAT ATAGATCTCT GTTAGGATGA	1080
	GACTAAGGGA TGAGGACATC TCTTTATAAA AGGCCCTAA GTAATGGATA AACAGAAACA	1140
	CTTAGAGGTG AGAAGGTCTG TCTTCAAGAT CCAAGGTAAG ATTGCCTTCA GTCTGATGTT	1200
60	TGTTCTCAAG GACTTATCCC CTACAATATT CTCCACTCC ATACTTCTCC TTCTACCCCA	1260

	CCATGTGCTC CCGTGCAC TC CAGATGGT CAGAGGGGTA ACCCAAGTCC TTAGAGAATT	1320
5	TGGGGACCAA TAGAATATGT GATGTGTGAA TTTTCTTTAA AAAACTTAAG GAGTCTTTGC	1380
	TACCTTCTGC TTGTTGAGTT GTTTTGGCAT TCATATTAAA AGCCAGCATC TCACTATTTA	1440
	TTGACAGGTT GGGCTGTGTG TGTGCGCATG TGTGTATACA TTTCCAGGCG TGCTGTGTC	1500
10	CTGTAGCTTT TTAAGAGGAA ACCCAGTCAT CCCACTATGA ATCTGGCATC TTCTTATGCT	1560
	TCTAGTGT TTGGCCATACA TCAACCAAGG GGTTAATTT ATCCAATGCT TGACGACATG	1620
	TTCAGGAGGG GCTGGATCAA ATTTTGAGAG GGTATGGA AAGGGAGGG GAGAAGAAAT	1680
15	TGACATTTAT TTTATTATTT ATTTTAAATG TTTACATCTT CTTTATGTTG TATCAAGCCT	1740
	GAATAGAAAC TGATAGCATT AAAATACTCC GTTCTCTCT CTCTCTCGC TTCCTTTTTT	1800
20	TTTTTTTTTA AATTAGGAT AACACATTTT TGTTCCTAAA GTGATTGTG ATTTGTGCTG	1860
	TATAAAGTGT ATAAAAGGTT CTGTTTTTAA AGGTGGATTT TCATTCCTCT GGGGACAGTG	1920
25	GTGCGCAAGA CATCTACATT GTAAGAGAAC ACAGTGAAG ATCCTGTCCT GATTCTCAAA	1980
	AATTATTTTC TCTGTATGAT TAAAAGT	2007

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(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 1291 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

	CTTTTAACCC TCCCCCTTCA CACACATACA TATCAGGTTG TTTTCTAGTT AAAAACC	60
	GTAGCTCAGA TTCTACTTTA ATGTCAGTGC AGATTGTCAT TGAATCATGC CATTATGTTT	120
45	TTTCTCATTT TTATGCTGTT GGTCTTAGT TTTTAAATTG ATATAAGAA CTCAGCAATG	180
	GTTTTATTTT CTACTCATAC TTAGGGTTTA GGAAACACTA CCACTAGTTA TCATTTAATC	240
	AACCTCAATG GTCTACTGAA ACAAAAATGG TAACTTTTCA TTAGTGGATT ATTTAGAGTT	300
50	ATAGTAGTTG TTTCCAGAAA ACACTTCTC ACAATTGTAC TTCCAATCA AATCATGTGA	360
	TCATACAGTT ATTCCCATGA AAGGCAGAAT GTTTGTTTCA AAATTAATCT AGTTTCTGT	420
55	ACATTTAAAT TTGAGAAGGT GACAACTGGC TCTTTTCCAG TCTTCCTTCA TGTCAGTTTT	480
	CTGATAGACC ACTATTGGCA AACAGTATCT GTCAACTACC AAATGTGTAA AATTTTCTGT	540
60	ATTTCACTTT GTCTTATTG TAAATAGTGA ACTAAAACCT TTGGCAGATC AGCAACATTT	600

GCTGAGCCTG TTTTTTAAGC TAATGTGTAT TCTTACTAAT GTTCCTATCA AGAATGGATT 660
 TGTAATATAT GCTGTCTATT TCTAATGTTT ACATTCATAT TTTGAGGTTC TATCTTATTT 720
 5 TAATAGAGAA CAGACTTCTC AAAAAATCTT CAGAAGCAGC TTATTATTGA AATATCGAAA 780
 TATTGAAATA AACCCGGTGG GTTAGATTAC TCATCTGTCC ACCAAGTGGG ACATTTCAT 840
 10 GGACTGGGGG CTTAAAGGAC TTAGAAGAGA CCTGTAAAGTA AATCCTGAAA ATGAGCCAAT 900
 CCCCACTTGA ATGGTTACTG GAGTAAACCC ACCTTTACCA CCCCAATTAC AGCACCCGAG 960
 GCCGATAAAC CAACTTGGCT CTGGTTCATT TTTCTTTTCT TCATTTGTGA TGCTCAGATT 1020
 15 CAAAATGTGT GTTCTACACT GTTACAGGCT TCTCTTTTGT TTGATTAAAG ATTTTAGTCC 1080
 TACTTTTGTA TGGACACATT AGAATATTCA GAGACCAAAA TAGAAGAATT TGCTGTTAGA 1140
 TATTTTTCAG AAGTCAGCAG ATTTGTGGCA AATCATTTAT TTGCCTTTTT AAAAATTCAT 1200
 20 TTAAGCAGTT CAGAGAGTAG ACTACTCAGA AAATTATTTT ACGTAATTGT CTAAGAGGTC 1260
 AATATTTTTT AATGCATATT GAATCAAATA A 1291

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(2) INFORMATION FOR SEQ ID NO: 137:

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- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1906 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

GGCACGAGGA CCTACTTTTG TAACAGACCA TGGTGTGTGC CAAGGTAAAA CCACAGTGAT 60
 40 ATTTTGGGAT GCTTTGTCTG CAATCTTGAC TTGTTTTGTC AGTATCATT TTCAGACTTC 120
 AAATTGTGAA TCTTTTAAAC ATCTTGATAA TTTGTTGTG AGAGCTGTTT ATTCTAAAAT 180
 45 GTAATGAAAT TCAGTCTAGT TCTGCTGATA AAGATCATCA GPTTTGAAAG GTTACTGATT 240
 TTCCTCTTCC CTCTTAGTTT TTTACCCAAT ATATGGAGAA GAGTAATGGT CAATCTTAAC 300
 ATTTTGTTTT AATTGTTTAA TAAAGCTGCT GGGCAGTGGT GCAGCATTC TACCTAGTGT 360
 50 CATAAAAGCA AAATACTTAC ATAGCTTTCT TAAAATATAG GAATGACATT ACATTTTTAG 420
 GAGAAAGTAA GTTGCTTTGC ACCGCCTACT TAATTCCTTT CCATATATTG TGATACAAAC 480
 TTTTGAATAT GGAATCTTAC TATTTGAATA GAAATGTGTA TGTATAATAT ACATACATAC 540
 55 ATAAGCATAT ATGTGTGTGT GTGTGTGTAT ATATATATAT ATGCATGCTG TGAAACTTGA 600
 CTACACAACA TAAATCACTT TTTAAATCC AGGAACGGT AGTCTGACAC GGTGATTATC 660
 60 CTTTTGAGGC TGAATCCGTT ATTAACCTGT TATTTAGGTT TTAATCCAG TAGCAAGGGA 720

TTCTAAGTTA GTTGCACTTA CATGATTATT GTGATTTAAA ACTAAGAATA AAGGCTGCAT 780
 5 TTTCAAAGAT AAATTGGAAT TGCTGTGGT GAAATAACAA CCAAAATACT GAATCTGATG 840
 TACATACAGG TTTCTACAGG AAGAGATGGT ATAATTTACA ATTTGGAGAT TTAATAACCA 900
 GGGCTACCCA GAAAAAGTGA CTGTATAACA TGGTACCAAT AAGTAAGGGA TGCTCTCTCG 960
 10 GTTTGCTTTT GCCACTTTCA AGATTTTAAC TTCTCAGGTT ATTAATCAAA ATTATTGTAT 1020
 AAGTTAGCCA ATAGAATTTT TAGGTTAAAA CAACAGATGG GGGGTTGTG GAGTGTTTAA 1080
 TGTCATGGG ATTTTITAGTA GCATAGACCC TTTGTTCTGC ATTTGAATGT TTCGTATATT 1140
 15 TTTGTTTCAC AGTTAATCTT CCTCCCCAA GTTTGCTATT CAAATCAACT GCCTGAATGA 1200
 CATTTCTAGT AGTCTGATGT ATTTTCTGA GGAATAGTTT GTGATTCCAA TGCAGGTGTC 1260
 20 TTCATTACCA TTACCTCTAC ACTGCAGAAG AAGCAAACT CCTTTATTAG AATTACTGCA 1320
 CATGTGTATG GGGAAAATAG TTCTGAAAGG CTAGAATGAT ACAAGTGAGC AAAAGTTGGT 1380
 CAGCTTGGCT ATGGAGTGGT GGCAATAATC TCTAAACATT CCAAAGACC ATGAGCTGAA 1440
 25 CCTAACTCC CTGGGAATC TGAACAAAG GAATATGAAA ATTGCCATT GAAAAGTAC 1500
 CAGCTAATCT GGACCTCAGA GATAGATCAG CCAGTGGCCC AAAGCCATT CAAGTACAGA 1560
 30 AATTATAGAG ACTACAGCTA AATAAATTG AACATTAAAT ATAATTTTAC CACTTTTGT 1620
 CTTTATAAGC ATATTTGTAA ACTCAGAACT GAGCAGAAGT GACTTTACTT TCTCAAGTTT 1680
 GATACTGAGT TGACTGTCC CTTATCCCTC ACCCTTCCCC TTCCCTTTCC TAAGGCAATA 1740
 35 GTGCACAACT TAGGTTATTT TTGCTCCGA ATTTGAATGA AAACTTAAT GCCATGGATT 1800
 TTTTCTTTT GCAAGACACC TGTATCAT CTTGTTTAAA TGTAAATGTC CCCTTATGCT 1860
 40 TTTGAAATAA ATTTCTTTT GTAAAAAAA AAAAAAAA AAAAAA 1906

45 (2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1935 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

55 TCTGAATAA TGCTAACAGA TCCCCCTGAG GGATTCTTGA TGGGCTGAGC AGCTGGCTGG 60
 AGCTAGTACT GACTGACATT CATTGTGATG AGGGCAGCTT TCTGCTACAG GATTCTAAGC 120
 60 TCTATGTTTT ATATACATTT TCATCTGTAC TTGCACCTCA CTTACACAA GAGGAACTA 180

	TGCAAAGTTA GCTGGATCGC TCAAGGTCAC TTAGGTAAGT TGGCAAGTCC ATGCTTCCCA	240
	CTCAGCTCCT CAGGTCAGCA AGTCTACTTC TCTGCCTATT TTGTATACTC TCTTTAATAT	300
5	GTGCCTAGCT TTGGAAGTC TAGAATGGGT CCTGCTGTCY TTTTACTTTT GAAGAAATCA	360
	GTTTCTGCCT CTTTTTGGA AAGAAAACAA AGTGCAATTG TTTTTTACTG GAAAGTTACC	420
10	CAATAGCATG AGGTGAACAG GACGTAGTTN AGGCCCTTCCT GTAAACAGAA AATCATATCA	480
	AAACACTATC TTCCCATCTG TTTCTCAATG CCTGCTACTT CTGTAGATA TTTCAATTTCA	540
	GGAGAGCAGC AGTTAAACCC GTGGATTTTG TAGTTAGGAA CCTGGGKTCA AACCCCTCTC	600
15	CACTAATTGG CTATGTCTCT GGACAAGTTT TTTTTTTTTT TTTTTTTTAA ACCCTTCTG	660
	AACTTTCACT TTCTATGTCT ACCTCAAAGA ATTGTGTGTA GGCTTGAGAT AATGCATTTG	720
20	TAAAGGGTCT GCCAGATAGG AAGATGCTAG TTATGGATT TACAAGGTGT TAAGGCTGTA	780
	AGAGTCTAAA ACCTACAGTG AATCACAATG CATTTACCCC CACTGACTTG GACATAAGTG	840
	AAAAGTAGCC AGAAGTCTCT TTTTCAAATT ACTTACAGGT TATTCAATAT AAAATTTTGT	900
25	TAATGGATAA TCTTATTTAT CTAAACTAAA GCTTCCGTGT TATACACACT CCTGTTATTC	960
	TGGGATAAGA TAAATGACCA CAGTACCTTA ATTTCTAGGT GGGTGCCTGT GATGGTTCAT	1020
30	TGTAGGTAAG GACATTTTCT YTTTTTCAGC AGCTGTGTAG GTCCAGAGCC TCTGGGAGAG	1080
	GAGGGGGGTA GCATGCACCC AGCAGGGGAC TGAAGTGGGA AACTCAAGGT TCTTTTACT	1140
	GTGGGGTAGT GAGCTGCCTT TCTGTGATCG GTTTCCTAG GGATGTTGCT GTTCCCTCC	1200
35	TTGCTATTCG CAGCTACATA CAACGTGGCC AACCCAGTA GGCTGATCCT ATATATGATC	1260
	AGTGCTGGTG CTGACTCTCA ATAGCCCCAC CCAAGCTGGC TATAGGTTTA CAGATACATT	1320
40	AATTAGGCAA CCTAAAATAT TGATGCTGGT GTTGGTGTGA CATAATGCTA TGGCCAGAAC	1380
	TGAAACTTAG AGTTATAATT CATGTATTAG GGTCTCCAG AGGGACAGAA TTAGTAGGAT	1440
	ATATGTATAT ATGAAAGGGA GGTATTAGG GAGAACTGGC TCCCACAGTT AGAAGGCGAA	1500
45	GTGCGACAAT AGGCCGTCTG CAAGCTGGGT TAGAGAGAAG CCAGTAGTGG CTCAGCCTGA	1560
	GTTCAAAAAC CTCAAAACTG GGAAGCTGA CAGTGCAGCC AGCCTTCAGT CTGTGGCCAA	1620
50	AGGCCAAGAG CCCCTGGCAA CCAACCCACT GGTGCAAGTC CTAGATTCCA AAGGCTGAAG	1680
	AACCTGGAGT CTGATGTCCA AGAGCAGGAA GAGTGAAGA AAGCCAGAAG ACTCAGCAA	1740
	CAAGGTAGAC AGTGTCTACC ACCAYAGTGG CCATACCAA GAGGCTACCG ATTCTTCCT	1800
55	GCTACCTGGA TCCCTGAAGT TGCCCTGGTC TCTGCACCTT CTAAACCTAG TTCTTAAGAG	1860
	CTTCCATTA CATGAGCTGT CTCAAAGCCC TCCAATWAAT TCTCAGTGTA AGYTTCAAAA	1920
60	AAAAAAAAA AAAAA	1935

(2) INFORMATION FOR SEQ ID NO: 139:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1446 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

10

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

15	NGCCCCCTTG GCACAAGTCA GATGAAGCAC GTTCTGCCGG GGAGGCCCTC AMCTTCCAGA	60
	GAGGACAGAC ACAGATTTCG TGCTGGGGGA GGGAGGAGTC CACGCATCCT GATGCTGCCT	120
	GGAAOCTTAT TTTCCCGTGG CCAGGATGCA TTTCTCTGAG TGGAAACAGG TTCTTGCA TG	180
20	TGGATGTGTG TTTCCCCAGG CAGACGGCCC CTCTYTTCCC AGCACTTCCC TGCCTCCCCC	240
	AGGCCTCAGG CCAGCACCCA GTTCCTCCTC ACATGGCAGG TGAGCACAGA CTTCTAGTTG	300
	GCAGGAGCTG AGGAGGGTGA ACAAACCCCG AGGGAGGCCG GGCCCTTGCT CCCGAGTTGG	360
25	GGGGAGGGGG TGTGGCAACG TGCCCCCGC AGAGGCCACG CATGTTTGAC CAAAGCCCTC	420
	ATTGTGGTCC GAGGACAGCC TTTTCCCCAG GCCTCARAGC ATTGCTCATC CGTGCCAAAC	480
30	TGGGTAGGTG GATTTGAGCG GAAAGACTCC CAAAATGTGC CAAGAATTTC CCRGTCCAG	540
	GCAGGCAGG GGAAACTAAG GGCAAGCAGG ATACAGGGCG AGGGATGTGG CAGGTGAGGG	600
	GGCTCCCGCC TGTGCCCTT CTCTCACCA TGTCTCCCC ACCCTGCTC AGTTCTCCGT	660
35	TCCCCCTCAT CTCCGTCCCC CTCTTTGAAG CTGTCCCCAT CTCAGTGTCA GACCAGCCTT	720
	CTCTCAKCT GACCACCCTC CTCTGACCSA CGCCCCCTCC TTGTCTGAAA AAAGGAGCCT	780
40	TGAATGGTGG AGGGAGGCAG TGGGGAGAAA GGTCTCACCG GACAGGTGAG GAGAATGAGG	840
	TCAGCGGTGC TGGGGAACAG ATGGAGGGGG CAGTGGGGAC AGGGCTTGGG CAGACACCAG	900
	CAGGAATAAT TTGAAATGTG TGAGGTGACT CCCCAGAGGC CTTGGGCTTG GCATTTTGGG	960
45	AAAAGAATGA TGTCTGGAAG GGCTTAAGGG ACACAGTGA CGAGGGGAGA GTCCTCATCT	1020
	GCTGGCATTT TGTGGGTGT TAGTGCCAAA CTTGAATAGG GGCTGGGGTG CTGTCTTCCA	1080
50	CTGACACCCA AATCCAGAAT CCCTGGTCTT GAGTCCCCAG AACTTTGCCT CTTGACTGTC	1140
	CCTTCTCTTC CTACCTCCAT CCATGGAAAA TTAGTTATTT TCTGATCCTT TCCCCTGCCT	1200
	GGTCTAGCTC CTCTCCAAAC AGCCATGCCC TCCAAATGCT AGAGACCTGG GCCCTGAACC	1260
55	CTGTAGACAG ATGCCCTCAG AATTGGGGCA TGGGAGGGGG GSTGGGGGAC CCCATGATTC	1320
	AGCCACGGAC TCCAATGCCC AGCTCCTCTC CCCAAAACAA TCCOGACAAT CCCTTATCCC	1380
60	TACCCCAACC CTTTGGCGCT CTGTACACAT TTTTAAACCT GGCAAAAGAT GAAGAGAATA	1440

TTGTAA

1446

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(2) INFORMATION FOR SEQ ID NO: 140:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1109 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

TTTTTTTTTT	TTTGATATGA	AATGTCTTT	CTCCATTGCA	GAAATAAGCT	AGGGAAACAC	60
TAACCCAAAA	ACTTTCTGTA	GAGCTGTTCC	TTTGGAGGCA	GCATCACTTA	TTGGCAGTAA	120
AGACTCAGTA	TAAAGCACC	AGCATCCCTA	CTTGGGTGAT	GGGGATTAAT	TTTATAGCAT	180
TCCATTTTCC	TAGTGCCACA	TGTGAAATTG	GATTTTGATG	ATCTTAATCT	ATATTCTACC	240
CTTATAATAA	AAGATCAAAA	GATATATCTC	CTATGAACAG	ATTGGAGATA	GGAGATGAAA	300
AGTTGGGAGG	ATGTCTTTAT	TCTAATGTGA	GGGTAGGGAA	AATGTGGATA	ACATTACTGG	360
GGTGARGGAG	GCATGTCTCT	TTAGTTGGAG	TTCTCATTTT	TATTCTCCAG	TACTGACTTG	420
TGGGGAAAGC	ATACTTTTTC	ACTGCCAGGT	ACTGAATGCA	GAGGCTCAGT	GAAGTATATA	480
TGTGGGAAGT	GCATGCATTT	CGTTTATTAG	CAAACATAGC	TGGATTAAGA	CAAAGTTGTT	540
GGTTTGAAAA	GGGGTTAAAG	CCTTAAGTGA	ACAAATCTAG	CTAACAGTGA	ATGAACTAGG	600
TAATATAACT	TGCATATTTT	TAATTCCTT	TGGTTAAAGG	TCCCCCATA	TTCTCTGTTC	660
GGAGACATGA	GAAGTATGAT	TACTTCAGTG	TTAGTTTCT	TAATTTTTTT	TTTCCCCTAT	720
TTGTCCCTTG	TCACMTTGT	GCAAGCTAGA	AATCTGTGGG	TTATACATAG	GGCAGCTCTT	780
TGTGAAAGTG	GTTTATTCCA	CTGGAGAAAG	GGGATTGAAA	ATCAGTTAGA	ACCAATGTAT	840
TTCTTGCCCC	ACGGAACACT	ATTCTTATAA	GATAGCTGAA	AGAAGCTGCT	GTGAGGAGCT	900
CAGCTCCAAA	CACAGGATCA	GCACCTTGTA	TAGGAATTCC	CATGAATTAT	GACTTCTCAT	960
TCTGTTTAT	CAGAGTGCAT	ATATGTCCTA	CTTCAGGAAA	AGTAAAACAG	TCATTTACGA	1020
AAGAAAGTCA	ATCTGTATCC	TAAGCATTTT	AATAAAAAGT	TAAAACAAAA	AATTAAAAGG	1080
GACACTCGAG	GGGGGGCCCG	AAACCCAAT				1109

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(2) INFORMATION FOR SEQ ID NO: 141:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

TAGGACTAAC TTAAATTCCTT TTATTCATCT TTTATTTATT AAAAAATTTT ATTTCTTTGA 60
10 ATTTTCCTGT AATTTCTTA RGCTCTCTA TAAATGTTA TATTCATGTG AACCATACCT 120
CATTATCCTT AACATTTACT CTCAAAAGC TTTTATTTT TATTTTTTTG AAGGTAGTTT 180
15 TTCTGTGTGT ACTCTGTAAC ATGATTTTGC TTTCAAATCA TTGTTGTGCC CCCATACAAA 240
ATGCCTTTTA TTTTGTAGGA TCGTGGACTT TTTAGTATGG CATGAGTGTG CTAAAAGCCA 300
GATATCTTTC CACATTCACT GGTGGCTTTG ACACCTAGTT TTTAATCTCC CATCCTTACT 360
20 TTAAACCTG ACAGTGCAGT CCTCAGTCAG GCCCAGGACC GGGCTGAGGC CCTTGTGGA 420
GATGCTGCAC CACCAGCAGA AGGCTGAGAC CTGGTTACCT GTACCTGTTT ACTTGTATA 480
AAAAGAATTA TCTAAAA 497
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(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

ATGAGGCAGA GGCAAGCTGC CTGCCAAGCC CCTCCCTCAA GGAATGGCCT TGCCAGGAA 60
40 TGCCACACAC ACATACCTC TTCTTTTTTT CTAGTCAAAC TCTTGTATAT TCCTTGGCTT 120
GCCTCCCTCC TTCTCTCCC TCTCAACCTT TTACTTCTGG TTTCTATTTT ATGGGATTG 180
45 GGGTTGAAGT TAAACTTACA ACAGTGGCGC CAACACCAAG TCTTGCAGGA AAAAAATACA 240
AAGAAATTTA ACAAAAAAAA AAAAAAAA 269

50

(2) INFORMATION FOR SEQ ID NO: 143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1269 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

	TTGATTGACT ATGGTCTCTC CGGCTACCAG GAAGAGTCTG CCGAAGTGAA GGCCATGGAC	60
5	TTCATCACCT CCACAGCCAT CCTGCCCTG CTGTTGGGCT GCCTGGGGCT CTTGGGCTC	120
	TTCCGGCTGC TGCAGTGGGT GCGCGGGAAG GCCTACCTGC GGAATGCTGT GGTGGTGATC	180
	ACAGCGCCCA CCTCAGGGCT GGGCAAAGAA TGTGCAAAG TCTTCTATGC TCGGGTGCT	240
10	AAACTGGTGC TCTGTGGCCG GAATGGTGGG GCCCTAGAAG AGCTCATCAG AGAACTCACC	300
	GCTTCTCATG CCACCAAGGT GCAGACACAC AAGCCTTACT TGGTGACCTT CGACCTCACA	360
15	GACTCTGGGG CCATAGTTGC AGCAGCAGCT GAGATCCTGC AGTGCTTTGG CTATGTCGAC	420
	ATACTTGTC ACAAATGCTGG GATCAGCTAC CGTGGTACCA TCATGGACAC CACAGTGGAT	480
	GTGGACAAGA GGGTCATGGA GACAACTAC TTTGGCCAG TTGCTCTAAC GAAAGCACTC	540
20	CTGCCCTCCA TGATCAAGAG GAGGCAAGGC CACATTGTG CCATCAGCAG CATCCAGGGC	600
	AAGATGAGCA TTCCTTTTCG ATCAGCATAT GCAGCCTCCA AGCAGCAAC CCAGGCTTTC	660
25	TTTGACTGTC TCGTGCCGA GATGGAACAG TATGAAATTG AGGTGACCGT CATCAGCCCC	720
	GGCTACATCC ACACCAACCT CTCTGTAAAT GCCATCACCG CGGATGGATC TAGGTATGGA	780
	GTTATGGACA CCACCACAGC CCAGGGCCGA AGCCCTGTGG AGGTGGCCCA GGATGTTCTT	840
30	GCTGCTGTGG GGAAGAAGAA GAAAGATGTG ATCCTGGCTG ACTTACTGCC TTCCTTGGCT	900
	GTTTATCTTC GAACTCTGGC TCCTGGGCTC TTCTTCAGCC TCATGCCTCC AGGGCCAGAA	960
35	AAGAGCGGAA ATCCAAGAAC TCCTAGTACT CTGACCAGCC AGGGCCAGGG CAGAGAAGCA	1020
	GCACCTTTAG GCTTGCTTAC TCTACAAGG ACAGTTGCAT TTGTTGAGAC TTTAATGGAG	1080
	ATTTGTCTCA CAAGTGGGAA AGACTGAAGA AACACATCTC GTGCAGATCT GCTGGCAGAG	1140
40	GACAATCAAA AACGACAACA AGCTTCTTCC CAGGGTGAGG GGAAACACTT AAGGAATAAA	1200
	TATGGAGCTG GGGTTTAAACA CTAAAACTA GAAATAAACA TCTCAAACAG TAAAAAATAA	1260
45	AAAAAAAC	1269

(2) INFORMATION FOR SEQ ID NO: 144:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1944 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

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AAAAGGCAAA CTATAGGATA ACACAGAGCC CTTTTTGAAA ATAAATTGGC ATTGGAGTGT 60

	TTTACCCCTCT AGCTGTTTTA CTTAGAATGT AACATATGCT GCCTACCCAC CTCAAAATGT	120
	CTGTACTGCA AGAGGGCCCT GGGCCTCTGC TTTCCATATT CAOGTTTGGC CAGAGTTGTA	180
5	GTCCCAAAGA AGAGCATGGG TGGCAGATGG TAGGGAATG AACTGGCCTG TGCAATGGGC	240
	ATGGAGCACA AGGGGTCACA GCATGCCTCC TGCCTTACCG TGGCAGTACG GAGACAGTCC	300
10	AGAACATGGT CTTCTTGCCA CGGGGTGTG TTGTCTCTGG TGGTGTGCA TGTCTGTGGC	360
	TCACCTTTAT TCTTGAAACT GAGGTTTACC TGGATCTGGC TACTGAGGCT AGAGCCCACA	420
	GCAGAAATGG GTTGGGCCCTG TGGCCCCCAA ACTAGGGGGT GTGGGTTCAT CACAGTGTG	480
15	CCTTTTGTCT CCTAAAGATA GGGATCTACT TTTGAAGGA ATTGTTCCTC CCAAATAAAT	540
	TTGCTTTACC TTGGTCCTTT CTTTGTGTCC AGTATTCAAG TGGTATAGCT CTGAGCAGGG	600
20	TCACATTGG CCAAACCTGA CACTGTCTTG CTGCATTCTC CTTTGGCAA CATCAGGGTC	660
	AGAATTGAG ATAGCCCTTC CTAGGGCACT GGACTTTCTG GCATGGGGGC TGTGTTTGCA	720
	CAAGTTATTT TCATGTTACC TGGAGAGTGT CCAGAGGCTG CTCTGAGGCT GAGGTGTGTT	780
25	CCCCCTTGCC TGGTTCAGC TGTGAGAGG ATACCATCCT AGGGTCTGGG AATCCAAGGC	840
	CACGAGACTC CTTGGTTTGT GGTCCGAGAT CCTGTACTAA GGAGGCTCTG GCCAGAGGAA	900
30	CAGACCAGCT TTTGCACAAT GAAGCGCAAG GGAACAAGTG GTTTGCTGG TGTCTACCT	960
	GTCTGAACC TGGTCTGTG GGCCATTGAA AAGTTAGATC TGTGATCTCT GGGGTTTTTG	1020
	TGGCTTTGTT CAATGCTTCC ACTCTAGGGC AGGCAGAGCA GTCTATACTC TCCCAAGCCT	1080
35	GCTTGACCTC CAAGTAGAGC TGATACAGAG ATCTGTGAAT ATTGTGATAG AAATTCTTTG	1140
	GTATTCATAC ATTTGAGCTG CAAGTCAGCA ATTTCCAGG TACCATGTAA GCTATAAAAC	1200
40	AGTCATTCTT AAAGACAGAG GATAGCTGTG ACTCATGGGA TCATGAGGTC CATGGCTGGT	1260
	TGCAGGTGCC CTTTTCCTT CTCAGGTTT TGTCTCTTCC TGTGTTGTCC CCAGCAAGGG	1320
	AGAGACTGTG GGGTGGATTG GGAGAACAGA TTAGGAGTAT AGCAAATGAA CCCAGAATGG	1380
45	AACAGTGGGG AGCTAACTGT GAATGAGGAG AGTACCTGCT GCAGGACCTG GAGGTCAGGT	1440
	GTGAATGCTG TATTGGCACA GGAATAAAT ATCCTGGCGT CTGGAGCCTT CACCTCTCCG	1500
50	TCAAGTCCTT CCTGTGATAC TGCCATGGCA CAGGATCTGA GTTGCAGCTC TGCACCCTAA	1560
	ATCACACCCT GGGCATGTG TGGGCTGCAG GGCTGCCAGG TTCTGTACTT GTGTCCAGCT	1620
	GTGGCCCTGG ATGCTGGAGC TGGAGGGTTT TCTGTGCTCA GACTGTAGCC TGTAAGCTCTT	1680
55	GGCCTGTGTA GAGCCCCCTC CTGTGCCCTC AGTGGCTGTC GTTTGTTAAC ATCATCAGGA	1740
	AGATGGGAAA GGTGAGGCAG AATTTTCTG CCTACAAAG GGTGGAAGAG AAAGGACACA	1800
60	GTATTTTCAT GAATTTACCA TATATCTTTG TTTTCTTCA ACGAAAAAGT TAATGAGGC	1860

AATGTCATCT GCTCAAAGTT GAGTGGTTTA TTCACAATAA ACTGTAAGTT TCTGATTATA 1920
AAAAAAAAAA AAAAAAAAAA AAAG 1944

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(2) INFORMATION FOR SEQ ID NO: 145:

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1021 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

TCGACCCACG CGTCCGGGGT GCGCAACGGG GAGTTCGGGC TGGAGACCCG TGCTCTGGGC 60
20 CGGCGCCTTC ACCATGGCCT CGGCAGAGCT GGACTACACC ATCGAGATCC CGGATCAGCC 120
CTGCTGGAGC CAGAAGAACA GCCCCAGCCC AGGTGGGAAG GAGGCAGAAA CTCGGCAGCC 180
25 TGTTGGTGATT CTYTTGGGCT GGGGTGGCTG CAAGGACAAG AACCTTGCCA AGTACAGTGC 240
CATCTACCAC AAAAGGGGCT GCATCGTAAT CCGATACACA GCCCCGTGGC ACATGGTCTT 300
CTTCTCCGAG TCACTGGGTA TCCCTTCACT TCGTGTTTTG GCCCAGAAGC TGCTCGAGCT 360
30 GCTCTTTGAT TATGAGATTG AGAAGGAGCC CCTGCTCTTC CATGTCTTCA GCAACGGTGG 420
CGTCATGCTG TACCGCTACG TGCTGGAGCT CCTGCAGACC CGTCGCTTCT GCCGCCGTGG 480
TGTTGGTGGC ACCATCTTTG ACAGCGCTCC TGGTGACAGC AACCTGGTAG GGGCTCTGGG 540
35 GGCCCTGGCA GCCATCCTGG AGCGCCGGGC CGCCATGCTG GGCCTGTTCG TGCTGGTGGC 600
CTTTGCCCTG GTGGTGTTC TGTTCACGT CCTGCTTGCT CCCATCACAG CCNTCTTCCA 660
40 CACCCACTTC TATGACAGGC TACAGGACGC GGGCTCTCGC TGGCCCGAGC TCTACCTCTA 720
CTCGAGGGCT GACGAAGTAG TCCTGGCCAG AGACATAGAA CGCATGGTGG AGGCACGCCT 780
GGCACGCCGG GTCTGGGCG GTTCTGTGGA TTTCTGTGCA TCTGCACAG TCAGCCACCT 840
45 CCGTGACTAC CCTACTTACT ACACAAGCCT CTGTGTGAC TTCATGCGCA ACTGCGTCCG 900
CTGCTGAGGC CATTGCTCCA TCTCACCTCT GCTCCAGAAA TAAATGCCTG ACACCTCCCC 960
50 ACAAAAAAAAA AAAAAAAAAA ACTCGAGGGG GGGCCCGGTA CCCAATTCGC CCTATAAAGG 1020
T 1021

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(2) INFORMATION FOR SEQ ID NO: 146:

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1285 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

	GGCACGAGGA GGGCCACGGC AGCCATCGCG CTTTGCAGTT CGGTCTCCTG GTGTACGGCC	60
	AACGCCAAGT AGGGGATTGC GTTCCCTCCA GTCGCAGACC CTATCAGATT TGGATATGTC	120
10	CTTCATATTT GATTGGATTT ACAGTGGTTT CAGCAGTGIG CTACAGTTTT TAGGATTATA	180
	TAAGAAACT GGTAAACTGG TATTTCTTGG ATTGGATAAT GCAGGAAAAA CAACATTGCT	240
15	ACACATGCTA AAAGATGACA GACTTGGACA ACATGTCCCA ACATTACATC CCACTTCCGA	300
	AGAACTGACC ATTGCTGGCA TGACGTTTAC AACTTTTGAT CTGGGTGGAC ATGTTCAAGC	360
	TCGAAGAGTG TGGAAAACT ACCTTCCTGC TATCAATGGC ATTGTATTTC TGGTGGATTG	420
20	TGCAGACCAC GAAAGGCTGT TAGAGTCAA AGAAGAACTT GATTCACTAA TGACAGATGA	480
	AACCATTGCT AATGTGCCTA TACTGATTCT TGGGAATAAG ATCGACAGAC CTGAAGCCAT	540
25	CAGTGAAGAG AGGTTGCGAG AGATGTTTGG TTTATATGGT CAGACAACAG GAAAGGGGAG	600
	TATATCTCTG AAAGAACTGA ATGCCCGACC CTTAGAAGTT TTCATGTGTA GTGTGCTCAA	660
	AAGACAAGGT TACGGAGAAG GCTTCCGCTG GATGGCACAG TACATTGATT AACACAACT	720
30	CACATTGGTT CCAGGTCTCA ACGTTCAGGC TTAATCAGAG ATTTGATTGC TCAACATGCA	780
	TAACCTGAAT TCAATAGACT TTTGCTGGTT ATAAACAGA TGTTTTTTAG ATTATTAATA	840
35	TTAAATCAAC TTAATTGAA TGAGAATTGA AACTGATTC AAGTAAGTTT GAGTATCACA	900
	ATGTTAGCTT TCTAATTCCA TAAAGTACT TGGTTTTTAC AGTTTATAAT CTGACATCAC	960
	CCCAGCGCCA TTTGTAAAGA GCAACTTTCC AGCAGTACAT TTGAAGCACT TTTTAACAAC	1020
40	ATGAACTAT AAACCATATT TAAAGCTCA TCATGTTAAA TTTTATGT ACTTTTCTGG	1080
	AACTAGTTT TAAATTTTAG ATTATATGTC CACCTATCKT AAGGTACAG TTAATAATTA	1140
45	GCTTATTCAA TGATTGCATG ATGCCTTACA GTTTCAATA ACTTTTTTTC TTATGCAAAC	1200
	GTCATGCAAT AAAACAACT CTAATGTTTG GCAAAAAAAA AAAAAAAAAA NTCGAGGGGG	1260
50	GGCCCGTACC CAATTCGCCC TAAAG	1285

55 (2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
60 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

5	GGCACGAGGT GCGCAGGGG TCAGTGGTTC TCTCGGGTCT CGGCACAGGT GAGCACCOCTG	60
	ATGAAGGCCA CGGTCTTGAT GCGGCACCTG GCGGGGTGCA GGAGATCGTG GCGGCCCTCC	120
	GCAAGGGCGS CGGAGACCGG TTACAGGTGA TTTCTGATTT TRACATGACC TTGAGCAGGT	180
10	TTGCATATAA TGGAAAGCGA TGCCCTTCTT CTTACAATAT TCTGGATAAT AGCAAGATCA	240
	TCAGTGAGGA GTGTCGAAA GAGCTCACAG CGCTCCTTCA CCACTATTAC CCAATTGAGA	300
	TCGACCCACA CGGACCGTC AAGGAGAAGC TACCTCATAT GGTGGAATGG TGGACCAAAG	360
15	CGCACAACTCT CCTATGTCAG CAGAAGATTC AGAAGTTTCA GATAGCCAG GTGGTTAGAG	420
	AGTCCAATGC AATGCTCAGG GAGGGATATA AGACCTTCTT CAACACACTC TACCATAACA	480
20	ACATTCCCCT TTTTATCTTT TCTGCGGCA TTGGTGATAT CCTGGAAGAA ATTATCCGAC	540
	AGATGAAAGT GTTCCACCCC AACATCCACA TCGTGTCTAA CTACATGGAT TTTAATGAAG	600
	ATGGTTTTCT CCAGGGATTT AAGGGCCAGC TGATACACAC ATACAACAAG AACAGCTCTG	660
25	TGTGTGAGAA CTSTGGTTAC TTCCAGCAAC TTGAGGGCAA AACCAATGTC ATCCTGCTGG	720
	GAGACTCTAT CGGGACCTC ACCATGGCCG ATGGGGTTCC TGGTGTGCAG AACATTCTCA	780
30	AAATTGGCTT CCTGAATGAC AAGGTGGAGG AGCGGCGGGA NCGCTACATG GACTCCTATG	840
	ACATCGTGCT GGAGAAGGAC GAGACTCTGG ATGTGGTCAA CGGGCTACTG CAGCACATCC	900
	TGTGCCAGGG GGTCCAGCTG GAGATGCAAG GCCCTGAAG GCGCAGGCTN CCAGNCCGCC	960
35	TGCAGGCCGT GGTGAGGAGG GCGCCTCCC CAGAGTCTGC TCCCCGTGA ACACAGAGCA	1020
	GANGCCAGGG TGGCCAGCAG TGGCTGGGTC CTTCCGCGCC CCTCCGTCTT CCTTTCCCTG	1080
40	AGCACCTTCA TCACCAGAGG CTTGAAGGAA CCCCGCCATG TGGCAGGGCA CAGGCACTGT	1140
	TCCTGGTGAA CCTTGGACCA CAGCATGTCA GTGCTCTAGG GATTGTCTAC TCCAGGGATT	1200
	TTCTTCAAAA TTTTTAAACA TGGGAAGTTC AAACAAATAT AATGTGTGAA ACAGATCAAA	1260
45	ATTTTAAAAA TGAATAAAAA GCTGCTCTGA TTCAGGGGAT GTGGGTGGG GTAGAACCTG	1320
	GACCTCTTGG CCTGGGGGCA CATGGGATGC TTCTAGGAAC ACAGTTTGAG AACCACCAAA	1380
50	AAAAAA	1386

55 (2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2098 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

5	AGCCCTTCTC CCCGCGCTTG GGA CTCTGAC ATCTTAAGGC TGCACGGTCG TGTCCTTGTC	60
	TGGGTGAGGC CATGTCTGTG ATCCAAGGTT CCTGGAAC TG ACACAGGAAG GGGCTGTGAA	120
	CCCTAAGTGG GTGTMATCTC CTCRACOGA GGCTCTMAC CCTGGAGATG GCAGTTACTC	180
10	CTGGCCATGG TTGCTGAGCA TGGGCAGACC AGTGGAGGCC ACCCTACTGT GTTATCTGG	240
	CCTTCRATGA AGTGAGACCC TTGGGGAGAA CGGGCTGTGG ATGAAGGAGT GGACTGCAGC	300
15	CTTGGCCTAG CCACTGGGCT GGGATCTTCT GGGTCATGTG ACTGTGTATC CAGGAGCAGA	360
	AACTGTATT CTCAGGATTC AGGATCTACC CAGCACCAA GATGTATTTT CAGGAGAACA	420
	GACCTAGAAA TGGGCTGTG TGGCATTTCA GAGTCAGCA AAGCAGGCAG GGCCAGGGAG	480
20	CTTCTGTGGG TCTACACAAG AAGGTTCTTG TGAGGGCTAT CAGTTGTTCG CTCTAGCTT	540
	GCTGGTAACT TTGGCGCCTC CGCCAAGCCC TGCCAGACTC CCTGGCTGT GATGGCATT	600
25	TGTGCCATCC TGCTTTGTCC CCAGCCTCTG CAGGATGCCC TCCCTACCCA MCTYTYCCTG	660
	GGCCTTCCCT GTCCACTGGG CTGGATTTCAT GTTCAAACCA CTGGACTGGC AGGGCAACGA	720
	CTTCTTCCCA CCTCAAGATG AGGTCTCTGC CCCCTGTCT TGGCATAAAA ACACCTTTAA	780
30	AGCATGAGCC ATGTGCTTCT TTGCCCTTCT CTGTCTGTG TCAATCTTCT GCCTCCAGT	840
	CACTCCCTGG GGACTATGGG ATCACTGTCC CCCCACCTGT GTGGCCACAC CATGTGCTCT	900
35	GTCAATCCAG AACTGCCTCT GAGCTCCAGG CTGACCACAG ATCAGCCACA GCCTGATGCC	960
	TGCAGCCCCA CTTTGCTCAC CCTTCCCTC CCTTCTCT TCCCTCCACA CAGCAAGCCT	1020
	ACCTTTYTCC ATCCATGCTC ACCATAGCCC CCTTCTTGT GACCTGGACC CTCCATGTGA	1080
40	CCTGGCTGAG ACTGTCAGCC TCCTGGAGGA GTGGGGTCCA CCTTCTTCTT GCCCTATGCA	1140
	GTGCAAGCTT CACTTCTCAC CCAGCAAGGT TGA CTCTCT GCCTCCATGT CTCTGGGGCT	1200
45	TTGCTGTTCG CCTGAAACCT AGCTGGGCTG GTCTTGCTCC CAGCTTGCTT CCCCCTCTC	1260
	GGATGTCCCT TTGCAGGCCC CTGTGCTTCC TCCGGCACCA GTGTCTTGG CTGCCATGGC	1320
	AAGCTCATCA GGGGCTTGTA CCTGGTCAC CAAGCATGGT AGCAGCTGCC TGCATTGTAT	1380
50	CTCCATCTGG TCACGTCAGG TGCCAACCT TCATCCCCA TGTTTTCTTG GGCCATGGAG	1440
	GGCTGACCTC CGTTTCTGGG GAATGTGGCT GAGCTGTGGT AACCAGCTAC ACCCCAGGTG	1500
55	CTCTTTCCAT GGTGGTGCCT GCTCATCTTG CTGATGCAAA CTAGGAAGTT AGGCTGCATC	1560
	TCGGAGTGGC TTTCGCTGGA GAGGTGCTTT GCTGTCTCTC AGACTCAGTC ACTGTGTTC	1620
60	CTCCCCGCTT CTCTTATCTC CATGGCTGTT TGCAGCTCTC CCAGGTACTT TGGGGTCTGA	1680

GCTGGAATTC CTTGTGGTT TGCTCTCTG CTTCTCACTC TTGTATTAAG AAGGATTCCA 1740
 CAAAGGGAGA GTGGCATCCC TGCTGCTGCT GTGCCAGACC AGAGTTTCCT GAGGGGCCCT 1800
 5 GACCCTAACC CTCCAGCTCA GCCCTGTACA CCTGACCCCTG TAAATGAGTG GGGTTTGCTG 1860
 ACTGTAATCC CTGACACCAG TAAACCAAAA AGGACTCTTG GGGGCTCAGT GTGAGAGCCA 1920
 GGGTTACCTA CTCTGCCAAG TGAGGACAAA CTGCTAGGCT GTATCCATA ATTTTCAGGAT 1980
 10 GAGAAACATT AACAATAAAA ATTTGTAGTA AACATAACCT CATGANGACT AAAAAAAAAA 2040
 AAAAACTYGG GGGGGGCCG GTAACCCATT GGGCCCTTNG GGGGGGNGTT TTAAAATT 2098

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(2) INFORMATION FOR SEQ ID NO: 149:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1847 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

TCGACCCACG CGTCCGAACT GAGGCGGCGG CGGGAGCCGG TTGGKGTCTG GTCTTCGCGT 60
 30 CGGCCCCCGG GACCAGACGC TGCCCCCGGC GCGGGGAGAA GATGGTGCK AGCGGCCCTG 120
 GGCCCGCCAC GCGCCGCCAC GAGTGAGCCC AGCGGACCG CGGGCGTCCG CCGAGCAGCT 180
 GGCCCGGCTG GGCCCGGGG GCGCANTGCC CGCCGGGGCG GGGTGGAGCT GATCAGAATA 240
 35 ATGTTTCAGCA TCAACCCCTT GGAGAACCTG AAGGTGTACA TCAGCAGTCG GCCTCCCCCTG 300
 GTGGTCTTCA TGATCAGCGT AANGCCCATG GCCATAGCTT TCCTGACCCT GGGCTACTTC 360
 40 TTCAAATCA AGGAGATTAA ATCCCCAGAA ATGGCAGAGG ATTGGAATAC TTTTCTGCTA 420
 CGGTTCAATG ATTTGGACTT GTGTGTATCA GAGAATGAAA CCTCAAGCA TCTCACAAC 480
 GACACCACAA CTCCGAAAG TACAATGACC AGCGGGCAGG CCGAGCTTC CACCCAGTCC 540
 45 CCCCAGGCC TGGAGGACTC GGGCCCGGTG AATATCTCAG TCTCAATCAC CCTAACCTG 600
 GACCCACTGA AACCCCTTCG AGGTATTCC CGCAACGTCA CCCATCTGTA CTCAACCATC 660
 50 TTAGGGCATC AGATTGGACT TTCAGGCAGG GAAGCCACG AGGAGATAAA CATCACCTTC 720
 ACCCTGCCTA CAGGTGGAG CTCAGATGAC TGCGCCCTCC ACGGTCAGTG TGAGCAGGTG 780
 GTATTACAG CCTGCATGAC CCTCACGGCC AGCCCTGGGG TGTTCCTCGT CACTGTACAG 840
 55 CCACCGCACT GTGTTCTGA CACGTACAGC AACGCCACGC TCTGTACAA GATCTTCACA 900
 ACTGCCAGAG ATGCCAACAC AAAATACGCC CAAGATTACA ATCCTTTCTG GTGTTATAAG 960
 60 GGGGCCATTG GAAAAGTCTA TCATGCTTTA AATCCCAAGC TTACAGTGAT TGTTCAGAT 1020

5 GATGACCGTT CATTAATAAA TTTGCATCTC ATGCACACCA GTTACTTCCT CTTTGTGATG 1080
 GTGATAACAA TGTTTTGCTA TGCTGTTATC AAGGGCAGAC CTAGCAAATT GCGTCAGAGC 1140
 AATCCTGAAT TTTGTCCCGA GAAGGTGGCT TTGGCTGAAG CCTAATTCCA CAGCTCCTTG 1200
 TTTTGTGAGA GAGACTGAGA GAACCATAAT CCTTGCTGTC TGAACCCAGC CTGGGCTTGG 1260
 10 ATGCTCTGTG AATACATTAT CTTGCGATGT TGGGTTATTTC CAGCCAAAGA CATTTCAAGT 1320
 GCCTGTAACT GATTTGTACA TATTTATAAA AATCTATTCA GAAATTGGTC CAATAATGCA 1380
 CGTGCTTTGC CCTGGGTACA GCCAGAGCCC TTCAACCCCA CCTTGGACTT GAGGACCTAC 1440
 15 CTGATGGGAC GTTCCACGT GTCTCTAGAG AAGGATTCCT GGATCTAGCT GGTACGACG 1500
 ATGTTTTCAC CAAGGTCACA GGAGCATTGC GTCGCTGATG GGGTTGAAGT TTGGTTTGGT 1560
 20 TCTTGTTTCA GCCCAATATG TAGAGAACAT TTGAAACAGT CTGCACCTTT GATACGGTAT 1620
 TGCATTTCCA AAGCCACCAA TCCATTTTGT GGATTTTATG TGTCTGTGGC TTAATAATCA 1680
 TAGTAACAAC AATAATACCT TTTTCTCCAT TTGCTTGCA GGAACATAC CTTAAGTTTT 1740
 25 TTTTGTTTG TTTTGTTTT TTTGTTTTT GTTTTCCTTT ATGAAGAAAA AATAAAATAG 1800
 TCACATTTTA ATACTACCAA AAAATGGACA AAAAAAGTCG AGGGGGG 1847

30

(2) INFORMATION FOR SEQ ID NO: 150:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1569 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

GACGCTGACG AGAGAAGGCC TCTTCCTTGA GGGTTGGTGC TGTGTTGCAG TGACCGTGGC 60
 45 GGATTACGCC AACTCGGATC CGCGGTCGT GAGGTCTGGA CGAGTCAAGA AAGCCGTAGC 120
 CAACGCTGTT CAGCAGGAAG TAAATCTCT TTTGCGCTTG GAAGCCTCTC AGGTTCTCTG 180
 AGAGGAAGCT CTTTCTGGGG CTGGTGAGCC CTGTGACATC ATCGACAGCA GTGATGAGAT 240
 50 GGATGCCCGAG GAGGAAAGCA TCCATGAGAG AACTGTCTCC AGAAAAAGA AAAGCAAGAG 300
 ACACAAAGAA GAACTGGACG GGGCTGGAGG AGAAGAGTAT CCCATGGATA TTTGGCTATT 360
 55 GCTGGCCTCC TATATCCGTC CTGAGGACAT TGTGAATTTT TCCCTGATTG GTAAGAATGC 420
 CTGGAAGTGC ACTTGCACTG CTGCCTTTTG GACCAGGTTG TACCGAAGCA CTACACGCTG 480
 GATGCTTCCC TGCCTTTGCG TCTGCGACCA GAGTCAATGG AGAAGCTGCG CTGTCTCCGG 540
 60

	GCTTGTGTGA TCCGATCTCT GTACCATATG TATGAGCCAT TTGCTGCTCG AATCTCCAAG	600
	AATCCAGCCA TTCCAGAAAG CACCCCCAGC ACATTAAAGA ATTCCAAATG CTTACTTTTC	660
5	TGGTCAGAA AGATTGTTGG GAACAGACAG GAACCAATGT GGGAAATCAA CTTCAAGTTC	720
	AAAAAACAGT CCCCTAGGTT AAAGAGCAAG TGTACAGGAG GATTGCAGCC TCCCCTTCAG	780
10	TACGAAGATG TTCATACCAA TCCAGACCAG GACTGCTGCC TACTGCAGGT CACCAACCTC	840
	AATTTCACTCT TTATTCCGAT TGTCATGGGA ATGATATTTA CTCTGTTTAC TATCAATGTG	900
	AGCACGGACA TCGGCATCA TCGAGTGAGA CTGGTGTTC AAGATTCCCC TGTCCATGGT	960
15	GGTCGAAAC TCGCAGTGA ACAGGGTGTG CAAGTCATCC TGGACCCAGT GCACAGCGTT	1020
	CGGCTCTTTG ACTGGTGGCA TCCTCAGTAC CCATTCTCCC TGAGAGCGTA GTTACTGCTT	1080
20	CCCATCCCTT GGGGGCAGCC TCGAGTGTAG TCCATTAGTA ATCAGATTCC AGTTTGGACA	1140
	GGGTGGCTGG ATTGTATATC TCGTTAGTAA TGTACATGCT CTTCAGGTC TAGGGCTCCT	1200
	GTTAGGGGAG GGAGAAATGT TGAATCAAGA GGGAAAACAA CTACTATGAT TTATAAACAT	1260
25	ATTTTAATGT AAAAATTGTC ATTTAAAAGG AGTGGCCCTG TTTTCTGTGT TAAAACCCCA	1320
	TTTGGTGCTA TTGAGTTTGT TCTTTATTCT TTTATCCCAG TGAAAATTGT TGATCTTGCT	1380
30	GTAGGGAAAA ATTAACTCT TTGAATCTCC AAACAAGGAA GTTTCAGCAT TCCCTTATGG	1440
	ATCAGAGGAA CCTTAGAGGC CTGAAATTGT TGCTTCCAGT TTAGCTGCCC CTCAAATTCA	1500
	AGTGAATATT TTCCCTTCTC CCTTTACCCT TCTCCAGAAA TAAAGCAGGT GACAGGGTTT	1560
35	CAGAACTCT	1569

40 (2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1540 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

50	CCCACGCGTC CGGAAGGATT GACCAGTTAA CCAACATCTT AGCCCCCATG GCTGTTGGCC	60
	AGATTATGAC ATTTGGCTCC CCAGTCATCG GCTGTGGCTT TATTTGCGGA TGGAAGTTGG	120
55	TATCCATGTG CGTGGAGTAC GTCTGCTCT GGAAGGTTTA CCAGAAAACC CCAGCTCTAG	180
	CTGTGAAAGC TGSTCTTAAA GAAGAGGAAA CTGAATTGAA ACAOCTGAAT TTACACAAAG	240
	ATACTGAGCC AAAACCCCTG GAGGGAAGTC ATCTAATGGG TGTGAAAGAC TCTAACATCC	300
60	ATGAGCTTGA ACATGAGCAA GAGCCTACTT GTGCCTCCCA GATGGCTGAG CCCTTCCGTA	360

5 CCTTCCGAGA TGGATGGGTC TCCTACTACA ACCAGCCTGT GTTCTGGCT GGCATGGGTC 420
TTGCTTTCCT TTATATGACT GTCCTGGGCT TTGACTGCAT CACCACAGGG TACGCCTACA 480
CTCAGGGACT GAGTGGGTTT CATCCTCAGT ATTTTGATGG GAGCATCAGC TATAACTGGA 540
ATAATGGGAA CTGTAGCTTT TACTTGGCTA CGTCGAAAAT GTGGTTTGGT TCGGCAGGTC 600
10 TGATCTCAGG ATGGGCACAG CTTTCTGTG TGATCTGTG TGTGATCTCT GTATTCATGC 660
CTGGAAGCCC CCTGGACTTG TCCGTTTCTC CTTTGAAGA TATCCGATCA AGGTTTCATT 720
AAGGAGAGTC AATTACACCT ACCAAGATAC CTGAAATTAC AACTGAAATA TACATGTCTA 780
15 ATGGGTCTAA TTCTGCTAAT ATTGTCCCGG AGACAAGTCC TGAATCTGTG OCCATAATCT 840
CTGTCACTCT GCTGTTTGA GCGTCATTG CTGCTAGAAT CCGTCTTTGG TCCTTTGATT 900
20 TAACTGTGAC ACAGTTGCTG CAAGAAAATG TAATTGAATC TGAAAGAGGC ATTATAAATG 960
GTGTACAGAA CTCCATGAAC TATCTTCTTG ATCTTCTGCA TTTCATCATG GTCATCCTGG 1020
CTCCAAATCC TGAAGCTTTT GGCTTGCTCG TATTGATTTC AGTCTCCTTT GTGGCAATGG 1080
25 GCCACATTAT GTATTTCCGA TTGCCCCAAA ATACTCTGGG AAACAAGCTC TTTGCTTGGG 1140
GTCTGATGC AAAAGAAGTT AGGAAGGAAA ATCAAGCAAA TACATCTGTT GTTTGAGACA 1200
30 GTTTAACTGT TGCTATCCTG TTACTAGATT ATATAGAGCA CATGTGCTTA TTTTGTACTG 1260
CAGAATTCCA ATAAATGGCT GGGTGTTTTG CTCTGTTTTT ACCACAGCTG TGCCTTGAGA 1320
ACTAAAAGCT GTTTAGGAAA CCTAAGTCAG CAGAAATTAA CTGGATTAAAT TTCCCTTATG 1380
35 TTGAGGGCCA TGGRAAAAAA ATTGGGAAAA GGAAAACTC AGTTTTAAAT ACGGGAGACT 1440
ATAATGGATA ACACTGRATT CCCCTATTTC TCATGAGTAG ATACAATCTT ACGTAAAAGA 1500
40 GTGGTTAGTC ACGTGAATTC AGTTATCATT TGACAGATTC 1540

45 (2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1719 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

55 TACTTATGAG GTCAATTGGA AATAAGAACA CCATTTTACT GGGTCTAGGA TTTCAAATAT 60
TACAGTTGGC ATGGTATGGC TTTGGTTTCA AACCTTGGAT GATGTGGGCT GCTGGGGCAG 120
TAGCAGCCAT GTCTAGCATC ACCTTTCCTG CTGTCACTGC ACTGTGTTCA CGAACTGCTG 180
60

	ATGCTGATCA ACAGGGTGTC GTTCAAGGAA TGATAACAGG AATTCGAGGA TTATGCAATG	240
	GTCTGGGACC GGCCTCTAT GGATTCATTT TCTACATATT CCATGTGGAA CTTAAAGAAC	300
5	TGCCAATAAC AGGAACAGAC TTGGGAACAA ACACAAGCCC TCAGCACCAC TTTGAACAGA	360
	ATTCCATCAT CCTGGCCCT CCTTCCTAT TTGGAGCCTG TTCAGTACTG CTGGCTCTGC	420
10	TTGTTGCCTT GTTTATTCCG GAACATACCA ATTTAAGCTT AAGGTCCAGC AGTTGGAGAA	480
	AGCACTGTGG CAGTCACAGC CATCCTCATA ATACACAAGC GCCAGGAGAG GCCAAAGAAC	540
	CTTTACTCCA GGACACAAAT GTGTGACGAC TGAAATCAGG AAGATTTTTC TATCAGCACC	600
15	CAGGCTTAG TTTTCACCTC TAGTTCTGGA TGTACATTCC ATTTCCATCC ACAGTGTACT	660
	TTAAGATTGT CTTAAGAAAT GTATCTGCAT GAACTCCGTG GGAACATAAG GAAGTGGGAA	720
20	CTTAGAACCA GACAGTTTC CAAAGATGTT ACAATTCTT TTGAAAAACC TTTTGTATTAT	780
	TAGCACCAAT TTCTYGCCAC TAAGCTATTT GTTTTATTAT ACATCCTTTA ATTAATAACT	840
	ATATATGTAA CTTCTTAGAT ATTAGCAAAT GTCTCTGCTA CCATTTCTTT AAGGTGTTGA	900
25	GCTTTAATC TATGCTGACT CAGTGAGACA CAGTAGGTAG TATGGTTGTG GACCTATTTG	960
	TTTTAACATT GTAAAATTTT GAGTCAGATT TTAATATTGT AAAATCTTGG GTCAAATAAT	1020
30	TCAAAGCCTT AATGCAGATG CACTAAACA AAGAAATGGT AAATGAATTG TTTGCATTTA	1080
	AAAAAAAAAA CTCTTAAGAA AACTGTACTA AATCTGAATC ATGTTTGTAG CTTGTTTGCA	1140
	GTACTTTTAA ACATTATTCA CTACTGTTT TGAAGTGAGA AAGTATCAGC CATTTAGCAT	1200
35	TTAAGTTGGG GTATTTAGAG CCTGTAATCT AAATGCTGGC TCAAATTTAT TCCCAGCTA	1260
	CTTCTTATAC CACTATTCTT TTAATGTTTG CATAATCATA AGCACCTCAA CACTTGAATA	1320
40	CATAATCTAA AAATTATATA GTAAAGCTGG TAGCCTTGAA AATGTCAGTG TGATATCTAT	1380
	TATGTAGATA AATATATATA GTGGCCTTTC AGGACTGTCA CAGTAACACT TTATTTACAG	1440
	AGCTAATGTT TGTCTTAAAT TTTCAGGACC CTAGAGGAGA GCTTTATACA ATTACCGATG	1500
45	TGAATTTCTC TAAAGTGAT ATTTTGTGT CCAGTTATAT TATTTAAAAA AGTGTTACTT	1560
	TGTAAAAATT GTATATAAAG AACTGTATAG TTTACACTGT TTTCATCTTG TGTGTGGTTA	1620
50	TTGCTTAATG CTTTTTAAAC TTGGAACACT CACTATGGTT AAATAAGGTC TTAAAAGAAA	1680
	TGTAAATATT YGTTAATAA AGTTAAATAT TTTAATGAT	1719

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(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 863 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

5 GGCACGAGGG AAGCCGGGAC GATGTCGCA TGACAACCGA CGTTGGAGTT TGGAGGTGCT 60
TGCCTTAGAG CAAGGGAAAC AGCTCTCATT CAAAGGAACT AGAAGCCTCT CCCTCAGTGG 120
10 TAGGGAGACA GCCAGGAGCG GTTTTCTGGG AACTGTGGGA TGTGCCCTTG GGGGCCGAG 180
AAAACAGAAG GAAGATGCTC CAGACCACTA ACTACAGCCT GTGCTCTCT CTGCAGTTCC 240
15 TGCTGCTGTC CTATGACCTC TTTGTCAATT CCTTCTCAGA ACTGCTCCAA AAGACTCCTG 300
TCATCCAGCT TGTGCTCTTC ATCATCCAGG ATATTGCAGT CCTCTTCAAC ATCATCATCA 360
TTTTCTCAT GTTCTTCAAC ACCTTCGTCT TCCAGGCTGG CCTGGTCAAC CTCTATTCC 420
20 ATAAGTTCAA AGGGACCATC ATCCTGACAG CTGTGTAATT TGCCCTCAGC ATCTCCCTTC 480
ATGTCGGGT CATGAACCTA CGCTGGAAAA ACTCCAACAG CTTCATATGG ACAGATGGAC 540
25 TTCAAATGCT GTTTGTATTC CAGAGACTAG CAGCAGTGTT GTACTGCTAC TTCTATAAAC 600
GGACAGCCGT AAGACTAGGC GATCCTCACT TCTACCAGGA CTCTTTGTGG CTGCGCAAGG 660
AGTTCATGCA AGTTCGAAGG TGACCTCTTG TCACACTGAT GGATACITTT CCTTCCTGGA 720
30 TAGRAGGCCA CATTGCTGC TTTGCAGGG AGAGTTGGGC CCTATGCATG GGGCAAACA 780
GGTGGGATTT TCCAAGGGAA GGTTTCAGAA TTAGGCNTGT TGTTCAGCC ATTTCCAAGG 840
35 AAGGGGAAGG GTTCCCTNC CCT 863

(2) INFORMATION FOR SEQ ID NO: 154:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

50 AACAGCAAAA AAGAATGATT TCTTCTGAAA TTGTGGAACA TGAGGATTCA AGTTTTTATT 60
TTGTACTAG GTGCTGGAGG AACATCCCAG TTCACAAAGC CCCCATCTCT TCCTCTGGAG 120
CCAGAGCCTG CGGTGGAATC AAGTCCAAC TAAACATCAG AACAAATAAG AGAGAAATAA 180
55 GAATAGAATG AATGACCCCA AAATARGTT TTCTTGGGCG AGGATGTGCT GGATTAGGAA 240
AGGTGACATG ACACAGGCAG AGCAGAGTGG CACCCACCAC AGAATACAGT GTGTGTTATT 300
ACGAGGAGCC AGCAGTTGAG CCTAAGGTCC TTCTACCTAC CTGGTATTGG CATTGAGGT 360
60

	CGGAAACCCCT CTA CTGCCCC ATAAGCCAGG AAAAGTGAAA AGAGAACACA GTTCCTTTAA	420
	GAAGCTGGCAG CAAGGCTTGA GGCCTTATGT ATGTAGCTGA GTCAGCAAGG TACATGATGC	480
5	TGCTCTGCTT CAAAAGGACT TTTCTCTCCT AGCTGACTGA CTCCTTCCTT AGTTCAAGGA	540
	ACAGCTGAGA CAGACCTCTG CTGAGTAGCT CTGTGATGAC AAAGCCTTGG TTTAACTGAG	600
10	GTGATCCTCA GGTGTGAGG TTTATTAGTC CCCAAGGCAA ACACAAATAT TAGATTAATA	660
	ATCCAACCTT AATAGTATAC ATTTAAAGA AAAAAACAA AAGCCCTGGA AGNTTGAGGC	720
	CAAGCCTGCT GAGTATTGCA GCTGCATTG CCCAAAGGGA ATCCAGAACA AGTCCCTCCC	780
15	TGTATTTTGT TCTTGAGAGG GGTGAGTCTA GAAGCTAGAT CCTATCAGGA TGAGGAGCAG	840
	CAGCCAGGG CTGTCTGGA TCAGCACCAA CGATTTTAAA GAAAAAGGA AGAGTTTCTT	900
20	AGATGAGTAA TTGTTATTGA AGATAGTCAG TGATAACCAC TGACCAGATG CTATCAATAC	960
	ACTATGTGTC CTTTTAGAA TAAAGATTAC ATATCATCAT TCCTTTGGGG AAAATGTGTA	1020
	TTGAGGTATA AAAACAAGAG ATTATAATAA AAAANTAAAA GAACCCTAAA AAAAAAAAC	1080
25	CTCGTGCCGA ATCCCTGCA G	1101

30 (2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 2031 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

40	CAATTAACCC GTTTGAGGCC TAGGTGTTT GGCAAGCCCC NGGCCTAAAG TTTTAATTGC	60
	GCAGAGCCAA GGGCTGAAA GGAAGGGAAA GGGGAGGGTA GCGGGAGGGT AGCAGGTGAG	120
45	TTCTAGGGC TGGAAGGTTT AGCAGCAGCC TGGTGCACTG CCCTGTCTATC AAGACAAACC	180
	CACGGTCTC CTGGGTGCCT ACCAAGCTTG GTTGTACAA AAGCAAGGTG GGAGTCTATT	240
	TTGTACATG AGATACATCA CACTTACCTG TGGGCCAGTA TTGTGAAGTG AGTCTGAGTT	300
50	GTTTACACTG ATGCCTTCCC TGCCACCAC AAATGTGTGA CATAGTCTTC AGAATGATAC	360
	CACCCCTTTC CCCAGCTCCC AACCAAGAGC TGGTTCTAGG CCTGTGTTAT ATGTCATATT	420
55	TAGCGTTTTT ATATATGACC TTGATTCTT GTTGTGTGTA TTTTAGCACA GTGTATGCAC	480
	CTTCATTTAA ATACATCTGT GTGCATACAG ATAOCATAT ATGTGTGTGC GTATGCATAT	540
	ATCTCTCATC TGTAGTTTCC AAGAGTTCAG CTGAAGCAGA TGGAGTCCTG CAGCCCAGGA	600
60	GACACCCTGC ATCCCTGCTA ATAGTGTTTG CCACAAGTAT TAGTGAGTCT TCCTTATTAA	660

TATTTTCATT TCAGAAGACT GAAGCAAAGC TGATAGTGT TGCTGTTTCT TTGGCAGCTA 720
AGTGAGGGTC TTGGGATGAC TTGCTGTGTT CCTCAAGCTG CACTTTGGGG CCATCTCTGC 780
5 AGTATTAAGC CCCCTTTTGT CTGCGTGTA CTCTGTCTGT GCCTGTGTGT GTGTGTGATA 840
GTCACCTTG CATGGCTTC ATGTCTGGTT TGTGGCATTT GGGGATAAGT GCTGAACCAAG 900
10 AGCATTTGCA GTTGTGTTGA GGCCTCGTTG CCAATGATAG ATCACTCCTG TTGACCTGGT 960
ATGTCTGCTT GCTGCTGCT TTTCTTGCT TTCTCTTGGA AGAGGAAAGG ACTCTGGTCA 1020
GGCCCAGGCT GAGTGAGATG AGCTGCAGCT GGCTCATGGC CTTCTTAGAG CAGAGAGAGG 1080
15 AGTATGTCAT TTTACTAAGT TCCTAAACAA ACATTTATGC AGGCAACACT CCTTGCGAT 1140
CCAGAACTG AGGCACAATA GGGTTATGAC TTGCTCAAGA ATATGTAGCT GCTAGGGGGT 1200
20 AAATCAAGGC ATCACAATTT CTGTCAGCG GGCAGGAATA GGCTGTGAAT TGCTAGCACT 1260
TTTTTTTAA GCAATTACTT TTTGACTTGT TCCTCTGAAA GTGCAAGAGG CGTACACCTT 1320
TCCCAATGT AGACTAGAAT CTGCAGGATG CCACCCACTG TATAGTTCTG CTTTCCAGA 1380
25 GAGGAAGAAC TTTTAGAAAC CAAATGATCT TAATTGTTAT TGCCACCCCC TGGCTTTTCC 1440
GGGTAGAAA TTCACAGTAG GAATGATTGT TAAGAGAGAG TGCTTGGAAC CATGGGTAA 1500
30 CAGGAAAGGC TACCTAACTT CACATATCTG CAACCAGAGC AGCCACCAAG CATTACTTAG 1560
CAGCAGGAAA ATGATTGTAT TTGAGTTCTT GTGTGTCCAA AACTGAGGCA CCATGTTCTT 1620
TGAAACATG CCACCTCAAG GCTGGGCGCG GTGGCTCACA CCTGTTAATC CCAGCACTTT 1680
35 GGGAGGCCGA GCGGGGCGGA TCACCGGAGT CGGGGAGTTT GAGACCAGCC TGGACCAACA 1740
TGGGAGAAAC CCCATCTCTA CCTAAAAATA CAAAATTAGC CGGGCGTGGT GGCATGCGCC 1800
40 TATAATCTCA GCTACTTGGG AGGGYTGAGG CAGGRGAATT GCTTGAACCC RGGANGGCGG 1860
AGGTTTGCGG TTGAGTTGAG GATCGTGCCA TTGCACTTCC GGGCCTTGGG GCAACAACAG 1920
CAAAAAYTCC GTCTTCAAMW MRTGCCGAAT TCGATATCAA GCTTATCGAT ACCGTGACC 1980
45 TCGAGGGGGG GCCCGGTACC CAATTCGCCC TATAGNGATC GTATTACAAT C 2031

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(2) INFORMATION FOR SEQ ID NO: 156:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1981 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

	CCTGCACCTT	GAGCCCTTCA	CCCCCTCCGAG	TTCCCCCCAG	GTGGGCTTCC	TTGATTCCT	60
	TTTCTTGGTA	TCAACGTTTG	ATTGGAAGAA	CAACCCCTC	TTTGTCAACC	TCAATAATGA	120
5	GCTCACTGTG	GAGGAGCAGC	TCGGGCACAG	CTCMCCGTYA	TGGTCAITGT	TACCCCCCAA	180
	GACCGCAAAA	ACTCTGTGTG	GACACAGGAT	GGACCCCTCAG	CCCAGATCCT	GCAGCAGCTT	240
10	GTGGTCTCGG	CAGCTGAAGC	CCTGCCCATG	TTAGAGAAGC	AGCTCATGGA	TCCCCGGGGA	300
	CCTGGGGACA	TCAGGACAGT	GTTCCGGCCG	CCCTTGGACA	TTTACGACGT	GCTGATTTCG	360
	CTGTYTCTTC	GCCATATCCC	GCGGCACCGC	AGGCTTGTGG	ACTGCCCAGY	TGCCTCTCTC	420
15	TGCCGGGGCC	TGCTCAGCCA	GCCGGGGGCC	TCATCCCTGA	TGCCCGTGCT	GGGTNATGAT	480
	CCTNCTCAGC	TCTATCTGAC	GCAGCTCAGG	GAGGCCTTTG	GGGATCTGGC	CCTTTTCTTC	540
20	TATGACCAGC	ATGGTGGAGA	GGTATTGGT	GTCTCTGGA	AGCCACCAG	CTTCCAGCCG	600
	CAGCCCTTCA	AGGCCTCCAG	CACAAAGGGG	CGCATGGTGA	TGTCTCGAGG	TGGGGAGCTA	660
	GTAATGGTGC	CCAATGTGA	AGCAATCCTG	GAGGACTTTG	CTGTGCTGGG	TGAAGGCCTG	720
25	GTGCAGACTG	TGGAGGCCCG	AAGTGAGAGG	TGGACTGTGT	GATCCCAGCT	CTGGAGCAAG	780
	CTGTAGACCG	ACAGCAGGAC	ATTGGACCTC	TAGAGCAAGA	TGTCAGTAGG	ATGACCTCCA	840
30	CCCTCCTTGG	ACATGAATCC	TCCATGGAGG	GCCTGCTGGC	TGAACATGCT	GAATCATCTC	900
	CAACAAAACC	CAGCCCCAAC	TTTCTCTCTG	ATGCTCCAGC	ATTGGGGCAG	GGGCATGGTG	960
	GCCCCATGTAG	TCTCCTGGGC	CTCACCATCC	CAGAAGAGGA	GTGGGAGCCA	GCTCAGAGAA	1020
35	GGAAGTGAAC	CCAGGAGATC	CATCCACCTA	TTAGCCCTGG	GCCTGGACCT	CCCTGCGATT	1080
	TCCCACCTCT	TTCTTAGTCT	TCTTCCAGAA	ACAGAGAAGG	GGATGTGTGC	CTGGGAGAGG	1140
40	CTCTGTCTCC	TTCTGTCTGC	CAGGACCTGT	GCCTAGACTT	AGCATGCCCT	TCACTGCAGT	1200
	GTGAGGCCTT	TAGATGGGAC	CCAGCGAAAA	TGTGGCCCTT	CTGAGTCACA	TCACCGACAC	1260
	TGAGCAGTGG	AAAGGGGCTA	TATGTGTATG	AATAGACCAC	ATTGAAGGAG	CACAATGCCC	1320
45	TCCTGTGTG	ATGCCACTTC	CCAGGGTGA	GACAGTGGAA	AAGAACCGAG	GACAGGAAAG	1380
	GATTGGGTAG	GTGAAGGGGT	CAGGGGACTG	GTAGTCACCC	AATCTTGGAG	AGGTGCAAAA	1440
50	AGCACTGGGG	GCTACCCGTT	AGCTGCATCT	GCCCTGGCTG	TTTGCCCGTT	CATGTCACAA	1500
	ACTGCCACTA	CTATGTACCT	GCACTGGGGT	TGCAGAGATG	GGGAGACTC	AAGTCTTACT	1560
	CCCCAGGAGC	TCCCAGGGCC	CAAGGAGGAG	AATGCTGCCT	CCTTTCAGTC	TGGTCTACAC	1620
55	CCACTTCTG	GTAGCCTCTC	TGCTTCCTGT	AATTCTGGCT	GTPTTTCAG	ACTCAGCTCA	1680
	AATAGTCCCC	CTCCTTAAGC	CCATCCCTCG	CCCCCAGCCT	GAGGTGATCT	TTCCCTCCTC	1740
60	TGAAGTATTA	GAGCAGTTAC	TGTCTGTTC	GTTCTGTTGG	CAGGCACACA	CAGTGGCATA	1800

AATTCTATTG TTTTGAATC TGATTTAAAA TTAAATGCA GCTGGGCGTG GTGGCTCATG 1860
 CTTGTAATCC CAACACTTAG GGAGTMAGGR GAATCACTTG ASCYCAGGAG TYCTAGACCA 1920
 5 ATCTGGGCAA MAGAGAGACC CCATCTCTTT TAAATAAAAA GTTAAATGTC TTAAAAAAA 1980
 A 1981

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(2) INFORMATION FOR SEQ ID NO: 157:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 915 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

GAATTCGGCA CGAGCGGGC CATGGCGCTC CTGCTTTCGG TGCTGCGTGT ACTGCTGGGC 60
 GGCTTCTTCG CGCTCGTGGG GTTGGCCAAG CTCTCGGAGG AGATCTGGC TCCAGTTTCG 120
 25 GAGCGATGA ATGCCCTGTT CGTGCAGTTT GCTGAGGTGT TCCCGCTGAA GGTATTTGGC 180
 TACCAGCCAG ATCCCTGAA CTACCAAATA GCTGTGGGCT TTCGGAAC TCTGGCTGGG 240
 30 TTGCTGCTGG TCATGGGCC ACCGATGCTG CAAGAGATCA GTAAC TTGTT CTTGATTCTG 300
 CTCATGATGG GGGCTATCTT CACCTTGGCA GCTCTGAAAG AGTCACTAAG CACCTGTATC 360
 CCAGCCATG TCTGCCTGGG GTTCCTGCTG CTGCTGAATG TCGGCCAGCT CTTAGCCAG 420
 35 ACTAAGAAG TGGTCAGACC CACTAGGAAG AAGACTCTAA GTACATTCAA GGAATCCTGG 480
 AAGTAGAGCA TCTCTGTCTC TTTATGCCAT GCAGCTGTCA CAGCAGGAAC ATGGTAGAAC 540
 40 ACAGAGTCTA TCATCTTGTT ACCAGTATAA TATCCAGGGT CAGCCAGTGT TGAAAGAGAC 600
 ATTTTGTCTA CCTGGCACTG CTTTCTCTTT TTAGCTTAC TACTCTTTTG TGAGGAGTAC 660
 ATGTTATGCA TATTAACATT CCTCATGTCA TATGAAAATA CAAAATAAGC AGAAAAGAAA 720
 45 TTAAATCAA CCAAAATCT GATGCCCCAA ATAACCACTT TTAATGCCTT GGTGTAAGTA 780
 TACCTCTGAA CTTTTTCTG TGCCTTTAAA CAGATATATA TTTTTTTTWA ATGAAAATAA 840
 50 AACCATATAT CCTATTTTAT TTCTCTCTTT TAAACCTTA TAACTATAA MAAAAAAA 900
 AAAAAAAA CTGA 915

55

(2) INFORMATION FOR SEQ ID NO: 158:

60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2117 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

	AGAGCGAAGC GAGGGTGGCG CGGGTCCGGG CATGAAGCTG GGCCGGGCCG TGCTGGGCCT	60
10	GCTGCTGCTG GCGCCGTCCG TGGTGCAGGC GGTGGAGCCC ATCAGCCTGG GACTGGCCCT	120
	GGCCGGCGTC CTCACCGGCT ACATCTACCC GCGTCTCTAC TGCCCTCTCG CCGAGTGTCTG	180
	CGGGCAGAAG CGGAGCCTTA GCGGGAGGC ACTGCAGAAG GATCTGGACG ACAACCTCTT	240
15	TGACAGCAT CTTGCAAAGA AAATCATCTT AAATGCCGTG TTTGGTTTCA TAAACAACCC	300
	AAAGCCCAAG AAACCTCTCA CGCTCTCCCT GCACGGGTGG ACAGGCACCG GCAAAAATTT	360
20	CGTCAGCAAG ATCATCGCAG AGAATATTTA CGAGGGTGGT CTGAACAGTG ACTATGTCCA	420
	CCTGTTGTG GCCACATTGC ACTTTCCACA TGCTTCAAAC ATCACCTTGT ACAAGGATCA	480
	GTTACAGTTG TGGATTGAG GCAACGTGAG TGCCCTGTGCG AGGTCCATCT TCATATTTGA	540
25	TGAAATGGAT AAGATGCATG CAGGCCTCAT AGATGCCATC AAGCCTTTCC TCGACTATTA	600
	TGACCTGGTG GATGGGGTCT CCTACCAGAA AGCCATGTC ATATTCTCA GCAATGCTGG	660
30	AGCAGAAAGG ATCAGAGATG TGGCTTTGGA TTTCTGGAGG AGTGGAAAGC AGAGGGAAGA	720
	CATCAAGCTC AAAGACATTG AACACGGTT GTCTGTGTCG GTTTTCAATA ACAAGAACAG	780
	TGGCTTCTGG CACAGCAGCT TAATTGACCG GAACCTCATT GATTATTTG TTCCCTTCCT	840
35	CCCCCTGGAA TACAAACACC TAAAAATGTG TATCCGAGTG GAAATGCAGT CCCGAGGCTA	900
	TGAAATTGAT GAAGACATTG TAAGCAGAGT GGCTGAGGAG ATGACATTTT TCCCCAAGA	960
40	GGAGAGAGTT TTCTCAGATA AAGGCTGCAA AACGGTGTTC ACCAAGTTAG ATTATTACTA	1020
	CGATGATTGA CAGTCATGAT TGGCAGCCGG AGTCACTGCC TGGAGTTGGA AAAGAAACAA	1080
	CACTCAGTCC TTCCACACTT CCACCCCCAG CTCCTTTCCC TGGAAGAGGA ATCCAGTGAA	1140
45	TGTTCTGTG TGATGTGACA GGAATTCTCC CTGGCATTGT TTCCACCCCC TGGTGCCCTG	1200
	AGGCCACCCA GGGACCACGG GCGAGGACGT GAAGCCTCCC GAACACGCAC AGAAGGAAGG	1260
50	AGCCAGCTCC CAGCCCACTC ATCGCAGGGC TCATGATTTT TTACAAATTA TGTTTTAATT	1320
	CCAAGTGTTT CTGTTTCAAG GAAGGATGAA TAAGTTTAT TGAAAATGTG GTAACTTTAT	1380
	TTAAAATGAT TTTTAACATT ATGAGAGACT GCTCAGATTC TAAGTTGTTG GCCTTGTGTG	1440
55	TGTGTTTTTT TTTAAGTTCT CATCATATT ACATAGACTG TGATGTATCT TTACTGGAAA	1500
	TGAGCCCAAG CACACATGCA TGGCATTGTG TCCACAGGAG GGCATCCCTG GGGATGTGGC	1560
60	TGGAGCATGA GCCAGCTCTG TCCCAGGATG GTCCCAGCGG ATGCTGCCAG GGGCAKTGAA	1620

GTGTTTAGGT GAAGGACAAG TAGGTAAGAG GACGCCCTTCA GGCACCACAG ATAAGCCTGA 1680
 AACAGCCTCT CCAAGGGTTT TCACCTTAGC AACAAATGGGA GCTGTGGGAG TGATTTTGGC 1740
 5 CACACTGTCA ACATTTGTTA GAACCACTCT TTTGAAAGAA AAGTATTTCC AACTTGTAC 1800
 TTGCCAGTCA CTCGGTTTGG CAAAAGGTGG CCCTTCACTG TCCATTCCAA ATAGCCCACA 1860
 CGTGCTCTCT GCTGGATTCT AAATTATGTG AATTTTGCCA TATTAAATCT TCCTCATTTA 1920
 10 TACTATTATT TGTTACGTTT AATCAGAATC CCCGAAACCT CCTATAAAGC TTAGCTGCCC 1980
 CTTCTGAGGA TGCTGAGAAC GGTGTCTTTC TTTATAAATG CAAATGGCTA CCGTTTAC 2040
 15 ATAAATTTT GCATGTGCAA AAAAAAAAAA ANAAAAAAAA AAAATCCCGG GGGGGGGCCG 2100
 GTAACCAATT TGNCCCC 2117

20

(2) INFORMATION FOR SEQ ID NO: 159:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2395 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

TGTTCCTTAA TCCTTTTCT AAAAAAGGGG GAAATCCCG ATGGATTTTA GGGATTGGTC 60
 TGGTGTACAG TGTGTTTAT TGCACACCTA AATCCTGATT ATAGGCTTTT CATTCTCCG 120
 35 CAAAGCCTTT ATTTTGGCAG TTAAGCCAAA TGTGTTTCC AGAAAGTTAG TTATTTTCTC 180
 CTCCTTCTTT CCTTCTTTC CTCCTTTTTC CCCGTCGAC CCCAAACGTT ATTGTCCAAA 240
 40 CATGACTGGA CAGCAGCTTT TGTTCCTTGA CCCTGTAATA TGACAGTCTG CTAATATTGA 300
 CAGAAGGTGC AGTTTPTGGG TTATAGTCGT GATTTTCGCT AATCAATCAT ATTAGCAGGA 360
 AAAAAAKGA CTGTTTCTG TTGTACTTGA GTCTTAAGAA AAAGTGGCCC ATAGTTTAGT 420
 45 GGACAATTTT CAAAGGCTTT AGTACCACCT GTATTTCAAA ATGGGGGACC CAACTCCCG 480
 GAAGAAACAA GCTCTGAACA GACTACGTGC TCAGCTTAGA AAGAAAAAG AATCTCTAGC 540
 50 TGACCAGTTT GACTTCAAGA TGTATATTGC CTTGTATTTC AAGGAGAAGA AGAAAAAGTC 600
 AGCACTTTT GAAGTGCTG AGGTATACC AGTCATGACA AATAATTATG AAGAAATAT 660
 CCTGAAAGGT GTGCGAGATT CCAGCTATTC CTTGGAAAGT TCCCTAGAGC TTTTACAGAA 720
 55 GGATGTGGTA CAGCTCCATG CTCCTCGATA TCAGTCTATG AGAAGGGATG TAATTGGCTG 780
 TACTCAGGAG ATGGATTTC TCTTTGGCC TCGGAATGAT ATTGAAAAA TCGTCTGTCT 840
 60 CCTGTTTTCT AGGTGAAAG AATCTGATGA GCCTTTTAGG CCTGTTTAGG CAAATTTGAG 900

	TTTCATCATG GTGACTATGA AAAACAGTTT CTGCATGTAC TGAGCCGCAA GGACAAGACT	960
5	GGAATCGTTG TCAACAATCC TAACCACTCA GTGTTTCTCT TCATTGACAG ACAGCACTTG	1020
	CAGACTCCAA AAAACAAAGC TACAATCTTC AAGTTATGCA GCATCTGCCT CTACCTGCCA	1080
	CAGGAACAGC TCACCCACTG GGGCAGTTGG CACCATAGAG GRTCACCTCC GTCCTTATAT	1140
10	GCCAGAGTAG AGTACTGACC AGCAAAATGG AGAAGATCAG AGAATGCAGC AGCAGTTTTT	1200
	TTTCTTGTTT TCTTACCACT TTATTCTTTC AGAGTTTAAA GAAAATGGAC TCATGCACAG	1260
	AACACTATGC ATTTTGAAAC TTGTTTCATCC TGGATTTTTT TAAATCATTT TTATCTCAGA	1320
15	ACTTAAACAA AAATTAGATG TCGTGCACGG ACTGTGTGAA AGAAGATGCT TTGCATATTT	1380
	GCTGCACTGC ATCAGTATCT TACTAAAAAT GTGAAATGAA AGGACTATTG TACTCTGAAA	1440
20	TGCTTAAATG TATCTGAAAG CACAAGGTGA TACTCATTTT TATGGTCTTC CCATTTGTGC	1500
	TGGTTTTTGC CTCTTTGACA TCTGTCACTA GTATTTAGAG GGTGAGAAGT GAATGTAACA	1560
	GGTATAAATA ACATTTTTAA AAACAATAAC TTTGCTATAA TCACAGTTGT TCCAGAGCAC	1620
25	TGTCAGATAC ATTCTAATGA CCAGAACTGG TTTAAAAAAA GAAAATACAA CCATGGGAAA	1680
	GAAATCTTAA ATGAAAAACG CATCTCATTG TAGGCATTTT TGCCTCATAT TTTACTGGGC	1740
30	CATGTTTGTT TCCTGGTACT CATGTATTTT TTTTTCAG ATCTCTTTCC CCAAGTTGCT	1800
	ATTGTAAGAG TATTCTGCTG CGTGTGGATG CAGTTATACA CATTAAAGCA GATCTGGAGT	1860
	CTGAAGTAGC TATAAAGCAG CTATAAACA GAAATACATG CATAGCTGCA GAAACCATGA	1920
35	TAGGTAGAGG ACTTTTCTTT TGGTTTGTGTT TTGTTTGTGTT TTGTTTGTGTT TTTGGTTTTA	1980
	CAGAGAAGAG ATTTTATATTA CAAAGAAAAA AATTCAGTG AATTGTGCAG AAATGCTGGT	2040
40	TTTACACCA TCCTAAAGAA AAACCTTACA AGGGTGTGTT GGAGTAGAAA AAAGTTATA	2100
	AAGTTGGAAT CTTAAATTGT AAAATTAACC ATTGAGTGTG AAAGTTCTAA AAGCAGAACT	2160
	CATTTTGTGC AATGAACATA AGGAAAGACT ACTGTATAGG TTTTTTTTTT TTCTCCTTTT	2220
45	AAATGAAGAA AAGCTTTGCT TAAGGGTGC ATACTTTTAT TGGAGTAAAT CTGAATGATC	2280
	CTACTCCTTT GGAGTAAAAC TAGTGCTTAC CAGTTTCCAA TTGTATTTAG CTTCTGGTTG	2340
50	GAATTTGAAA AAAAAAGAAA AAAAGAAAAA GAAACCTAA ATAAAAATAGG TGAAA	2395

55 (2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2120 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

5	CCCCGGATAC CGCCTGACGT AGTGCCAATC ACACCTCTCG CGTCTCGGCG CCTCGGAGGC	60
	TAATGAGGAC GCCTGGCGAA ACGCAGTAAC GGATTTCGGG GTGGACCTTC GCTTTAAGGC	120
	TCGTGAGTTC TTCGGCCCAA CCCAGAGGAA GCGGGAGAGC AGTTTACGAC AGCGCGGGTC	180
10	GTGTTTACGG CGGCGCCCGC TGCGCGCGCA TGTTCCTCTT TTTCTCGGTT TCTCAAGAGT	240
	GCTGCTGCTA ACGCGGTCCC CGGCACGCAC CATCTGTTGC CATCCCGGCC GGCCGAGGCA	300
15	TTGCAGATTT TGAAGATGG CAAAGTTCAT GACACCCGTG ATCCAGGACA ACCCCTCAGG	360
	CTGGGGTCCC TGTGCGGTTT CCGAGCAGTT TCGGGATATG CCCTACCAGC CGTTCAGCAA	420
	AGGAGATCGG CTAGGAAAGG TTGCAGACTG GACAGGAGCC ACATACCAAG ATAAGAGGTA	480
20	CACAAATAAG TACTCTCTC AGTTTGGTGG TGGAAGTCAA TATGCTTTATT TCCATGAGGA	540
	GGATGAAAGT AGCTTCCAGC TGGTGGATAC AGCGCGCACA CAGAAGACGG CCTACCAGCG	600
25	GAATCGAATG AGATTTGCCC AGAGGAACCT CCGCAGAGAC AAAGATCGTC GGAACATGTT	660
	GCAGTTCAAC CTGCAGATCC TGCCTAAGAG TGCCAAACAG AAAGAGAGAG AACGCATTGG	720
	ACTGCAGAAA AAGTTCAGG AACAAATTTGG GGTTAGGCAG AATGGGATC AGAAATCACA	780
30	GAAACCCCGA GACTCTTCAG TTGAAGTTGG TAGTGATTGG GAAGTGAAAG AGGAAATGGA	840
	TTTTCTCTAG TTGATGAAGA TGCGCTACTT GGAAGTATCA GAGCCACAGG ACATTGAGTG	900
35	TTGTGGGGCC CTAGAATACT ACGACAAAGC CTTTGACCGC ATCACCACGA GGAGTGAGAA	960
	GCCACTGCGG ASATNCAAGC GCATCTTCCA CACTGTCAAC ACCACAGACG ACCCTGTCAT	1020
	CCGCAAGCTG GCAAAACTC AGGGGAATGT GTTTGCCACT GATGCCATCC TGGCCACGCT	1080
40	GATGAGCTGT ACCCGCTCAG TGTATTCTCG GGATATTGTC GTCCAGAGAG TTGGGTCCAA	1140
	ACTCTTCTTT GACAAGAGAG ACAACTCTGA CTTTGACCTC CTGACAGTGA GTGAGACTGC	1200
45	CAATGAGCCC CCTCAAGATG AAGGTAATTC CTTCAATTCA CCCGCAACC TGGCCATGGA	1260
	GGCAACCTAC ATCAACCACA ATTTCTCCCA GCAGTGCTTG AGAATGGGGA AGGAAAGATA	1320
	CAACTTCCCC AACCCAAACC CGTTTGTTGA GGACGACATG GATAAGAATG AAATCGCCTC	1380
50	TGTTGCGTAC CGTTACCGCA GTGGNAAGCT TGGAGATGAT ATTGACCTTA TTGTCTGTTG	1440
	TGAGCAAGAT GCGGTATGA CTGGAGCCAA CGGGGAAGTG TCCTTCATCA ACATCAAGAC	1500
55	ACTCAATGAG TGGGATCCA GGCAGTGTAA TGGCGTTGAC TGGCGTCAGA AGCTGGACTC	1560
	TCAGCGAGGG GCTGTCAATTG CCACGAGCT GAAGAACAAC AGCTACAAGT TGGCCCGGTG	1620
60	GACCTGCTGT GCTTTGCTGG CTGGATCTGA GTACCTCAAG CTTGGTTATG TGTCTCGGTA	1680

CCACGTGAAA GACTCCTCAC GCCACGTCAT CCTAGGCACC CAGCAGTTCA AGCCTAATGA 1740
GTTTGCCAGC CAGATCAACC TGAGCGTGGA GAATGCTGG GGCATTTTAC GCTGCGTCAT 1800
5 TGACATCTGC ATGAAGCTGG AGGAGGGCAA ATACCTCATC CTCAAGGACC CCAACAAGCA 1860
GGTCATCCGT GTCTACAGCC TCCCTGATGG CACCTTCAGC TCTGATGAAG ATGAGGAGGA 1920
AGAGGAGGAG GAAGAAGAGG AAGAAGAAGA GGAAGAACT TAAACCAAGTG ATGTGGAGCT 1980
10 GGAGTTTGTC CTTCCACCGA GACTACGAGG GCCTTTGATG CTTAGTGGAA TGTGTGTCTA 2040
ACTTGCTCTC TGACATTTAG CAGATGAAAT AAAATATATA TCTGTTTAGT CTTAAAAAAA 2100
15 AAAAAAAAAA AAAAAAAAAAN 2120

20 (2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 900 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

30 GGAAGCTGAA GTCCTTCCAG ACCAGGGACA ACCAGGGCAT TCTCTATGAA GCTGCACCCA 60
CCTCCACCCT CACCTGTRAC TCAGGACCAC AGAAGCAAAA GTTCTCACTC AAACCTGGATG 120
CCAAGGATGG GCGCTGTTC AATGAGCAGA ACTTCTTCCA GCGGGCCGCC AAGCCTCTGC 180
35 AAGTCAACAA GTGAAGAAG CTGTACTGA CCCCCTGCT GGCCATCCCT ACCTGCATGG 240
GTTTCGGTGT TCACCAGGAC AAATACAGGT TCTTGGTGT ACCCAGCCTG GGGAGGAGCC 300
40 TTCAGTCGGC CCTGGATGTC AGCCCAAAGC ATGTGCTGTG CAGAGAGGTC TGTGCTGCAG 360
GTGGCCTGCC GGCTGCTGGA TGCCCTGGAG TTCTCCATG AGAATGAGTA TGTTCATGGA 420
AATGTGACAG CTGAAAATAT CTTGTGGAT CCAGAGGACC AGAGTCAGGT GACTTTGGCA 480
45 GGCTATGGCT TCGCMTCCG CTATTGCCCA AGTGCAAAAC ACGTGGCCTA CGTGAAGGC 540
AGCAGGAGCC CTCACGAGGG GGACCTTGAG TTCATTAGCA TGGACCTGCA CAAGGGATGC 600
50 GGGCCCTCCC GCGCRGCGA CCTCCAGAGC CTGGGCTACT GCATGCTGAA GTGGCTCTAC 660
GGGTTTCTGC CATGGACAAA TTGCCTTCCC AAMAMTGAGG ACATCATGAA GCAAAAACAG 720
AAGTTTGTG ATAAGCCGGG GCCCTTCGTG GGACCTGCG GTCCTGGAT CAGGCCCTCA 780
55 GAGACCTGC AGAAGTACCT GAAGGTGGTG ATGGCCCTCA CGTATGAGGA GAAGCCGCC 840
TACGCCATGC TGAGGAACAA CCTAGAAGCT TTGCTGCAGG ATCTGCGTGT GTCTCCATAT 900

60

(2) INFORMATION FOR SEQ ID NO: 162:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1003 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

GGCACGAGAT GAGGGGCACC CAGTGCTTCT AGGGCAGGCT GGGTGGTGGT CCCCTAGGTA 60
15 TCAGCCTCTC TTACTGTACT CTCGGGAAT GTTAACCTTT CTATTTTCAG CCTGTGCCAC 120
CTGTCTAGGC AAGCTGGCTT CCCCATTTGC CCCTGTGGGT CCACAGCAGC GTGGCTGCC 180
CCCAGGGCCA CCGCTTCTTT CTTGATCCTC TTTCCTTAAC AGTGACTTGG GCTTGAGTCT 240
20 GGCAAGGAAC CTGTCTTTTA GCTTCACCAC CAAGGAGAGA GGTGACATG ACCTCCCCGC 300
CCCTTCACCA AGGCTGGGAA CAGAGGGGAT GTGGTGAGAG CCAGGTTCTT CTGGCCCTCT 360
25 CCAGGTGTT TTCCACTAGT CACTACTGTC TTCTCCTTGT AGCTAATCAA TCAATATTCT 420
TCCCTTGCTT GTGGGCAGTG GAGAGGCTGC TGGGTGTACG CTGCACCTGC CCACTGAGTT 480
GGGGAAGAG GATAATCAGT GAGCACTGTT CTGCTCAGAG CTCCTGATCT ACCCCACCCC 540
30 CTAGGATCCA GGAAGTGGTC AAAGCTGCAT GAAACCAGGC CCTGGCAGCA AACCTGGGAA 600
TGGCTGGAGG TGGGAGAGAA CCTGAATTC TCTTTCCCTC TCCCTCCTCC AACATTACTG 660
35 GAACTCTATC CTGTTAGGAT CTTCTGAGCT TGTTCCTCTG CTGGGTGGGA CAGAGGACAA 720
AGGAGAAGGG AGGGTCTAGA AGAGGCAGCC CTCTTTTGTG CTCIGGGSTA AATGAGCTTG 780
ACCTAGAGTA AATGGAGAGA CAAAAGCCT CTGATTTTTA ATTTCCATAA AATGTTAGAA 840
40 GTATATATAT ACATATATAT ATTTCTTTAA ATTTTGTAGT CTTGATATG TCTAAAAATC 900
CATTCCTCT GCCCTGAAGC CTGAGTGAGA CACATGAAGA AAAGTGTGTT TCATTAAAG 960
45 ATGTTAATTA AATGATTGAA ACTTGAAAAA AAAAAAAAAA AAA 1003

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(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2196 base pairs

(B) TYPE: nucleic acid

55

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

60 AAGAAGCGGC ACACGGATGT GCAGTTCTAC ACAGAAGTGG GAGAGATAAC CACGGACTTG 60

	GGGAAACATC AGCATATGCA TGACCGAGAT GACCTCTATG CTGAGCAGAT GGAACGAGAA	120
5	ATGAGGCACA AACTGAAAAC AGCCTTTAAA AATTTCATTG AGAAAGTAGA GGCTCTAACT	180
	AAGGAGGAAC TGGAAATTGA AGTGCCCTTT AGGGACTTGG GATTTAACGG AGCTCCCTAT	240
	AGGAGTACCT GCCTCCITCA GCCCACTAGT AGTGCGCTGG TAAATGCTAC GGAATGGCCA	300
10	CCTTTTGTGG TGACATTGGA TGAGGTAGAG CTGATCCACT TTRAGCGGGT CCAGTTTCAC	360
	CTGAAGAACT TTGATATGGT AATCGTCTAC AAGGACTACA GCAAGAAAGT GACCATGATC	420
15	AACGCCATTC CTGTAGCCTC TCTTGACCCC ATCAAGGAAT GGTGAATTTC CTGCGACCTG	480
	AAATACACAG AAGGAGTACA GTCCCTCAAC TGGACTAAAA TCATGAAGAC CATGTGTGAT	540
	GACCCTGAGG GCTTCTTCGA ACAAGGTGGC TGGTCTTTCC TGGAGCCTGA GGGTGAGGGG	600
20	AGTGATGCTG AAGAAGGGGA TTCAGAGTCT GAAATTGAAG ATGAGACTTT TAATCCTTCA	660
	GAAGATGACT ATGAAGAGGA AGAGGAGGAC AGTGATGAAG ATTATTTCATC AGAAGCAGAA	720
25	GAGTCAGACT ATTCTAAGGA GTCATTGGGT AGTGAAGAAG AGAGTGGAAG GGATTGGGAT	780
	GAAGTGGAGG AAGAAGCCCC AAAAGCGGAC CGAGAAAGTC GTTACGAGGA AGAAGAAGAA	840
	CAAAGTCGAA GTATGAGCCG GAAGAGGAAG GCATCTGTGC ACAGTTCGGG CCGTGGCTCT	900
30	AACCGTGGTT CCAGACACAG CTCTGCACCC CCCAAGAAAA AGAGGAAGTA ACTTCTGAAC	960
	TTTGGCCCTG AGCTCCATTC TTCTCCAGC CAACCCCTGA AAATTTTACA TGACATAGAA	1020
35	ACTGTATTTT TCCTTTCGTT TTCATTGAA GTTTTGCCAT TTGTGTTTAT GGGTTTAGGG	1080
	GGCCATTTGT GTGGACCAAT CTACTCGGGG AATTCCAGGC CCACCAGGAC ACGTGCCAAT	1140
	GGCCCCATTC AGATGGCAAG GGAGGAGGTG TTCTTGAAGA CAGGAGGAGG CTCCCGCTGT	1200
40	TAATAAATAT TGTTCATTC TTCTCTCTTC CTGTACCTT CTGCCAAGAC ATTGATGGCT	1260
	TCTGACATCT TATTTGGTGT CTCAAAGCTG TATTTCCAAG ACAGTGGTAC AAGGTGACCC	1320
45	TTAATTACCC GTATCATGGT TCTTGACCAG CACATTCAAT CCTCCAACCT ACCCTACTGC	1380
	CATGACCTTC CGCACATCTC TAAGTTTAT CTTTGCAATA CTCAGGTTC TCGGAAATTT	1440
	GCTAATGGTT GTGATAAAAC ATACAGCTTG AGCCAGTGAG GCAGATTGGG CTGGTGCTTT	1500
50	CGTCTGAGTT TTCCTGCTTT CTGCGCTCGT GCAGATTCTG AGGTATATCT GCTGCCTTGG	1560
	AAGACATAAG AAGCAGTGAT ACTCCCTGGC TCGGTTATTT TCTCCATACA ATGCACACAT	1620
55	GGTACAATGA TAGAAGGCAA AATTGCCACT GTCTTCTTTT TTTTCTCATA TATCTAAGGA	1680
	AGATATATCA GGTGTGCGCT CATGTACCGC TTCTAGTGAA ATGTAGAGGA AGGCTCAAAG	1740
	GAGTCAACAT TTAGATCTGG AAGGGACAAG TCATGCCTTG GGCCTAGAAT ACCCTGATGA	1800
60	GAAAAGAGAA GAGGAAGGGA GGCATATCT ACAACANCA CCTCTCGGCA CTGCTGCTCC	1860

TTATTTTAAC TTGTCTTGC ATTGTCTGT ATTTATCACA GTTCTGTG AACAGCTTTT 1920
 CAAGTATTTG GGGAGTTTAT CTTGCCATCC TCCCCTTCTG GTTCTCTGCA CCCACCTGTC 1980
 5 CCACTGCAGT TCCTTCOGTG CTCTGTGACT TTAAGAGAAG AAGGGGGGAG GGGTCCCGGA 2040
 TTTTATGTTT GTTGTMTTTC TCTCCTTAGC AGTAGGACTT GATATTTTCA ATTTTGAAG 2100
 10 AACTAAAAGA TGAATAAACT GGGTTTTTTT TGTGTGTTGT TTTGTAAAA AAAAAAAAAA 2160
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA 2196

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(2) INFORMATION FOR SEQ ID NO: 164:

(i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 1945 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

GCACAGAGTC GGGCGGACGG ACAGGGAGAG GAGGAGAGGG GGTCTGCGCG CGGCCGCTAC 60
 CCAGAAGCCA GCGGACGGCA GCACGGAGTG GGCTGTCCCC GAGCCCAGCC CCGAGCGAGC 120
 30 CCCCCCCCCG CCCCCGMAGG ACGCGCCTYC CAGCCAGCCC GACTYCTAGG AGGAGGGGAG 180
 GCGGAAAGC AGCTCAAGCC TCACCCACCG CCCTGCCCCC AGCCCCGCCA CTCCCAGGCT 240
 35 CCTCGGGACT CGGCGGTCC TCCTGGGAGT CTCGGAGGGG ACCGGCTGTG CAGACGCCAT 300
 GGAGTGGTG CTGGTCTTCC TCTGCAGCCT GCTGGCCCCC ATGGTCTCTG CCAGTGCAGC 360
 TGAAAAGGAG AAGGAAATGG ACCCTTTTCA TTATGATTAC CAGACCCTGA GGATTGGGGG 420
 40 ACTGGTGTTC GCTGTGGTCC TCTTCTCGGT TGGGATCCTC CTTATCCTAA GTCGCAGGTG 480
 CAAGTGCAGT TTCAATCAGA AGCCCCGGC CCCAGGAGAT GAGGAAGCCC AGGTGGAGAA 540
 45 CCTCATCACC GCCAATGCAA CAGAGCCCCA GAAAGCAGAG AACTGAAGTG CAGCCATCAG 600
 GTGGAAGCCT CTGGAACCTG AGGCGGCTGC TTGAACCTTT GGATGCAAAT GTCGATGCTT 660
 AAGAAAACCG GCCACTTCAG CAACAGCCCT TTCCCCAGGA GAAGCCAAGA ACTTGTGTGT 720
 50 CCCCCACCTT ATCCCTCTA ACACCATTC TCCACCTGAT GATGCAACTA AACTTGCCTT 780
 CCCCCTGCA GCTGCGGTG CTGCCACCT CCCGTGATGT GTGTGTGTGT GTGTGTGTGT 840
 55 GTGACTGTGT GTGTTTGCTA ACTGTGGTCT TTGTGGCTAC TTGTTGTGG ATGGTATTGT 900
 GTTGTGTAGT GAACTGTGGA CTCGCTTTC CAGGCAGGGG CTGAGCCACA TGGCCATCTG 960
 60 CTCTCCCTG CCCCCGTGC CCTCCATCAC CTTCTGCTCC TAGGAGGCTG CTTGTGCCC 1020

	GAGACCAGCC CCTCCCTG ATTTAGGGAT GCGTAGGGTA AGAGCACGGG CAGTGGTCTT	1080
	CAGTCGTCTT GGGACCTGGG AAGGTTTGCA GCACCTTTGTC ATCATTCTTC ATGGACTCCT	1140
5	TTCACTCCTT TAACAAAAAC CTGCTTCCT TATCCACCT GATCCAGTC TGAAGGTCTC	1200
	TTAGCAACTG GAGATACAAA GCAAGGAGCT GGTGAGCCCA GCGTTGACGT CAGGCAGGCT	1260
10	ATGCCCTTCC GTGGTTAATT TCTTCCAGG GGCTTCCACG AGGAGTCCCC ATCTGCCCCG	1320
	CCCTTCACA GAGCGCCCGG GGATTCCAGG CCCAGGCTT CTA CTCTGCC CCTGGGGAAT	1380
	GTGTCCCTG CATATCTTCT CAGCAATAAC TCCATGGGCT CTGGGACCCT ACCCTTCCA	1440
15	ACCTTCCCTG CTCTGAGAC TTCAATCTAC AGCCAGCTC ATCCAGATGC AGACTACAGT	1500
	CCCTGCAATT GGTCTCTGG CAGGCAATAG TTGAAGGACT CCTGTTCCGT TGGGGCCAGC	1560
20	ACACCGGAT GGATGGAGG AGAGCAGAGG CCTTTGCTTC TCTGCCTACG TCCCCTAGA	1620
	TGGGCAGCAG AGGCAACTCC CGCATCCTTT GCTCTGCCG TCRGTGGTCA GAGCGGTGAG	1680
	CGAGGTGGT TGGAGACTCA GCAGGCTCCG TGCAGCCCTT GGAACAGTG AGAGGTGAA	1740
25	GGTCATAACG AGAGTGGGAA CTCAACCCAG ATCCCCCCCC TCCTGTCTC TGTGTCCCCG	1800
	CGAAACCAA CCAAACCGTG CGCTGTGACC CATGTCTGTT CTCGTATCG TGATCTATCC	1860
30	TCAACAACAA CAGAAAAAG GAATAAATA TCCTTTGTTT CTTAGTGAAA AAAAAAAAAA	1920
	AAAAAAAAA AAAAAAAAAA CTCGA	1945

35

(2) INFORMATION FOR SEQ ID NO: 165:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2933 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

45

	GGGTCGACCC ACGCGTCCGG CAGCGTCGT TTGAGTCGTT GCTGCCGCTG CCCCCCCCCG	60
	GATCAGGAGC CAGTGTATAC CGCCGCCCCA CCGCTTGGT GCCGTAGAG GAAACGAGAA	120
50	GGAGGCGGCC TCGGTTTGT CGCCGAGCT CGCCCMYGY CYGGRAGAGC CGAGCCCCG	180
	CCCACTGGT CGCTGCCAC CSCTCGTAGC CGTTACCGC GGGCCGCCAC AGCCGCGGC	240
55	CGGAGAGGC GCGGCCATG GCTCTGGAG CCGATTCAA AGGTGATGAC CTATCAACAG	300
	CCATTCTCAA ACAGAAGAAC CGTCCAATC GGTAAATGT TGATGAAGCC ATCAATGAGG	360
	ACAACAGTGT GGTGTCTTG TCCAGCCCA AGATGGATGA ATTGCAGTTG TTCCGAGGTG	420
60	ACACAGTGT GCTGAAAGGA AAGAAGAGAC GAGAAGCTGT TTGCATCGTC CTTCTGATG	480

	ATACTTGTC	TGATGAGAAG	ATTCGGATGA	ATAGAGTTGT	TCGGAATAAC	CTTCGTGTAC	540
5	GCCTAGGGGA	TGTCATCAGC	ATCCAGCCAT	GCCCTGATGT	GAAGTACGGC	AAACGTATCC	600
	ATGTGCTGCC	CATTGATGAC	ACAGTGAAG	GCATTACTGG	TAATCTCTTC	GAGGTATACC	660
	TTAAGCCGTA	CTTCCTGGAA	GCGTATCGAC	CCATCCGGAA	AGGAGACATT	TTTCTTGTCC	720
10	GTGGTGGGAT	GCGTGCTGTG	GAGTTCAAAG	TGGTGGAAAC	AGATCCTAGC	CCTTATTGCA	780
	TTGTTGCTCC	AGACACAGTG	ATCCACTGCG	AAGGGGAGCC	TATCAAACGA	GAGGATGAGG	840
15	AAGAGTCCTT	GAATGAAGTA	GGGTATGATG	ACATTGGTGG	CTGCAGGAAG	CAGCTAGCTC	900
	AGATAAAGGA	GATGGTGGAA	CTGCCCCTGA	GACATCCTGC	CCTCTTTAAG	GCAATTGGTG	960
	TGAAGCCTCC	TAGAGGAATC	CTGCTTTACG	GACCTCCTGG	AACAGGAAAG	ACCCTGATTG	1020
20	CTCGAGCTGT	AGCAAATGAG	ACTGGAGCCT	TCTTCTTCTT	GATCAATGGT	CCTGAGATCA	1080
	TGAGCAAATT	GGCTGGTGAG	TCTGAGAGCA	ACCTTCGTAA	AGCCTTTGAG	GAGGCTGAGA	1140
25	AGAATGCTCC	TGCCATCATC	TTCATTGATG	AGCTAGATGC	CATCGCTCCC	AAAAGAGAGA	1200
	AAACTCATGG	CGAGGTGGAG	CGGCGCATTG	TATCACAGTT	GTGACCCCTC	ATGGATGGCC	1260
	TAAAGCAGAG	GGCACATGTG	ATTGTTATGG	CAGCAACCAA	CAGACCCAAC	AGCATTGACC	1320
30	CAGCTCTACG	GCGATTGGT	CGCTTTGACA	GGGAGGTAGA	TATTGGAATT	CCTGATGCTA	1380
	CAGGACGCTT	AGAGATTCTT	CAGATCCATA	CCAAGAACAT	GAAGCTGGCA	GATGATGTGG	1440
35	ACCTGGAACA	GTAGCCAATG	AGACTCACGG	GCATGTGGGT	GCTGACTTAG	CAGCCCTGTG	1500
	CTCAGAGGCT	GCTCTGCAAG	CCATCCGCAA	GAAGATGGAT	CTCATTGACC	TAGAGGATGA	1560
	GACCATTGAT	GCCGAGGTCA	TGAACTCTCT	AGCAGTTACT	ATGGATGACT	TCCGGTGGGC	1620
40	CTTGAGCCAG	AGTAACCCAT	CAGCACTGCG	GGAAACCGTG	GTAGAGGTGC	CACAGGTAAC	1680
	CTGGGAAGAC	ATCGGGGGCC	TAGAGGATGT	CAAACGTGAG	CTACAGGAGC	TGGTCCAGTA	1740
45	TCCTGTGGAG	CACCCAGACA	AATTCCTGAA	GTTTGGCATG	ACACCTTCCA	AGGGAGTTCT	1800
	GTTCTATGGA	CCTCCTGGCT	GTGGGAAAAC	TTTGTGGGCC	AAAGCCATTG	CTAATGAATG	1860
	CCAGGCCAAC	TTCATCTCCA	TCAAGGGTCC	TGAGCTGCTC	ACCATGTGGT	TTGGGGAGTC	1920
50	TGAGGCCAAT	GTCAGAGAAA	TCTTTGACAA	GGCCCGCCAA	GCTGCCCCCT	GTGTGCTATT	1980
	CTTTGATGAG	CTGGATTCTA	TTGCCAAGGC	TCGTGGAGGT	AACATTGGAG	ATGGTGGTGG	2040
55	GGCTGCTGAC	CGAGTCATCA	ACCAGATCCT	GACAGAAATG	GATGGCATGT	CCACAAAAAA	2100
	AAATGTGTTT	ATCATTGGCG	CTACCAACCG	GCCTGACATC	ATTGATCCTG	CCATCCTCAG	2160
	ACCTGGCCGT	CTTGATCAGC	TCATCTACAT	CCACITCCT	GATGAGAAGT	CCCGTGTTC	2220
60	CATCCTCAAG	GCTAACCTGC	GCAAGTCCCC	AGTTGCCAAG	GATGTGGACT	TGGAGTTCTT	2280

5 GGCTAAAATG ACTAATGGCT TCTCTGGAGC TGACCTGACA GAGATTTGCC AGCGTGCTTG 2340
 CAAGCTGGCC ATCCGTGAAT CCATCGAGAG TGAGATTAGG CGAGAACGAG AGAGGCAGAC 2400
 AAACCCATCA GCCATGGAGG TAGAAGAGGA TGATCCAGTG CCTGAGATCC GTCGAGATCA 2460
 CTTTGAAGAA GCCATGCGCT TTCCGCGCCG TTCTGTCAGT GACAATGACA TTCGGAAGTA 2520
 10 TGAGATGTTT GCCCAGACCC TTCAGCAGAG TCGGGGCTTT GGCAGCTTCA GATCCCTTC 2580
 AGGGAACCAG GGTGGAGCTG GCCCCAGTCA GGCAGTGA GCGGCACAG GTGGCAGTGT 2640
 ATACACAGAA GACAATGATG ATGACCTGTA TGGCTAAGTG GTGGTGGCCA GCGTGCAGTG 2700
 15 AGCTGGCCTG CCTGGACCTT GTTCCCTGGG GGTGGGGGCG CTGCCCCAGG AGAGGGACCA 2760
 GGGGTGGGCC CACAGCCTGC TCCATTCTCC AGTCTGAACA GTTCAGCTAC AGTCTGACTC 2820
 20 TGGACAGGGG GTTCTGTGTG CAAAAATACA AAACAAAGC GATAAAATAA AAGCGATTTT 2880
 CATTGTGTAA AAAAAAAAAA AAAAAAAT CCGGGGGGGG GCCCGAACCA TTT 2933

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(2) INFORMATION FOR SEQ ID NO: 166:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2243 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

TCGGAGAGCC GCGGGCGNG CGCCTCTCGG CCAGGAAGCG CCTCTTGGAC GCGTGTNACC 60
 GATGCCCAGA AGTGGCCTTG GGCTGGGGAT CACCATAGCT TTTCTAGCTA CGCTGATCAC 120
 40 GCAGTTTCTC GTGTATAATG GTGTCTATCA GTATACATCC CCAGATTTC TCTATATTGG 180
 TTCTTGCGTC CCTGTATAT TTTTCTCAGG AGGCGTCACG GTGGGGAACA TAGGACGACA 240
 45 GTTAGCTATG GGTGTTCCTG AAAAGCCCCA TAGTGATTGA GTCTTCAAAA CCACCGATTTC 300
 TGAGAGCAAG GAAGATTTTG GAAGAAAATC TGACTGTGGA TTATGACAAA GATTATCTTT 360
 TTTCTTAAGT AATCTATTTA GATCGGGCTG ACTGTACAAA TGACTCCTGG AAAAACTCT 420
 50 TCACCTAGTC TAGAATAGGG AGGTGGAGAA TGATGACTTA CCTGAAGTC TTCCCTTGAC 480
 TGCCCGCACT GCGCCTGTC TGTGCCCTGG AGCATTCTGC CCAGGCTACG TGGGTTGAGG 540
 55 CAGGTGGCAG CTTCCCAAGT ATTGATTTTC ATTCATGTGA TTAAAACAAG TTGCCATATT 600
 TCAAAGCCTT GAACTAAGAC TCAATTACCA ACCCGCAGTT TTGTGTCAGT GCCCAAAGGA 660
 60 GGTAGGTGA TGGTGCTTAA CAAACATGAA GTATGGTGTA ATAGGAATAA TATTTATCCA 720

	AAAGATTTT AAAAATAGGG CTGTGTTTAA AAAAAAAAC AAAACARGAA AAGCAGCAGT	780
	GATTATAGAG AGGTCACACT CTAAGTGGGG TCGCGCGTG GCCACGCTTC ACGGTCACGC	840
5	TCGTCCGTCC TGCAGTGGCG TGTTTACATG GTCACACGTG TGTGTATCAC CAGTGGGTCA	900
	ACTGCTTGTC ATTCTCCCG TGGCAGTTTG TGTAGACAAT CTTACTGAGC AAAAGGCAAT	960
10	GAAAAGTCTT GGTTCACACA CTGCGATATA TTGGAATTTT CACCTCAGTT TATGAAGTTT	1020
	ATTTGCGAAAT CCATAGTCAT CTAAGAATGA ATACCTGTCT GCCATGTATT TCAATCTTAG	1080
	TGAGCCAAAA TTGTTTGT TTACTACAG AATAGAGATG ACTGTTTTTT GCCACAGCCC	1140
15	TATGGRATTT GCAATCTGTG ATTGCCTTGT AAAAAGGAGA GTGCATATGG CACTGCATTA	1200
	AACGTGTGGT GTTCTAGTC AATGATATTG GTGAGCACAA TGTATTCATT TAATGGCATA	1260
20	GACCATACCA GACCTAATTT GCAAGTATTG GGTCTTAAAC TTCAAGTGCA ATGTATATGA	1320
	AAACCAATCT GAGCCTTGTA TCTCTTAAAT ATTTATTTTT TTAAACGTGT GAGATGTTTG	1380
	AGAGAAGGTT CTCCATTCAT TTCAGTGCTG CCTGGAGGAA ACTCGGCAAT GATTCTTTTC	1440
25	AGTTGTGAAG TTCCTTTCGT GTTACACCTT CCACCTGAACC CTCAACCTTC GAAATACTCC	1500
	AGTTTTGTGG GTTTGGTCAT TTTTACTTAT AAATTTACCT TTTTGTATTT TGCAATTTAC	1560
30	ATGTGTTTGG TTTGTTTTAA ATTCTGTGAA AGTGGCTTGA TTAAAAGACT CCTTTTAAAT	1620
	GGAAGCCACC AGTCAGCAGA ATGGAAGCTT AGAGGAACTT GCCTGTGAGC GCTGGTCTTT	1680
	GTGTTTGGTT TTGTGATGTA ACGATCTTTG CTGGGGTTTT TGCTTTGTT TTGAGGGAAA	1740
35	TGTCTTGAG TAAATTTTAA GTTCCTGGAG TTAATTTGTT TTACAGGAAT TTTGTTTTTT	1800
	AAAAAATAG GATCATTCCT AACTTTGGAA TGACCCCTT ATATATTTTC TGAAAATGAA	1860
40	AACAGTTACA TGAAAAAAT TTCCAATGAA GATGTCAGCA TTTTATGAAA AACCAGAAGT	1920
	TATTAGATGA AAGCAGCGAG TGAATCTTTA AAACAGACTT GATCACGCAC ACACAATAAG	1980
	TCTTTCTCTC CGAAACCGGA AGTAAATCTA TATCTGTTAG AAATAATGTA GCCAAAAGAA	2040
45	TGTAAATTG AGGATTTTTT TGCCAATAGT TTATAGAAAA TATATGAACC AAAGTGATTT	2100
	GAGTTTGTA AAATGTAAAA TAGTATGAAC AAAATTGCA CTCTACCAGA TTTGAACATC	2160
50	TAGTGAGGTT CACATTCATA CTAAGTTTTC AACATTGTGT TCTTTTGTGA TTCATTTTTT	2220
	ACTTTTATTA AAGGTCAAA ACC	2243

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(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1816 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

5	GGTGGGNAGC TTTNAAATTC CCCTTACWGG GGCGCTNTAA GGGGAAACCT TCCCGGAATT	60
	TTCCGGTTCGA CCCACGGCTC CGGCCAGCCT AGGAGAAGAA GTTCGTAGTC CCAGAGGTGA	120
10	GGCAGGAGGC GGCAGTTTCT GGCGGGTGAG GCGGAGCTG AAGTGACAGC GGAGGCGGAA	180
	GCAACGGTCG GTGGGGCGGA GAAGGGGGCT GGCCCCAGGA GGAGGAGGAA ACCCTTCCGA	240
	GAAAAACAGCA ACAAGCTGAG CTGCTGTGAC AGAGGGGAAC AAGATGGCGG CGCCGAAGGG	300
15	GAGCCTCTGG GTGAGGACCC AACTGGGGCT CCCGCCGCTG CTGCTGCTGA CCATGGCCTT	360
	GGCCGGAGGT TCGGGGACCG CTTCGGCTGA AGCATTTGAC TCGGTCTTGG GTGATACGGC	420
20	GTCTTGCCAC CGGGCCTGTC AGTTGACCTA CCCCTTGCAC ACCTACCTTA AGGAAGAAGA	480
	GTTGTACGCA TGTCAGAGAG GTTGCAGGCT GTTTTCAATT TGTCAGTTTG TGGATGATGG	540
	AATTGACTTA AATCGAATA AATTGGAATG TGAATCTGCA TGTACAGAAG CATATTCCCA	600
25	ATCTGATGAG CAATATGCTT GCCATCTTGG KTGCCAGAAT CAGCTGCCAT TCGCTGAAT	660
	GAGACAAGAA CAACTTATGT CCCTGATGCC AAAAAATGCAC CTACTCTTTC CTCTAACTCT	720
30	GGTGAGGTCA TTCTGGAGTG ACATGATGGA CTCGACACAG AGCTTCATAA CCTCTTCATG	780
	GACTTTTTAT CTTCAAGCCG ATGACGGAAA AATAGTTATA TTCCRGCTTA AGCCAGRAA	840
	TCCCAGGTAC GCACCACATT TGGAGCCAGG AGCCCTACCA AATTTGRGRG RAWCMTCTCT	900
35	AAGCAAAATG TCCNTCAKMT CGSMAATGAG AAATTCACAA GCGCACAGGA ATTTTCTTGA	960
	AGATGGAGAA AGTGATGGCT TTTTAAGATG CCTCTCTCTT AACTCTGGGT GGATTTTAAC	1020
40	TACAACTCTT GTCCCTCTCGG TGATGGTATT GCTTTGGATT TGTTGTGCAA CTGTGTGCTA	1080
	CACGCTGTTG GACGCAATAT AGTTTCCCTC TGAGAAGCTG AGTATCTATG GTGACTTGGA	1140
	GTTTATGAAT GAACAAAAGC TAAACAGATA TCCAGCTTCT TCTCTTGTGG TTGTTAGATC	1200
45	TAAAACTGAA GATCATGAAG AAGCAGGGCC TCTACCTACA AAAGTGAATC TTGCTCATTC	1260
	TGAAATTTAA GCATTTTCTT TTTAAAAGAC AAGTGTAATA GACATCTAAA ATTCCACTCC	1320
50	TCATAGAGCT TTTAAAATGG TTTTATTGGA TATAGGCCTT AAGAAATCAC TATAAAATGC	1380
	AAATAAAGTT ACTCAAATCT GTGAAAAAAA AAAAAAAAAA AAAAAAAAC TCGAGGGGGG	1440
	GCCCCTTACC AAKTCGCCCT ATWGTGADTB GTATTMTAT TTTACTAATA TCTGTAGCTA	1500
55	TTTTGTTTTT KGCTTKGGTT ATKGTTTTTY TCCCTTYTCT WAGCTATRAG CTGATCATKG	1560
	CYSCCTCTCA CCTCCTGCCA TGATACTGTC AGTTACCTTA GTTAACAAGC TGAATATTTA	1620
60	GTAGAAATGA TGCTTCTGCT CAGGAATGGC CCACAAATCT GTAATTTGAA ATTTAGCAGG	1680

AAATGACCTT TAATGACACT ACATTTTCAG GAACTGAAAT CATTAAAATT TTATTTGAAT 1740
 AATTATGTGC TGAAAAAAAA AAAAAAAAAA AMMRARASK RRWACTCGA GGGGGGCCCC 1800
 5 GGTACCCNAT TCGCCG 1816

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(2) INFORMATION FOR SEQ ID NO: 168:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 945 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

20 AGAAACCGTT GATGGGACTG AGAAACCAGA GTTAAACCT CTTGGAGCT TCTGAGGACT 60
 CAGCTGGAAC CAACGGGCAC AGTTGGCAAC ACCATCAACT TCTCCCAAGC AGAGAAACCC 120
 25 GAACCCACCA ACCAGGGGCA GGATAGCCTG AAGAAACATC TACACGCAGA AATCAAAGTT 180
 ATTGGGACTA TCCAGATCTT GTGTGGCATG ATGGTATTGA GCTGGGGAT CATTTTGGCA 240
 TCTGCTTCCT TCTCTCCAA TTTTACCCAA GTGACTTCTA CACTGTTGAA CTCTGCTTAC 300
 30 CCATTCATAG GACCCCTTTT TTTTATCATC TCTGGCTCTC TATCAATGC CACAGAGAAA 360
 AGGTTRACCA AGCTTTTGGT GCATAGCAGC CTGGTTGGAA GCATTCTGAG TGCTCTGTCT 420
 35 GCCCTGGTGG GTTTCATTAT CCTGTCTGTC AAACAGGCCA CCTTAAATCC TGCCTCACTG 480
 CAGTGTGAGT TGGACAAAA TAATATACCA ACAAGAAGTT ATGTTTCTTA CTTTATCAT 540
 GATTCACTTT ATACCACGGA CTGCTATACA GCCAAAGCCA GTCTGGCTGG AACTCTCTCT 600
 40 CTGATGCTGA TTTGCACTCT GCTGGAATTC TGCCTAGCTG TGCTCACTGC TGTGCTGCGG 660
 TGGAACAGG CTTACTCTGA CTTCCTGGG AGTGTACTTT TCCTGCCTCA CAGTTACATT 720
 45 GGTAAATCTG GCATGTCTC AAAAATGACT CATGACTGTG GATATGAAGA ACTATTGACT 780
 TCTTAAGAAA AAAGGGAGAA ATATTAATCA GAAAGTTGAT TCTTATGATA ATATGGAAAA 840
 GTTAACCATT ATAGAAAAGC AAAGCTTGAG TTTCTTAAAT GTAAGCTTTT AAAGTAATGA 900
 50 ACATTAAAA AAACCATTAT TTCACTGTCA TTAAAGATA ATGTG 945

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(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 902 base pairs
 60 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

5	GGCAGAGCCA CAGGAAGGAT GAGGAAGACC AGGCTCTGGG GGCTGCTGTG GATGCTCTTT	60
	GTCTCAGAAC TCCGAGCTGC AACTAAATTA ACTGAGGAAA AGTATGAACT GAAAGAGGGG	120
10	CAGACCTGG ATGTGAAATG TGACTIONACG CTAGAGAAGT TTGCCAGCAG CCAGAAAGCT	180
	TGGCAGATAA TAAGGGACGG AGAGATGCCC AAGACCCTGG CATGCACAGA GAGGCCCTCA	240
	AAGAAITCCC ATCCAGTCCA AGTGGGGAGG ATCATACTAG AAGACTACCA TGATCATGGT	300
15	TTACTGCGCG TCCGAATGGT CAACCTTCAA GTGGAAGATT CTGGACTGTA TCAGTGTGTG	360
	ATCTACCAGC CTCCCAAGGA GCCTCACATG CTGTTCCGATC GCATCCGCTT GGTGGTGACC	420
20	AAGGGTTTTT CAGGGACCCC TGGCTCCAAT GAGAATICTA CCCAGAATGT GTATAAGATT	480
	CCTCTACCA CCACTAAGGC CTTGTGCCCC CTCTATACCA GCCCCAGAAC TGTGACCCAA	540
	GCTCCACCCA AGTCAACTGC CGATGTCTCC ACTCCTGACT CTGAAATCAA CCTTACAAAT	600
25	GTGACAGATA TCATCAGGGT TCCGGTGTTC AACATTGTCA TTCTCCTGGC TGGTGGATTG	660
	CTGAGTAAGA GCCTGGTCTT CTCTGTCTCG TTGTCTGTCA CGCTGAGGTC ATTTGTACCC	720
30	TAGGCCCACG AACCCAOGAG AATGTCTCTT GACTTCCAGC CACATCCATC TGGCAGTTGT	780
	GCCAAGGGAG GAGGGAGGAG GTAAAAGGCA GGGAGTTAAT AACATGAATT AAATCTGTAA	840
35	TCACCRGCTA AAAAAAAAAA AAAAAAAAACN CGANCCINGG TTTTCAGCTC CATCAGCTCC	900
	TT	902

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(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 1883 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

50	AGAAAACAAC TGAAAACCA CATTTTTCTA CATAAGCTG GGGAGGTAGC TGAGAACTTG	60
	GCACTGCGCA CACATACTAG GTTGAAAGAG AGTTGAGGAA ACCAGAAGGC CAAGTGGATC	120
55	TGCTGGCAAA CCCTGAACCT GTCTCCTGCG CTGCTCTAC AGTTCTGAAG TTGAAAATCC	180
	TTTTCATGCC TAGCATCTGC TTGAGTTATA AACCCCAAGG CAGCCATGTC ATAGACTAGT	240
60	GTTTACTCTT GTTTTGACTT TGTTTAAATG CTTCTAAGA OCCAAGTGCC TCCTGCTGTT	300

	TCTTCCTTTG TGGTAGCCTC TGGCCATCTG GGACCTCAAT CCCCAGCTTT CCCACTTTCA	360
	GCAGTCCTTT GCTCTCTTTG CTTCTACCTC AAATAGCCCC AGGAGTGGGC TTTAGTCTCC	420
5	AATATGGAGC ATYTCAAGCT TCTCCTGGGG GATGGGGATT GGGATGGGCA GAATCTGTTT	480
	TGGWCTCTCC GGTATTTTCC AGTGGGTGTA AAAGCAGAGC TGGGCCTTTC CCTCTCTTAT	540
10	CCCTGAGGGT GGGTAAGAAG GACTGTATCT ACACCTGTTC TTCCCTACCT TCTCTTTTGT	600
	TAGGGAGGCC TCATTCTAAG TTCCTCAAGA GAGTCCTTGG CTTAAAGCTG TAGCAAGGGT	660
	GTGCTAGGTG GGGGATTTGG AGCAAAACCG TCGAGTAGGC ATGATACTGG TATGGAGTGG	720
15	GCCTGCAAAA TCAGACAGAA ATGGCTTGAG AAGCCGCAGG GGAGCATGCC TGTCTCTCAG	780
	TGATAGAGTA TGGGAGGGAC CTCCCTAGCT TGGAAAATGA GAATTGAAGG GGTATGAAC	840
20	AAATAGGATG CCTAGTTGAG GATGTTCCCA AAGTTTGTG CAACTCTATC ATTAGTAGAT	900
	TTTATAAGCC ACAGAGACAA ACCAGAAACG GAATAATGTT ACTTTGGATG CTTTATTTTT	960
	TTGTTCTAGG TGTGGCTTTG TACATGCAGA AGAATGCTAT ATGCTGCACA TTTTGCTTTT	1020
25	AAAGTCTTAC GACTTTCCCC ATTTTAGTCT AATGGGAAGA TACAGATGTG CAAGTCTGCT	1080
	TTTTTGTTTT TTGTTATTAT TTTTTTTTTT TTGCTCTGTG TTATGGACAT TTTGAGACAT	1140
30	GCACAGAAGT GGAGAGGATG GTCCTTGGAC CCCATGTGTC CATCACCTAG CTGCATCACT	1200
	TATCAGCTAT GGTC AACCTG GTTTCATCTG TATCTCTCTC TTTTCACCTG TATTGTTTAT	1260
	TGAAAATCCA AGACACTATG CCAATGCAAC CGTGACTACT TTGGGAGATT GGTAGTCTCT	1320
35	TTTGATGGTG ATAGTGATGG GGTGCACTAT CATAATCACA TCAGGTCTGC TTTTGTCTTT	1380
	TAATGTTAAC TAATGAAGTT CCAGAGATGG GCCTTAGAAA TGTGTTTTAA GAATTAACAA	1440
40	GGAGTCTCAA AAAGAAATGA GAGGGATGCT TCCTTTCCCC TTGCATCTAC AAAACAAGAG	1500
	AGAGACTGTT CTGTTGTAAA ACTCTTTCAA AAATTCGTAT ATGGTAAGGT ACTTGAGACC	1560
	CTTCACCAGA ATGTCAATCT TTTTTTCTGT GTAACATGGA AACTTGTGTG ACCATTAGCA	1620
45	TTGTTATCAG CTGTACTGG TCTCATAACT CTGGTTTGG AAGAATAATT TGGAAATGT	1680
	TGCTGTGTTT TGTGAAAATA ACCTCCCCAA AATAATTAGT AACTGGTTGT TCTACTTGGT	1740
50	AATTTGACAC CCTGTTAATA ACGCAATTAT TTCGTGTGTC TTAAACAGTA TAAATAGTTG	1800
	TAAGTTTGCA TGCATGATGG AAAAATAAAA ACCTGTATCT CTGTTAAAAA AAAAAAAAAA	1860
	AAAAAAAAA AAAAAAAAAA AAA	1883
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(2) INFORMATION FOR SEQ ID NO: 171:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2100 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

	TACTTTTAGA TTTACTGCCT TCAAAAAGTG CCTATTCTGA GCAACATAAA CGTTATTCCT	60
10	TACATATGTA TGTACACACG GTACCCAGAG TGTACTGTG GCAGCCTTCA AAAACATACC	120
	ATCAGAAAGA GTAGGTGCTG AGATAAGGNA ACTTTGCCAA ATGNAAGAAA GTCACCTCACT	180
	TCCAATATCC CCTCTTCAAG CGGCTACCGT GRAASGGGCT GCAAACACAT TCCCTGAGCA	240
15	TCCCTTGCTG ATACAGCTTC TTTATATTTA TATCCTACTG GATGGTAGCA TATTGCTAAG	300
	GTTTCCTGTA CTCTGCTTCA AGGGAATGTA AGYTTTATGG CATTGAAACA TTTAGGAAAA	360
20	AAAAAGATGT TTAAGAGAAT TAATAGAGCC GTAGTCTGTA TTAGGATGTG TGTCAATATGT	420
	GTGTCTATA AACTAAGCAT CGGTGGGTTC AGAGTGTTAA AGTGTGAGCA CATTCCTTCT	480
	CCTTTTGTCT CTCAGGCTAA CATGAGAGAA AATAGAAAAG TCTTGGCTGT GGGGATTGGA	540
25	AGCTCAGGGG GCCAAATGTC CTTGCCAGAT CCTTAGAGCA TTACTTTGAC TCCTAAAAAT	600
	AGTAGTGTAT GTTATTTGAT GGCTTTTGTTC TCCATAGTTC CATCACTGAC AAAACTGTCA	660
30	ATACTGTTGA TGGAGCAGCA GCATAGCCTA GAGTGATGCA TTCTTACCCA GAGGTGGCAA	720
	TAGGAGAGGG TCCATGTAAA TAGGACGAGG TAGACAGTGC ATGATTGTAG GAGAAGGGTT	780
	GAAGGGAGGA CATGATTCCA AAAAAGATCG TTCTCAATGT GTCGTCTGAC TCAACCAGCT	840
35	GGCAGATTAC ACTTGCCAAG TCGTTCCTTT TCCTTCTAAG TCAGTTGGCT CCATATTCAC	900
	TTGAATATGC CTCTGTTTGG GCAAAGCAAG ATACCTCCAC TTAACCTTTA TCCAAGGAAG	960
40	CTCTTGGTGT CCTCTTGGTC ATAAAGTTGT CTCCTACCTA ACCCAGTTTC ACCAAATGGA	1020
	AGTAAAAGGG GACAAACTAT GGAAGATGGA CTCCATGCCA TTGCAGTCAG CCACCATTCCT	1080
	CTTTTCCATA TAAGGAGCCC CATTACATAA GCTACGGGTG AGGTGGAAC AGCTATGTTT	1140
45	CATAATTICA AGAGTGTGAC CACCTGCTC TAGTCATCAT CATGGATGA ATCCAGTTGA	1200
	CTCTTTGGCA AAAGGGTGAT ACTTTTCACT AAAAATGCCT ACTCTTCCTG TTGATGTTCC	1260
50	TTTTCTGTTT TTACCTTGTC CAATTTCAC ACTAGTCATT TTTTATATTT TTTAGAGGAT	1320
	CAGATTTTAG CGCTGAAAA TGAGTTCAAA AATTTCACTG TAATGTCATA AGGATGTTGG	1380
55	GATACAGAGA TTTTTTTTTT CCTTGGAAAC AAATGGACTG GGAAGAAACA CAGCATGGCT	1440
	TGCTCTGAG TTTCAATCTG ATGATTATGA CCATGGAAGA TAGTCTTATG TAAAGGTTAA	1500
	ATGGTGTTTA CAAGTGATA GATAAGGCGG AGATGGTGAG AAGCCGGGTT TTCTCTATGC	1560
60	TAAATGTGTC TACTAAGAGC AGCACTTCCT ACTAGCTAAG CACAATCATA GCCCCACCGT	1620

5 GATGAGCTGC TAGTCTGAAT AACATTCCCT GACTTAGGGA AAGGCACACA AAAACATATA 1680
 AAGAATATGT CTATTTTCAT ATGTGTGATA CTGACAGAGC CATGGTATTC CTAAAATATA 1740
 GGTTCCTCTT TTTTCTTGTA TTCTTAGCAA ATTGCATTTA TTTACTACAT TACAAACCAT 1800
 CACTGATGTA TCCAAAATAG CACACATAGT TCAGTATGAA AATAAGAGAA TAAAATCTGT 1860
 10 TATAAGCAAG TGATTTAGGT ATTTTCTTTT GTGTTTATGC ATTATCTGAC TATATTAAAA 1920
 CCTGTTTTTC TATTTACCTT CTATCAGTTT TCTCTACCAA TTATGTTTTT TCAATGCTCT 1980
 ATAAGAATGA ATATGGAAAT TATATTTCTT TTTTCTGTAA AAGAGTTGCA ACTACTTTAT 2040
 15 TATATTTAGA AATCCAATAA ACTTCTTATT ACATTTAAAA AAAAAAAAAA AAAACTCGAA 2100

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(2) INFORMATION FOR SEQ ID NO: 172:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1930 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

CCTTTGANTG TGGTCCCGGG TGCNGATTGG CAGCGCCTCC GCCGCGGCTC GTGGTTGTCC 60
 CGCCATGGCA CTGTGCGGGG GGCTGCCCGG GGAGCTGGCT GAGGCGGTGG CCGGGGGCCG 120
 35 GGTGCTGGTG GTGGGGCGGG GCGGCATCGG CTGCGAGCTC CTCAAGAATC TCGTGCTCAC 180
 CGGTTTCTCC CACATCGACC TGATTGATCT GGATACTATT GATGTAAGCA ACCTCAACAG 240
 40 ACAGTTTTTG TTTCAAAAGA AACATGTTGG AAGATCAAAG GCACAGGTG CCAAGGAAAG 300
 TGTACTGCAG TTTTACCCGA AAGCTAATAT CGTTGCCTAC CATGACAGCA TCATGAACCC 360
 TGAATAAAT GTGGAATTTT TCCGACAGTT TATACTGGTT ATGAATGCTT TAGATAACAG 420
 45 AGCTGCCCCG AACCATGTTA ATAGAATGTG CCTGGCAGCT GATGTTCTCT TTATTGAAAG 480
 TGAACAGCT GGGTATCTTG GACAAGTAAC TACTATCAAA AAGGGTGTGA CCGAGTGTTA 540
 50 TGAGTGTCAT CTAAGCCGA CCCAGAGAAC CTTTCTGGC TGTACAATTC GTAACACACC 600
 TTCAGAACCT ATACATGCA TCGTTGGGC AAAGTACTTG TTCAACCAGT TGTTTGGGGA 660
 AGAAGATGCT GATCAAGAAG TATCTCCTGA CAGAGCTGAC CCTGAAGCTG CCTGGGAACC 720
 55 AACGGAAGCC GAAGCCAGAG CTAGAGCATC TAATGAAGAT GGTGACATTA AACGTATTTT 780
 TACTAAGGAA TGGGCTAAAT CAACTGGATA TGATCCAGTT AAACTTTTTA CCAAGCTTTT 840
 TAAAGATGAC ATCAGGTATC TGTTGACAAT GGACAACTA TGGCGGAAAA GGAAACCTCC 900
 60

	AGTTCGGTTG GACTGGGCTG AAGTACAAAG TCAAGGAGAA GAAACGAATG CATCAGATCA	960
	ACAGAATGAA CCCAGTTAG GCCTGAAAGA CCAGCAGGTT CTAGATGTAA AGAGCTATGC	1020
5	ACGTCCTTTT TCAAAGAGCA TCGAGACTTT GAGAGTTCAT TTAGCAGAAA AGGGGGATGG	1080
	AGCTGAGCTC ATATGGGATA AGGATGACCC ATCTGCAATG GATTTTGTCA CCTCTGCTGC	1140
10	AAACCTCAGG ATGCATATTT TCAGTATGAA TATGAAGAGT AGATTTGATA TCAAATCAAT	1200
	GGCAGGGAAC ATTATTCCTG CTATTGCTAC TACTAATGCA GTAATGCTG GGTGATAGT	1260
	ATTGGAAGGA TTGAAGATTT TATCAGGAAA AATAGACCAG TGCAGAACAA TTTTTTTGAA	1320
15	TAAACAACCA AACCCAAGAA AGAAGCTTCT TGTGCCTTGT GCACTGGATC CTCCCAACCC	1380
	CAATGTGTAT GTATGTGCCA GCAAGCCAGA GGTGACTGTG CGGCTGAATG TCCATAAAGT	1440
20	GACTGTTCTC ACCTTACAAG ACAAGATAGT GAAAGAAAAA TTTGCTATGG TAGCACCAGA	1500
	TGTCCAAATT GAAGATGGGA AAGGAACAAT CCTAATATCT TCCGAAGAGG GAGAGACGGA	1560
	AGCTAATAAT CACAAGAAGT TGTCAGAATT TGGAATTAGA AATGGCAGCC GGCTTCAAGC	1620
25	AGATGACTTC CTCCAGGACT ATACTTTATT GATCAACATC CTTCATAGTG AAGACCTAGG	1680
	AAAGGACGTT GAATTTGAAG TTGTTGGTGA TGCCCCGGAA AAAGTGGGGS CCAAACAAGC	1740
30	TGAAGATGCT GCCAAAAGCA TAACCAATGG GCAGTGATGA TGGGAGCTTC AGCCCTCCAC	1800
	CTYCACAGCT TCAAGGAGGC AAGATGGACG TYTCYCATAG TTGATYCGGR TGAAGAAGRT	1860
	TCTCCAATAA TTGCCCGACG TTCAITGAAG GAAGGAGGAG GAGGCCCGCC AAGAGGGGAA	1920
35	TTTAGGNTTG	1930

40 (2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1509 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

50	GGCCCTGGCC TCTGGGCTGA GGCTTGCTAG GGA CTGGGG TGGCTCTAAG GGCAGGGAT	60
	AGGGCTGGGG AGCGCCGGCC TGTGGCCCTG ACCAGCCCTT TCTCGTGCRG GTTCCACCCC	120
55	GATGCAGGTG GTCACGTGCT TGACGCGGGA CAGCTACCTG ACGCACTGCT TCCTCCAGCA	180
	CCTCATGGTC GTGCTGTCTT CTCTGGAACG CACGCCCTCG CCGGAGCCTG TTGACAAGGA	240
	CTTCTACTCC GAGTTTGGGA ACAAGACCAC AGGAAGATG GAGAACTACG AGCTGATCCA	300
60	CTCTAGTCGC GTCAAGTTTA CCTACCCAG TGAGGAGGAG ATTGGGGACC TGACGTTTAC	360

	TGTGGCCCAA AAGATGGCTG AGCCAGAGAA GGCCCCAGCC CTCAGCATCC TGCTGTACGT	420
5	GCAGGCCTTC CAGGTGGGCA TGCCACCCCC TGGGTGCTGC AGGGGCCCCC TGGGCCCCAA	480
	GACACTCCTG CTCACCAGCT CCGAGATCTT CCTCCTGGAT GAGGACTGTG TCCACTACCC	540
	ACTGCCCGAG TTGCCAAAG AGCCGCGCA GAGAGACAGG TACCGGCTGG ACGATGGCCG	600
10	CCGCGTCCGG GACCTGGACC GAGTGCTCAT GGGCTACCAG ACCTACCCGC AGCCCTCACC	660
	CTCGTCTTCG ATGACGTGCA AGGTCATGAC CTCATGGGCA GTGTCAACCT GGACCACTTT	720
15	GGGGAGGTGC CAGGTGGCCC GGCTAGAGCC AGCCAGGGCC GTGAAGTCCA GTGGCAGGTG	780
	TTTGTCCCCA GTGCTGAGAG CAGAGAGAAG CTCATCTCGC TGTGGCTCG CAGTGGGAG	840
	GCCCTGTGTG GCCGTGAGCT GCCTGTCGAG CTCACCGGCT AGCCCAGGCC ACAGCCAGCC	900
20	TGTCGTGTCC AGCCTGACGC CTACTGGGGC AGGGCAGCAG GCTTTTGTGT TCTCTAAAAA	960
	TGTTTATCC TCCCTTTGGT ACCTTAATTT GACTGTCTC GCAGAGAATG TGAACATGTG	1020
25	TGTGTGTGT GTTAATTCCT TCTCATGTTG GGAGTGAGAA TGCCGGGCCC CTCAGGGCTG	1080
	TGGTGTGCT GTCACTCTC CACAGGTGGT ACAGCCGTGC ACACCACTGT CGTGTCTGCT	1140
	GTGTGGGAC CGTGTTAAC ACGTGACACT GTGGGTCTGA CTTTCTCTTC TACACGTCTT	1200
30	TTCTGAAGT GTCGAGTCCA GTCCTTTGTT GCTGTGCTG TTGCTGTGTC TGTGTCTGTT	1260
	GGCATCTTGC TGCTAATCCT GAGGCTGGTA GCAGAATGCA CATTGGAAGC TCCCACCCCA	1320
35	TATTGTCTCT CAAAGTGGAG GTCTCCCCTG ATCCAGACAA GTGGGAGAGC CCGTGGGGGC	1380
	AGGGGACCTG GAGCTGCCAG CACCAAGCGT GATTCTGCT GCCTGTATTC TCTATTCCAA	1440
	TAAAGCAGAG TTTGACACCG TCAAAAAAAA AAAAAAAAAA AAAAAAAAAA ATTNCTGCGG	1500
40	CCTCAAGGG	1509

45 (2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 3173 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

55	TGACCCAS GCGTCCGTGC TTTTCCACAG AAGGTTAGAC CCTGAAAGAG ATGGCTCAGC	60
	ACCACCTATG GATCTTGCTC CTTTGCCTGC AAACCTGGCC GGAAGCAGCT GGAAAAGACT	120
60	CAGAAATCTT CACAGTGAAT GGGATTCTGG GAGAGTCAGT CACTTTCCT GTAAATATCC	180

	AAGAACCACG GCAAGTTAAA ATCATTGCTT GGACTTCTAA AACATCTGTT GCTTATGTAA	240
	CACCAGGAGA CTCAGAAACA GCACCCGTAG TTAGTGTGAC CCACAGAAAT TATTATGAAC	300
5	GGATACATGC CTTAGGTCCG AACTACAATC TGGTCATTAG CGATCTGAGG ATGGAAGACG	360
	CAGGAGACTA CAAAGCAGAC ATAAATACAC AGGCTGATCC CTACACCACC ACCAAGCGCT	420
10	ACAACCTGCA AATCTATCGT CGGCTTGGGA AACCAGAAAT TACACAGAGT TTAATGGCAT	480
	CTGTGAACAG CACCTGTAAT GTCACACTGA CATGCTCTGT AGAGAAAGAA GAAAAGAATG	540
	TGACATACAA TTGGAGTCCC CTGGGAGAAG AGGGTAATGT CCTTCAAATC TTCCAGACTC	600
15	CTGAGGACCA AGAGCTGACT TACACGTGTA CAGCCCAGAA CCCTGTCAGC AACAAITCTG	660
	ACTCCATCTC TGCCCGGCAG CTCTGTGCAG ACATCGCAAT GGGCTTCCGT ACTCACCACA	720
20	CCGGTTTGCT GAGCGTCTG GCTATGTCTT TTCTGCTTGT TCTCATTTCTG TCTTCAGTGT	780
	TTTTGTTCAG TTGTTCAG AGAAGACAAG ATGCTGCCTC AAAGAAAACC ATATACACAT	840
	ATATCATGGC TTCAAGGAAC ACCCAGCCAG CAGAGTCCAG AATCTATGAT GAAATCCTGC	900
25	AGTCCAAGGT GCTTCCCTCC AAGGAAGAGC CAGTGAACAC AGTTTATTCC GAAGTGCAGT	960
	TTGCTGATAA GATGGGAAA GCCAGCACAC AGGACAGTAA ACCTCCTGGG ACTTCAAGCT	1020
30	ATGAAATTGT GATCTAGGCT GCTGGGCTGA ATTCTCCCTC TGGAAACTGA GTTACAACCA	1080
	CCAATACTGG CAGGTTCCCT GGATCCAGAT CTCTCTGCC CAACTCTTAC TGGGAGATTG	1140
	CAAACTGCCA CATCTCAGCC TGTAAGCAAA GCAGGAAACC TTCTGCTGGG CATAGCTTGT	1200
35	GCCTAAATGG ACAAATGGAT GCATACCCCTT CCTGAAATGA CTCCTTCTG AATGAATGAC	1260
	AAAGCAGGTT ACCTAGTATA GTTTTCCCAA ACTTCTTCCC ATCATAGCAC ATGTAGAAAA	1320
40	TAATATTTTT ATGGCAGCT GGGATAAACA AGCAAGATTG CTCACTTCTG GAAGCTGCAT	1380
	ATGACTAGAG GCCTCTGTG ACTGGAGGTA ACAACCCTGC CCAGTAACTG TGGGAGAAGG	1440
	GGATCAATAT TTGTCACACC TGTAATAGGC CATGGCACAC CAGCCAAGAT GCTCTGCTCA	1500
45	CAGTCAGTAT GTGTGAAGAT CCCTGGTGG TGGCCTTCAC CACGCATCTT GAGCAAATTA	1560
	GGAAAATGTA CCCTTCGCTT GAGGCAGATG CAGCCCTTCC CCGAGTGCA TGGCTTGGAG	1620
50	AGCAGAAATG GGGCTGCATA TAAGCAGACT CATCCCTTTG TCTGGGAATC TTTGTGCAGG	1680
	GCATAACAGG CTTAGTAAGT CCAAACACAG ATGACAGTGC TGTGTGGGTC TCTGTCAGAG	1740
	TTGTGGCTCT CAGCCATGTA GACACACTCT CCAAATGGAG TGTGGAAAA TGTTCCTTCT	1800
55	GCAGGTCTA GAGACTGCTG GGACACTTTT CTGGAGTGC TACTTCAGAA GCCTTATAGG	1860
	ATTTTCTTTC TGGCCAAGAT TTCCTTCTGT ATCACTCCAA GCAGCCTCAG CAGAAGAAGC	1920
60	AGCCATGCCC AGTATTCCCA CTCTCCAAAA GGAAGTGACC AGCTTATATT TCTCACACTT	1980

	CTGGGGAAC T GGTATAATC CAACCATCAA AATAGAAGAC CTTGCAAGAA GCAGAGTCAT	2040
	TCTCCAGAAG GAACTTGGGA GATGATGGTG CAGATGATGA AACTGGGTTC ATCCCAGTTC	2100
5	CAAAGACTCA GAGAACTAGA GTTTAAGCTG AGGCAGAGTG CCGCCACCCT GGCATGCCCC	2160
	ACAAACAGAT CACCAGCCAG CTTACACAGG CATTAACTCT CCTCAATGAG GAAGAATCAT	2220
10	TCACAAC TGA GCAAGACATT CATATGATCA TTTAAGGAAG TGTTCCTT ATGTGTTAGC	2280
	AAGTATAATC GGCTAACTCC TAAATCCCAA TGAATAGTCC TAGGCTGGAC AGCAATGGGC	2340
	TGCAATTAGG CAGATAAAGA CATCAGTCCC AGTAAATGAA TCCATAGACT CATCTAGCAC	2400
15	CAACTACCAT TAGCACTATG TTAGGAGCTG CAAGGCCCCA AAGTAGAAGA TGTGCATAAT	2460
	GTCTGCTCTT GTGTAGCTCA GGAGACAATT CCAGCACAGA CACTACAGTT AACGCTGAAC	2520
20	TGCAGCTGCA AGTAATAGCA TGAACAGTCA GAAAAATACC TTATGAGGGG GCAGGGCTGA	2580
	AGCTGGGCC TGAAGGATGG ATGAAATTTG GATAGAGAAT GAGGAAGACA GAGGGCCTCC	2640
	AAGTGAGAGA AGCATGAAAA ATGAGCAGGG GCCTGGATCA GTGGGGTGTA TTCAGAGCAC	2700
25	CTCTCCAGAT GCACCATGCA TGCTCACAGT CCCTTGCTTA TGTGTGGCAG AGTGTCCAG	2760
	CCAGATGTGT GCGCCACCC CATGTCCATT TACATGTCT TCAATGCCA CCTCAAAGG	2820
30	TACCTCTCT GTAAAGCTTT CCCTGGTATC AGGAATCAAA ATTAATCAGG GATCTTTTCA	2880
	CACTGCTGTT TTTTCTCTT TGGTCCTTCT ATCACTAAAA CTCATCTCAT TCAGCCTTAC	2940
	AGCATAACTA ATTATTTGTT TTCTCACTA CATGTACAT GTGGGAATTA CAGATAAACG	3000
35	GAAGCCKGCT GGGGTGGTGG CTCACGCTG TAATCCCAAC ACTTGGGAG GCCAAGGCAG	3060
	GCGGATCACC TGAGGTCAGG ARTTCGAGAT TARCTGGCC AACATGGTGA AACCCCATNT	3120
40	NTACTAAAA TACGAAATTA GCCAGGTGTG GTGGCACACA TCTGTAGTCC CAG	3173

(2) INFORMATION FOR SEQ ID NO: 175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 991 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

55	AAATTGCGCA CAGCTGAGAG GAGACACAAG GAGCAGCCG CAAGCACCAA GTGAGAGGCA	60
	TGAAGTTACA GTGTGTTTCC CTTTGGCTCC TGGGTACAAT ACTGATATTG TGCTCAGTAG	120
	ACAACCACGG TCTCAGGAGA TGTCTGATTT CCACAGACAT GCACCATATA GAAGAGAGTT	180
60	TCCAAGAAAT CAAAAGAGCC ATCCAAGCTA AGGACACCTT CCCAAATGTC ACTATCCTGT	240

CCACATTGGA GACTCTGCAG ATCATTAAAGC CCTTAGATGT GTGCTGCGTG ACCAAGAACC 300
 TCCTGGCGTT CTACGTGGAC AGGGTGTTC AAGATCATCA GGAGCCAAAC CCCAAAATCT 360
 5 TGAGAAAAAT CAGCAGCATT GCCAACTCTT TCCTCTACAT GCAGAAACT CTGCGGCAAT 420
 GTCAGGAACA GAGGCAGTGT CACTGCAGGC AGGAAGCCAC CAATGCCACC AGAGTCATCC 480
 10 ATGACAACTA TGATCAGCTG GAGGTCCACG CTGCTGCCAT TAAATCCCTG GGAGAGCTCG 540
 ACGTCTTTCT AGCCTGGATT AATAAGAATC ATGAAGTAAT GTCCTCAGCT TGATGACAAG 600
 GAACCTGTAT AGTGATCCAG GGATGAACAC CCCCTGTGCG GTTFACTGTG GGAGACAGCC 660
 15 CACCTTGAAG GGAAGGAGA TGGGAAGGC CCCTTGCAGC TGAAAGTCCC ACTGGCTGGC 720
 CTCAGGCTGT CTTATTCCGC TTGAAAATAG CCAAAAAGTC TACTGTGGTA TTTGTAATAA 780
 20 ACTCTATCTG CTGAAAGGCG CTGCAGGCCA TCCTGGGAGT AAAGGGCTGC CTTCCCATCT 840
 AATTTATTGT GAAGTCATAT AGTCCATGTC TGTGATGTGA GCCAAGTGAT ATCCTGTAGT 900
 ACACATTGTA CTGAGTGGTT TTTCTGAATA AATTCCATAT TTTACCTAAA AAAAAAAAAA 960
 25 AAAAACTCGA GGGGGGGCCC GTACCCAATT T 991

30

(2) INFORMATION FOR SEQ ID NO: 176:

(1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1290 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

40

ACAGCCCTCT TCGGAGCCTG AGCCCGGCTC TCCTCACTCA CCTCAACCCC CAGGCGGCC 60
 CTCACAGGG CCCCTCTCCT GCCTGGACGG CTCTGCTGGT CTCCCCGTCC CCTGGAGAAG 120
 45 AACAAAGCCA TGGGTGCGCC CTGCTGCTG CCCCTRCTGC YCCTGCTGCW GCCGCCAGCA 180
 TTTCTGCAGC CTRGTGGCTC CACAGGATCT GGTCCAAGCT ACCTTTATGG GGTCACTCAA 240
 CCAAAACACC TCTCAGCCTC CATGGGTGGC TCTGTGGAAA TCCCTTCTC CTTCTATTAC 300
 50 CCCTGGGAGT TAGCCAYAGY TCCCRACGTG AGAATATCCT GGAGACGGG CCACTTCCAC 360
 GGGCAGTCCT TCTACAGCAC AAGCCCGCCT TCCATTCACA AGGATTATGT GAACCGGCTC 420
 55 TTTCTGAACT GGACAGAGGG TCAGGAGAGC GGCTTCCTCA GGATCTCAAA CCTGCGGAAG 480
 GAGGACCACT CTGTGTATTT CTGCCGAGTC GAGCTGGACA CCCGGAGATC AGGGAGGCAG 540
 CAGTTGCAGT CCATCAAGGG GACCAAACTC ACCATCACCC AGGCTGTCAC AACCACCACC 600
 60

	ACCTGGAGGC CCAGCAGCAC AACCACCATA GCCGGCCTCA GGGTCACAGA AAGCAAAGGG	660
	CACTCAGAAT CATGGCACCT AAGTCTGGAC ACTGCCATCA GGGTTGCATT GGCTGTCGCT	720
5	GTGCTCAAAA CTGTCAATTT GGGACTGCTG TGCCTCCTCC TCTGTGGTGG AGGAGAAGGA	780
	AAGGTAGCAG GGGCCCAAGC AGTGACTTCT GACCAACAGA GTGTGGGGAG AAGGGATGTG	840
10	TATTAGCCCC GGAGGACGTG ATGTGAGACC CGCTTGAGAG TCCTCCACAC TCGTTCCCCA	900
	TTGGCAAGAT ACATGGAGAG CACCTGAGG ACCTTTAAAA GGCAAAGCCG CAAGGCAGAA	960
	GGAGGCTGGG TCCCTGAATC ACCGACTGGA GGAGAGTTAC CTACAAGAGC CTTTCATCCAG	1020
15	GAGCATCCAC ACTGCAATGA TATAGGAATG AGGTCTGAAC TCCACTGAAT TAAACCACTG	1080
	GCATTTGGGG GCTGTTYATT ATAGCAGTGC AAAGAGTTCC TTTATCCTCC CCAAGGATGG	1140
20	AAAATACAAT TTATTTTGCT TACCATACAC CCCTTTTCTC CTGCTCCACA TTTTCCAATC	1200
	TGTATGGTGG CTGTCTTCTA TGGCAGAAGG TTTTGGGGAA TAAATAGCGT GANATGNTNC	1260
	TGACTNAAAA AAAAAAAAAA AAAAACTCGA	1290

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(2) INFORMATION FOR SEQ ID NO: 177:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2290 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

	TGGGGCCCTT TTTGGATGCT CTGGGTGTTT TTGCCAAGAG TTACAGGATG TCAAGTGTGG	60
40	GGAGCTCAGC ACCCTTGCTG TGGACCAGTG AAGGCTGTTT CAGACCAGGT GCTTCCAGAC	120
	ATTTCCAGGC TCCAGGAGAG AGGCTGGGAG CCCCCACAGA AAGCACAGGA AAATGCAAAA	180
45	AAAAAACAGT CTTTTTTTTT TTTTGTCTT TTATTATGAA AACAAAACAA ATGCCCCAGG	240
	AGAAGGTCC ATGATTACCA GAAACATCAA AGAGTACTTT CTACCATTTT TATCTGTGTG	300
	TGTTGAGGCC AGCATTGCAA TAAACAAGCT AAAGTACTTA CATTTGACTC ATTTTCAGTA	360
50	ACTGACATTT ACAGGAATAT ACTAGAAACG GCACTAAAAA GTTTAAGAAA AGTTACGGTA	420
	AACTTGCAATG CACATCATAC AGAAAAGTAA CATTTTAAAT ATAAAAAGA AAAACTTCCT	480
55	GGAAGCATTG TGCCAGTATT AAGGAACAGT GCTACTCTGG ATGTGACAAA TTCTGTATGT	540
	GGGTGTTACT CTTTCCCAAA AGACTGTCAG AGGCGTGAGT GCTGCAAAAG AACACAACA	600
	AAAACAACA CACAAAAAAA TGTGTCTTAC AGTTTGTAAG CAAGATGACA CTGCCCCACA	660
60	CAAAGAGGGG TCTGGAGTTC AGTTCACGCC CGAAGCCTGC CCCCTGGGCC TCCAGGGGTC	720

	ATTCAGAGTG TTCTCAAATC CAATTCCGAC ACACGACTTG TCACTACTCC TCTCCCCCTG	780
5	AAAAAAGCAT GTTAGAAGCT GOCCTACAGG TCTCAGCAGT GGGACAATCT AATTGAATCA	840
	CCGCAGCCTT CTAATACAGA AGAAACGGAC GTGACTGTCA CCCTCAGCCC GCCAGCAAGG	900
	GCGCTGAGGA AGTCATTAAT CCTTCGAAAC TCTGAAAAGA AACCAGTGT T GAAGTCTGGA	960
10	CAGAAAGCCT TAAAAAAGTG ACAGCACCAA TGCAGCTGCT CAGTGTACCC NCCGTGGGCT	1020
	GTCAGGGTCA GTGGCTTCTT TCTAGATGAA AGGAGCAGAG GCGAGCCGAC GCCACCGTCA	1080
15	CAGAGAACCA GCCGAGAAGG AAAGGCCCCA CGATGCTCCC TGTGCGCTGC CCCACAGCC	1140
	GGCCGCTCCC CCGACGGCTC ACACAGGCAG CACCTCACTG CCCTGTGGCT GGAGGGGCAT	1200
	TGCAAGGAGC GCGCCCGAGC CCCAGGCACC CCGGCTTAG GGTGTACGTA TCACCCAGCC	1260
20	CTGTGCTGGC AGCACGTTAC CAACCAGCCT GCGTGAAGAC CTGTCAACTG TCGTGTGTGA	1320
	ATTCTTTAAA TTCGGTTTAA ATAGTCCATT AAAGATCTGT TTAGAAAATA CCTTTGAAAA	1380
25	CGAGGGTAAC TTTAAAAAAT GGAAACTTTC AAATCCATTT ATATTTTAT TATAAACAAA	1440
	ACTTAATTAA AAGTTTAACA AACTGGCTGA AAACCTACCA AGTGTGAGAC TCACCAGCAA	1500
	TTTAAAAAAT GATAATTTAC CAGCATCTCC TCATCAGAGT TCCCTCTCCA GTAAGGGTAT	1560
30	ACCTACATCT GTAAGGGTCA GTGGACTCTG AATCAATTTT ATGGTTGTTT TAAAATCACC	1620
	GTGTATTAGG ATACTAATGA TAGTCCCTAT ATCCATCCAG AAATGCTGGC AGAAAGCACT	1680
35	GGCCACCATA CAGGACAGAC CACACCACAG CTCCATACCC AGCGTCTGCC TGGAGGCTCC	1740
	CCCAAGCTGA GGTCCGGGAG AATGCCTGGT TTCAGTCATT TCCGGACTAA CTGTGACAAC	1800
	GCGTGAGCAG GGAGCACCGT GCGAGTCTCC GGGAGGGAAT CCTCCTGGG CCCAGAGACT	1860
40	CCTCCACCCC TGGGGAGGGC AGACAGGCTC GGGARGGCCT GGCCAGGCCA CTGGAGGCTG	1920
	GCAGGGAGCA GGCATGTCCA CCGCAAGCC TGGGAGGCTA ACTCTGGCAT TCCTGGCCGG	1980
45	AGCCGCCATG CTCATTGGTG GGCCAGTTTG GGACATCCCC GTACTCAAAG ACCATATGGC	2040
	AGCCTCTGGG AAAACAAAAC CAAAACATCA CCTTCTATTA AACTCTGTAT ATTATTATTT	2100
	TTTACAATAG AAAGTTAAAA ATCAAGACTT AGATTTACTA TACATTTTTT CTCTCAGATT	2160
50	ACAAAGTTTA TATTATATAA CTGGGGTTCC CTAAATTGAT TTCTTTTAAA ACAGTCTTAA	2220
	AGAGACCAGA AGTGAATACA AAAGAACTAA ACAAATAAAA AAATTAGAAT GTGCTGTAGC	2280
55	TGAAAGCTGT	2290

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

GGCAGAGCC ATGCCTGGCC TCTCCTTGAT TCTTACAGTC ACTTGTGTGG CTGTTTCTGA 60
 CTCAGCAGCT ACCTGCATTG TGGCCAAAGG ATGACCTATT CCTTCTCAGG AGGGCAAAAA 120
 TGTGGAATAG TGTCTGTCCA TGCCTCTCCT CATGGGCTAC CACCTCTGCC ACCGTGGTTA 180
 ATCAGTAACA ACCAGGAGAG AAGCTGCTGG AACTGACCTC TGGGAACTCC CTGGGATGGT 240
 TTGGTGCAAG AATGTAGTAG GCATACACGT GGTGCGTGG ATCTGGGCCC TCCTGATGTG 300
 AGTAGAGAGG TAAAAGGCCA CCATCTCCTT GACCTCTGGG GAACTCATCC ACAAAGAAGA 360
 TGTTCCTCAAG ATGCTTCTGA AGATTGCCTA AAAATAGCCG GTTCCACCC CCGTGAATGC 420
 ATCCATTCTA GAATGCTCCT TCACCAGGAC CAGAGAACTG ATTTACAGAA GTGACATGAA 480
 AACATTCCAT CCCAGAATTT GCAGTAGCTC AAATTAAGTT TCTAGCTATT AAAAAGAAAA 540
 AAAAAAAAAA 549

30

(2) INFORMATION FOR SEQ ID NO: 179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1509 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

GGCAGAGGG CTCATTCATT CCGCGCGGG CCTGCCAGAC ACCTGCGCCC TTCTGCAGCC 60
 GCGCGCGCA TCGCGCGCG CAGCCCCAG CATGTGGGC CCAGACGTGG AGACGCGTC 120
 CGCCATCCAG ATCTGCCGA TCATGCGGCC AGATGATGCC AACGTGGCCG GCAATGTCCA 180
 CGGGGGGACC ATCTGAAGA TGATCGAGGA GGCAGGCGCC ATCATCAGCA CCCGGCATTG 240
 CAACAGCCAG AACGGGGAGC GCTGTGTGGC CGCCCTGGCT CGTGTGAGC GCACCGACTT 300
 CCTGTCTCCC ATGTGCATCG GTGAGGTGGC GCATGTCAGC GCGGAGATCA CCTACACCTC 360
 CAAGCACTCT GTGGAGGTGC AGGTCAACGT GATGTCCGAA AACATCCTCA CAGGTGCCAA 420
 AAAGTGACC AATAAGGCCA CCCTGTGGTA TGTGCCCTG TCGCTGAAGA ATGTGGACAA 480
 GGTCTCGAG GTGCCTCCTG TTGTGTATTC CCGGCANGAG CAGGAGGAGG AGGGCCGGAA 540
 GCGGTATGAA GCGCAGAAGC TGGAGCGCAT GGAGACCAAG TGGAGGAACG GGGACATCGT 600

60

	CCAGCCAGTC CTCAACCCAG AGCCGAACAC TGTCAGCTAC AGCCAGTCCA GCTTGATCCA	660
5	CCTGGTGGGG CCTTCAGACT GCACCTGCA CGCCTTGTG CACGGAGGTG TGACCATGAA	720
	GCTCATGGAT GAGGTGCGCG GGATCGTGGC TGCACGCCAC TGCAAGACCA ACATCGTCAC	780
	AGCTTCCGTG GACGCCATTA ATTTTCATGA CAAGATCAGA AAAGGCTGCG TCATCACCAT	840
10	CTCGGGACGC ATGACCTTCA CGAGCAATAA GTCCATGGAG ATCGAGGTGT TGGTGGACGC	900
	CGACCTGTT GTGGACAGCT CTCAGAAGCG CTACCGGGCC GCCAGTGCCT TCTTCACCTA	960
15	CGTGTGCGTG AGCCAGGAAG GCAGGTGCT GCCTGTGCC CAGCTGGTGC CCGAGACCGA	1020
	GGACGAGAAG AAGCGCTTTG AGGAAGGCAA AGGGCGGTAC CTGCAGATGA AGGCGAAGCR	1080
	ACAGGGCCAC GCGGASCYTC AGCCCTAGAC TCCCTCCTCC TGCCACTGGT GCCTCGAGTA	1140
20	GCCATGGCAA CGGGCCAGT GTCCAGTCAC TTAGAAGTTC CCCCCTTGGC CAAAAACCCA	1200
	ATTACATATG AGAGCTGGTG TTGTCTGAAG TTTTCGTATC ACAGTGTAA CCTGTACTCT	1260
25	CTCCTGCAA CCTACACACC AAAGCTTTAT TTATATCATT CCAGTATCAA TGCTACACAG	1320
	TGTTGTCCCG AGCGCCGGGA GCGTGTGGC AGAAACCCTC GGAATGCTT CCGAGCACGC	1380
	TGTAGGGTAT GGAAGAACC CAGCACCCT AATAAAGCTG CTGCTTGGCT GGAAAAAAAA	1440
30	AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1500
	AGAAAAAAN	1509

35

(2) INFORMATION FOR SEQ ID NO: 180:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

	AGCTGTATCA TAGGAAAGAT GGCCACACCG GCGGTACCAG TAAGTGCTCC TCCGGCCACG	60
50	CCAACCCAG TCCCGGGCGG GCGCCAGCC TCAGTTCCAG CGCCAACGCC AGCACCGGCT	120
	GCGGCTCCGG TTCCCGCTGC GGCTCCAGCC TGCACTCTCA GACCTGCGG CAGCAGCGGC	180
	TGCAACTGCG GCTCCTGGCC AGACCCCGGC CTCAGCGCAA NTCCAGCGCA GACCCAGCG	240
55	CCCCTCTGC CTGGTCTGC TCTTCCAGGG CCTTCCCCG GCGGCCGCGT GGTGAGGCTG	300
	CACCCAGTCA TTTTGGCCTC CATGTGTGAC AGCTACGAGA GACGCAACGA GGGTGCTGCC	360
60	CGAGTTATCG GGACCTGTT GGAAGTGTG GACAAACACT CAGTGGAGGT CACCAATTGC	420

	TTTTCAGTGC CGCACAAATGA GTCAGAAGAT GAAGTGGCTG TTGACATGGA ATTTGCTAAG	480
	AATATGTATG AACTGCATAA AAAAGTTTCT CCAAATGAGC TCATCCTGGG CTGGTACGCT	540
5	ACGGGCCATG ACATCACAGA GCACTCTGTG CTGNATOCAT GAGTACTACA GCGGAGAGGC	600
	COCCAAACCC ATCCACCTCA CTGTGGACAC AAGTCTOCAG AACGGCCGCA TGAGCATCAA	660
10	AGCCTACGTC AGCACTTTAA TGGGAGTCCC TGGGAGGACC ATGGGAGTGA TGTTCACGCC	720
	TCTGACAGTG AAATACGCGT ACTACGACAC TGAACGCATC GGAGTTGACC TGATCATGAA	780
	GACCTGCTTT AGCCCCAACA GAGTGATTGG ACTCTCAAGT GACTTGCAGC AAGTAGGAGG	840
15	GGCATCAGCT CGCATCCAGG ATGCCCTGAG TACAGTGTG CAATATGCAG AGGATGTACT	900
	GTCTGGAAAG GTGTCAGCTG ACAATACTGT GGGCCGCTTC CTGATGAGCC TGGTTAACCA	960
20	AGTACCGAAA ATAGTTCCCG ATGACTTTGA GACCATGCTC AACAGCAACA TCAATGACCT	1020
	TTTGATGGTG ACCTACCTGG CCAACCTCAC ACAGTCACAG ATTGCACTCA ATGAAAAACT	1080
	TGTAAACCTG TGAATGGACC CCAAGCAGTA CACTTGCTGG TCTAGGTATT AACCCAGGA	1140
25	CTCAGAAAGT AAGGAGAAAT GGGTTTTTTG TGGTCTGAG TCACACTGAG ATAGTCAGTT	1200
	GTGTGTGACT CTAATAAACG GAGCCTACCT TTTGTAAATT AAAAAAAAAA AAAAAAACCN	1260
30	SGRGGGGGGG CCCGGTCCCA TTSSCCCTTT NGTAATTCGT NTTACAATCC CCNGGC	1316

35 (2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 777 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

45	GGCATGWKCA GACATGACTT CTATTGCCAG GCTGGTCAAG TGGCAGGGTC ATGAGGGAGA	60
	CATCGATAAG GGTGCTCCTT ATGCTCCCTG CTCTGGAATC CACCAGCGGG CTATCTGCGT	120
	TTATGGGGCT GGGGACTAGA ATTGGATGCT TCAAAACCAT CACCTGTTGG CCAACAAGTT	180
50	TGACCCAAAG GTAGATGATA ATGCTCTTCA GTGCTTAGAA GAATACCTAC GTTATAAGGG	240
	CCATCTTATT GGGACCTGAA CTTTGAAGAC CACAMTATTG AAGAGGCGTT GCTTACCYGT	300
55	TGGGGGCCAA GAGGCATGTT ACCAAACATG GYYCARGAAM YTTGGYKGGG AMCARKKKKG	360
	GKKGGGARRM CMRGGGYTTG SCAAWTTC SK KGGCMWCCYT TTAGGGTAAR RRRGGGCKGTW	420
	ATTAGATTGT GGGTAAAGTA GGATCTTTTG CCCTTGCAAA TTTGCTGCCT GGGTGAATGY	480
60	TGCTTGTTCC TTCTCMACCC CTAACCCTAG TAGTTCCTCC ACTAACTTTC TCACTAAGTG	540

AGAATGAGAA CTGCTGTGAT AGGAGAGTG AAGGAGGGAT ATGTGGTAGA GCACTTGATT 600
 TCAGTTGAAT GCCTGCTGGT AGCTTTTCCA TTCTGTGGAG CTGCCGTTCC TAATAATTCC 660
 AGGTTTGSTA GCGTGGAGGA GAACTTTGAT GGAAGAGAA CCTTCCCTTC TGTACTGTTA 720
 ACTTAAAAAT AAATAGCTCC TGATTCAAAG TAAAAA AAAA AAAA 777

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(2) INFORMATION FOR SEQ ID NO: 182:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 791 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

GGCACAGATA ACTATGTACA TGTATTCCTT AAATGTTTTT TTAAGTTTTA TATTCCTGGC 60
 ACTGGTCTTC AAATGTGTAC ATGTGTGCCA GGGAGCAAAT GCCTTCTTGT TTCTGAAATT 120
 GGTCCTTITAG ACTGTTCTTT TTCCCATCT TCTCACCTCC TGCCCTCCT TCAGGGTACT 180
 TCCGTGCCA GAACCCCTCC AGGTCAGAGG CAGAAGAGAA GCCTCATGGG TCACAGCAGC 240
 AGATGTGGGC TGGAGATCTA TTCAATTGGT TTGGCCTTGA ATTTTCTGRA TGGTTTACTT 300
 GATCYTGGGA AAGANATATC TGCCAGGAA AAATGATAGN CCTTGACAAT GTTGAATGAT 360
 CCTGCACCAC CTGAAAGAC ATTTCTAATA TGGTTTGTC GCAAAGTGG TTAGTAGTCA 420
 TTTGTGCCCT GAGGTAGAAG TCCTCAGAAA TCAGCAGACT TCACTGATAA AATGCTGACT 480
 TGCCCTGGA CTGGGCTCTG TGAGAGTGGC CTCTGCACT GTGCACAGTA GGTGTGAACA 540
 CACCACACCT ACAGGGACCA CGTGGTGGC TGTGGACTAG CGGCAAGCT CCCTGCAGGC 600
 CCACTAATAG AATTCAGCTT TTAGCATGGG CTGTTTCATA CTGTTCTGAT GAAACTGATT 660
 TGGTTTCTTT CCTCCATACC CCTTCTGCAT TTCAGTGTTT TTGTTAGTT TCCTGGTTT 720
 TTAATTATAA CTACAAAATA AAATCTTTAG GCTATTCACC TTAGCTTAGT AAAAAA 780
 AAAAAAACT C 791

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(2) INFORMATION FOR SEQ ID NO: 183:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1405 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

5	AAATTGATTA ACAGCTTGAA AGAAGGCTCT GGTTTTGAAG GCCTAGATAG CAGCACTGCC	60
	AGTAGCATGG AGCTGGAAGA ACTTCGGCAT GAGAAAGAGA TGCAGAGGGA GGAAATACAG	120
	AAGCTGATGG GCCAGATACA TCAGCTCAGA TCCGAATTAC AGGATATGGA GGCACAGCAA	180
10	GTTAATGAAG CAGAATCAGC AAGAGAACAG TTACAGGWTG TGCATGACCA AATAGCTGGG	240
	CAGAAAGCAT CCAAACAAGA ACTAGAGACA GAACTGGAGC GACTGAAGCA GGAGTTCCAC	300
	TATATAGAAG AAGATCTTTA TCGAACAAAG AACACATTGC AAAGCAGAAT TAAAGATCGA	360
15	GACGAAGAAA TTCAAAACT CAGGAATCAG CTTACCAATA AAACTTTAAG CAATAGCAGT	420
	CAGTCTGAGT TAGAAAATCG ACTCCATCAG CTAACAGAGA CTCTCATCCA GAAACAGACC	480
20	ATGCTGGAGA GTCTCAGCAC AGAAAAGAAC TCCCTGGTCT TTCAACTGGA GCGCCTCGAA	540
	CAGCAGATGA ACTCGCCTC TGAAGTAGT AGTAATGGGT CTTGATTAA TATGTCTGGA	600
	ATTGACAATG GTGAAGGCAC TCGTCTGCGA AATGTTCTTG TTTCTTTTAA TGACACAGAA	660
25	ACTAATCTGG CAGGAATGTA CGAAAAGTT CGCAAAGCTG CTAGTTCAT TGATCAGTTT	720
	AGTATTGCC TGGGAATTT TCTCGAAGA TACCCCATAG CGCGAGTTT TGTAAATATA	780
30	TATATGGCTT TGCTTCACCT CTGGGTCATG ATTGTTCTGT TGAATTACAC ACCAGAAATG	840
	CACCAGGACC AACCATATGG CAAATGAACC AAGCCCAGTT GTTGCACTGA TTGGTTGTCT	900
	TTTTCTAGAC TTGGGATCTG CAAGAAGGCC AATGCTCTAA AATTCTGAG AACAGTGCAC	960
35	AAGATTATTT TATCACTACA AGCTTTTAAC TTTTAAAGTT ATTGTACAAG TATTCTACCT	1020
	AAATCTTCCA ATTTCTTTA AATGGTAAGA GTTTCTAAA CAGACAATA TTTAACAAGC	1080
40	TCAGCTCTGC TTTATCTGAG TTAGTGGTC CTAATATATA TGTAAGAGAA GATGGTGGG	1140
	TTGTTACCT CTGTACAGAC CATCTGTATG TTAGGTGACA TTGATTATGG GTTATAATCA	1200
	GGGAACTAA TTGTATTTAG TGACAAAAT AAAAAGTTTT TTTTATATA TTCAGTCTGC	1260
45	TTTTGGATTT TCATATATTT AACTTTGCAA AAAGATTAC TTTGTACATG TTACAGGCTT	1320
	GATTGGTGTA AATCTTTTAA TAAATACATA AATAAAGNA AAATATGCAT TTTCTTTTC	1380
50	TAAAAAAAAA AAAAAAAAAA CTCGA	1405

55 (2) INFORMATION FOR SEQ ID NO: 184:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1596 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

5	GTTCATGCACT GCGCCGGAGA ACTGTGCTCT TTGAGGCCGA CGCTAGGGGC CCGGAAGGGA	60
	AACTGCGAGG CGAAGGTGAC CGGGGACCGA GCATTTTCAGA TCTGCTCGGT AGACCTGGTG	120
	CACCACCACC ATGTTGGCTG CAAGGCTGGT GTGTCTCCGG ACACTACCTT CTAGGGTTT	180
10	CCACCCAGCT TTCACCAAGG CCTCCCCGTG TGTGAAGAAT TCCATCACGA AGAATCAATG	240
	GCTGTTAACA CCTAGCAGGG AATATGCCAC CAAAACAAGA ATTGGGATCC GCGTGGGAG	300
15	AACTGGCCAA GAACTCAAAG AGGCAGCATT GGAACCATCG ATGGAAAAA TATTTAAAT	360
	TGATCAGATG GGAAGATGGT TTGTTGCTGG AGGGGCTGCT GTTGGTCTTG GAGCATTGTG	420
	CTACTATGGC TTGGGACTGT CTAATGAGAT TGGAGCTATT GAAAAGGCTG TAATTTGGCC	480
20	TCAGTATGTC AAGGATAGAA TTCATTCCAC CTATATGTAC TTAGCAGGGA GTATTGGTTT	540
	AACAGCTTTG TCTGCCATAG CAATCAGCAG AACGCCCTGT CTCATGAACT TCATGATGAG	600
25	AGGCTCTTGG GTGACAATTG GTGTGACCTT TGCAGCCATG GTTGGAGCTG GAATGCTGGT	660
	ACGATCAATA CCATATGACC AGAGCCCAGG CCCAAAGCAT CTGCTTGGT TGCTACATTC	720
	TGGTGTGATG GGTGCAGTGG TGGCTCCTCT GACAATATTA GGGGGTCTC TTCTCATCAG	780
30	AGCTGCATGG TACACAGCTG GCATTGTGGG AGGCTCTTCC ACTGTGGCCA TGTGTGCGCC	840
	CAGTGAAAAG TTTCTGAACA TGGGTGCACC CCTGGGAGTG GGCCTGGGTC TCGTCTTTGT	900
35	GTCTCTATTG GGATCTATGT TTCTTCCACC TACCACCGTG GCTGGTGCCA CTCTTTACTC	960
	AGTGGCAATG TACGGTGGAT TAGTTCTTTT CAGCATGTC CTCTGTATG ATACCCAGAA	1020
	AGTAATCAAG CGTGCAGAAG TATCACCAAT GTATGGAGTT CAAAAATATG ATCCCATTA	1080
40	CTCGATGCTG AGTATCTACA TGGATACATT AAATATATTT ATGCGAGTTG CAACTATGCT	1140
	GGCAACTGGA GGCAACAGAA AGAAATGAAG TGACTCAGCT TCTGGCTTCT CTGCTACATC	1200
45	AAATATCTTG TTTAATGGG CAGATATGCA TTAATAGTT TGTACAAGCA GCTTTCGTTG	1260
	AAGTTTAGAA GATAAGAAAC ATGTCATCAT ATTTAAATGT TCCGGTAATG TGATGCCTCA	1320
	GGTCTGCCTT TTTTCTGGA GAATAAATGC AGTAATCCTC TCCCAAATAA GCACACACAT	1380
50	TTTCAATCTT CATGTTTGAG TGATTTTAAA ATGTTTGGT GAATGTGAAA ACTAAAGTTT	1440
	GTGTCAATGAG AATGTAAGTC TTTTCTTAC TTTAAAATTT AGTAGGTTCA CTGAGTAACT	1500
55	AAAATTTAGC AAACCTGTGT TTGCATATTT TTTKGGAGTG CAGMMTAWTG TAATTARAGC	1560
	ATTCCAGTAA NAGTGTNTTT AAAGTTGNTC TATATN	1596

(2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 2293 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

GCGCAGAGCC CGYACGAGCA GGACGACGAC GACAAGGGCG ACTCCAAGGA AACGCGGCTG 60
ACCCGTGATGG AGGAAGTGCT CCTGCTGGGC CTCAAGGACC GCGARGGTTA CACATCATTT 120
15 TGGAAATGACT GTATATCATC TGGATTACGT GGCTGTATGT TAATTGAATT AGCATTGAGA 180
GGAAGGTTAC AACTAGAGGC TTGTGGAATG AGACGTAAAA GTCTATTAAAC AAGAAAGGTA 240
20 ATCTGTAAAGT CAGATGCTCC AACAGGGGAT GTTCTTCTTG ATGAAGCTCT GAAGCATGTT 300
AAGGAACTC AGCCTCCAGA AACGGTCCAG AACTGGATTG AATTACTTAG TGGTGAGACA 360
TGGAATCCAT TAAAATTGCA TTATCAGTTA AGAAATGTAC GGAACGATT AGCTAAAAAC 420
25 CTGGTGGAAA AGGGTGATT GACAACAGAG AAACAGAACT TCCTACTTTT TGACATGACA 480
ACACATCCCC TCACCAATAA CAACATTAAG CAGCGCTCA TCAAGAAAGT ACAGGAAGCC 540
30 GTTCTTGACA AATGGGTGAA TGACCCCTCAC CGCATGGACA GCGGCTTGCT GGCCCTCATT 600
TACCTGGCTC ATGCCTCGGA CGTCCTGGAG AATGCTTTTG CTCCTCTTCT GGACGAGCAG 660
TATGATTTGG CTACCAAGAG AGTGGGCGAG CTTCTGACT TAGACCTGA AGTGAATGT 720
35 CTGAAGGCCA ACACCAATGA GGTCTGTGG GCGGTGGTGG CGGCGTTCAC CAAGTAACTC 780
TGCTCGGGGT GAACCATCTC CTTTCTCTC AAGTAAACCA GTAGTTTTC TTCTGTTGAC 840
40 TTCTGGTTTT CTGTAATTTG TACTTTCCCA CACTATAATT GGCTTCTGTT TTACAAAATG 900
GTGGGTGGCT TTTTCTTTTT TGTACGTGTA CAGGATTCTG CTGGTACGAG AGGCCTTCCT 960
CTTCTGTTT TTAaaaaaag TTTTACTGCC ATATTGGCAT TCCATTCCCT GTTGCCATCC 1020
45 TCACGTTAC CTGTTTGGG TTTCTGGTCT ACTTTGACTT TCAAAGTACC TCCAGCCTCC 1080
TCATACGCAC AGCTTTTGA TGACCTCAGC TTGAGTTTCT CCATATGTGC ATGTACATCT 1140
50 AGCATCTGC CTACAGTTCA GACAGAAGTC AAAAAAGGC CTTCAACTCA CCAAAGGTAA 1200
ATATCTGTAT CTATTAGGAC ATTTTTTACA TAGACTTCAG TTGAGATGTA TACTTAGCAA 1260
AATTATTTTT AAATTGAAAC AGCACAGTAA ATACTTAATA TAAATGTCC CTTGGATTTT 1320
55 GCTTCCCATG TAAATCTATT GTATTATTAC ACTTGTATA ATTTTAACTA TAAAGGTCCA 1380
ATTGTTTCAC AGAGCCAGTT TGGGATGGGC TGCATCCAT TTATGCTGTA TATAGTTTGA 1440
60 ATTATATATA AATTACCCCT TCTCTGGCC ACCCCTGCTC CCATCTTAGT ATTTTGCAAG 1500

ATCTAATCAG TTGTACACCT GGTGCCCTC GCTTGCTTCA ATCATGGTTA TTTGATGGCA 1560
 5 AAATCGACCT CTTGTGCTG AAGGAGAGAG AAAAGATGTG TGTCTGATTG GTCCCTGGGAT 1620
 TTTTIGAGCT GTGCCATTTA TGGTACTCTT TGCCTATGCA TCCCTTTTT AGATTTTTTT 1680
 TAAATTTTAT CTTACTGTTT TTATAATTTT TATTGGGAAG AGGCTTGTGA CCAGTACCAA 1740
 10 TCTTGAGITT CTTTTCTGT CCACAAGTAA ATTAATATCT GCTCTGAAAT GTCATTTATC 1800
 TACTCACACA TTCTTGGGGA AAAAAATCAA ATGTCAGTCC TAGCAGATGT TGCATGTAAA 1860
 TTGGTAGCAA GTAATGATTA CAACCCAGAG GATTAAGAAT TTTGTAACAG AAAGCTCTAT 1920
 15 GTTTTAATTT TTTATATACA ATTAGGATAA TTAGCATTGT CAGACTATAA ACCTTTGCTT 1980
 TTTAAAGITT ATTTTACTA TTCTTTATC ACTTTATTGT ATCATCACCA TTGGTTTCAT 2040
 20 AATGTAAATA CTATATGTTG AACAAATTAA ATGTCAAAT TTTTATTAC CATAGTCCAT 2100
 GTAATAGTG GGGCTTTCAG GTGTTTAGAG ATTTTTTTTG TTGTTGTAA CATTCATTGC 2160
 AAAAGTACTA GATGGTGTAT AACTCTAGAG TTGAATTTTA AGGGATTCCC TAATATGTAT 2220
 25 ACTATCTTTT TATCTGAAGT AATAAATAAA CAATGATCTT GAAAGTGCCY RAAAMAAAAA 2280
 AAAAAAAAA AAA 2293

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(2) INFORMATION FOR SEQ ID NO: 186:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

GGCACGAGGC GAGCCGGCGC ACCGTACGCT GGGACGTGTG GTTTCAGCTC GTGCGCCTCC 60
 45 CCGTGGGTTT GCGACGTTTA GCGACTATTG CGCCTGCGCC ACGCCGGCTG CGAGACTGGG 120
 GCGGTGGCTG CTGGTCCCGG GTGATGCTAG GCGGCTCCCT GGGCTCCAGG CTGTTGCGGG 180
 GTGTAGGTGG GAGTCACGGA CGTTTCGGG CCCGAGGTGT CCGGAAGGT GGCGCATG 240
 50 GGCGGCAGGG GAGAGCATGG CTCAGCGGAT GGTCTGGGTG GACCTGGAGA TGACAGGATT 300
 GGACATTGAG AAGGACCAGA TTATTGAGAT GGCCTGTCTG ATAAGTACT CTGATCTCAA 360
 55 CATTTTGGCT GAAGGTCTTA ACCTGATTAT AAAACAACCA GATGAGTTGC TGGACAGCAT 420
 GTCAGATTGG TGTAAGGAGC ATCACGGGAA GTCTGGCCTT ACCAAGGCAG TGAAGGAGAG 480
 TACAATTACA TTGAGCAGG CAGAGTATGA ATTTCTGTCC TTTGTACGAC AGCAGACTCC 540
 60

TCCAGGGCTC TGTCCACTTG CAGGAAATTC AGTTCATGAA GATAAGAAGT TTCTTGACAA 600
 ATACATGCCC CAGTTCATGA AACATCTTCA TTATAGAATA ATTGATGTGA GCACTGTTAA 660
 5 AGAACTGTGC AGACGCTGGT ATCCAGAAGA ATATGAATTT GCACCAAAGA AGGCTGCTTC 720
 TCATAGGGCA CTTGATGACA TTAGTGAAAG CATCAAAGAG CTTCAGTTTT ACCGAAATAA 780
 CATCTTCAAG AAAAAAATAG ATGAAAAGAA GAGGAAATTT ATAGAAAATG GGGAAAATGA 840
 10 GAAGACCGTG AGTTGATGCC AGTTATCATG CTGCCACTAC ATCGTTATCT GGAGGCAACT 900
 TCTGGTGGTT TTTTTTCTC ACGCTGATGG CTTGGCAGAG CACCTTCGGT TAACTTGCAT 960
 15 CTCCAGATTG ATTACTCAAG CAGACAGCAC ACGAAATACT ATTTTCTCC TAATATGCTG 1020
 TTCCATTAT GACACAGCAG CTCCTTTGTA AGTACCAGGT CATGTCCATC CCTTGGTACA 1080
 TATATGCATT TGCTTTTAAA CCATTTCTTT TGTTTAAATA AATAAATAAG TAAATAAAGC 1140
 20 TAGTTCTATT GAAATGCAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1200
 AAAAAAAAAA AN 1212

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(2) INFORMATION FOR SEQ ID NO: 187:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1605 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

GCTTCCGGAA GTTGCTTTTG TCCAAACATC CGGGCTTCTC CTTTTTGTGT TCCGGCCGAT 60
 40 CCCACCTCTC CTCGACCCTG GACGTCTACC TTCCGGAGGC CCACATCTTG CCCACTCCGC 120
 GCGCGGGGCT AGCGCGGGTT TCAGCGACGG GAGCCCTCAA GGGACATGGC AACTACAGCG 180
 GCGCCGGCGG GCGGCGCCCG AAATGGAGCT GGCCCGGAAT GGGGAGGGTT CGAAGAAAAC 240
 45 ATCCAGGGCG GAGGCTCAGC TGTGATTGAC ATGGAGAACA TGGATGATAC CTCAGGCTCT 300
 AGCTTCGAGG ATATGGGTGA GCTGCATCAG CGCTGCGCG AGGAAGAAGT AGACGCTGAT 360
 50 GCAGCTGATG CAGCTGCTGC TGAAGAGGAG GATGGAGAGT TCCTGGGCAT GAAGGGCTTT 420
 AAGGGACAGC TGAGCCGSCA GGTGGCAGAT CAGATGTGGC AGGCTGGGAA AAGACAAGCC 480
 TCCAGGGCCT TCAGCTTGTA CGCCAACATC GACATCCTCA GACCCTACTT TGATGTGGAG 540
 55 CCTGCTCAGG TGCGAACAGG GCTCCTGGAG TCCATGATCC CTATCAAGAT GGTCAACTTC 600
 CCCAGAAAA TTGCAGGTGA ACTCTATGGA CCTCTCATGC TGGTCTTCAC TCTGGTTGCT 660
 60 ATCTACTTCC ATGGGATGAA GACGTCTGAC ACTATTATCC GGGAGGGCAC CCTGATGGGC 720

	ACAGCCATTG GCACCTGCTT CGGCTACTGG CTGGGAGTCT CATCCTTCAT TTACTTCCTT	780
5	GCCTACCTGT GCAACGCCCA GATCACCATG CTGCAGATGT TGGCACTGCT GGGCTATGGC	840
	CTCTTTGGGC ATTGCATTGT CCTGTTTCATC ACCTATAATA TCCACCTCCA CGCCTCTTC	900
	TACCTCTTCT GGCTGTTGGT GGGTGGACTG TCCACACTGC GCATGGTAGC AGTGTGGTG	960
10	TCTCGGACCG TGGGCCCCAC ACAGCGGCTG CTCCTCTGTG GCACCTGGC TGCCTACAC	1020
	ATGCTCTTCC TGCTCTATCT GCATTTTGCC TACCACAAAG TGGTAGAGG GATCCTGGAC	1080
15	AACTGGAGG GCCCAACAT CCGCCCATC CAGAGGGTCC CCAGAGACAT CCTGCCATG	1140
	CTCCCTGCTG CTCGGCTTCC CACCACGTC CTCAACGCCA CAGCCAAAGC TGTGCGGTG	1200
	ACCTGCAGT CACACTGACC CCACCTGAAA TTCTTGGCCA GTCTCTTTC CCGCAGCTGC	1260
20	AGAGAGGAGG AAGACTATTA AAGGACAGTC CTGATGACAT GTTGTGTAGA TGGGTTTGC	1320
	AGCTGCCACT GAGCTGTAGC TCGTAAGTA CCTCCTTGAT GCNTGTGCGC ACTTCTGAAA	1380
25	GGCACAAGGC CAAGAACTCC TGGCCAGGAC TGCAAGGCTC TGCAGCCAAT GCAGAAAATG	1440
	GGTCAGTCC TTTGAGAACC CCTCCACC TACCCCTTCC TTCCTCTTTA TCTCTCCAC	1500
	ATTGTCTTGC TAAATATAGA CTGGTAATT AAAATGTTGA TTGAAGTCTG GAAAAAAA	1560
30	AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAC TCGAG	1605

35 (2) INFORMATION FOR SEQ ID NO: 188:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1516 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

45	ATTGGCATG AGGGGGTCAC GTGGTGGCTG GGCCGGGGAA ATGGCGGCTT CAGGAGAGAG	60
	CGGGACTTCA GGCGGGGAG GCAGACCGA GGAAGCATTT ATGACCTTCT ACAGTGAGGT	120
50	GAAACAAATA GAGAAGAGAG ACTCGGTTCT AACTTCGAAA AATCAGATTG AAAGACTGAC	180
	CGTCTTGGT TCCTCTTACT TCAATTTGAA CCCATTGAG GTTCTTCAGA TAGATCCTGA	240
	AGTTACAGAT GAAGAAATAA AAAAGAGGTT TCGGCAGTTA TCCATCTTGG TGCATCCTGA	300
55	CAAAAATCAA GATGATGCTG ACAGAGCACA AAAGGCTTTT GAAGCTGTGG ACAAAGCTTA	360
	CAAGTTGCTA CTGGATCAGG AGCAAAAGAA GAGGGCCCTG GATGTAATTC AGGCAGGAAA	420
60	AGAATACGTG GAACACACTG TGAAAGAGCG AAAAAACAA TTAAAGAAGG AAGGAAAACC	480

	TACAATTGTA GAGGAGGATG ATCCTGAGCT GTTCAAACAA GCTGTATATA AACAGACAAT	540
	GAAACTCTTT GCAGAGCTGG AAATTAAAAG GAAAGAGAGA GAAGCCAAAG AGATGCATGA	600
5	AAGGAAACGA CAAAGGGAAG AAGAGATTGA AGCTCAAGAA AAAGCCAAAC GGGAAAGAGA	660
	GTGGCAGAAA AACTTTGAGG AAAGTCGAGA TGGTCGTGTG GACAGCTGGC GAAACTTCCA	720
10	AGCCAATACG AAGGGAAGA AAGAGAAGAA AAATCGGACC TTCCTGAGAC CACCGAAAGT	780
	AAAAATGGAG CAACGTGAGT GACCGCCCAA GGTACAGGC ACAGAACCTT TCCCTGCTA	840
	TCTCCCTTCC TGCTTCGAAG GACTCATTCT TTCCTCCAC TTCCACCCCA ACATAGAGTA	900
15	GTATTGCTT TTTAGTCCAT TTTGTTTCA ATACGATTTA ATATCGATCA GAGTAATTCT	960
	TTGTACATT GAAATGAGG GCTTGGTTTA AAAAAAGACC TTTCCCTCTC CCTGCCCTA	1020
20	GAACAACCAG TATTAGAAGG TGCCACCATT GGTGCTGCCT TCTCTTCCA CAGCCTGTAA	1080
	CTCAGTGT TTGTACTTAC TGAATTGTGA TGGTTAGAAA CTTCGTGGAT AGTTTGTGGA	1140
	AATCATCCAA TTAAACATAC TGCTTAAAC AGTGTGCTG TGAATTCAGA GACAAGCCTG	1200
25	GAAGGGCAC CTTAGGAAGC CCTTCGCTT CAGTTGCTCG CTTCTGGTG TGCTCCCTTC	1260
	GAAGGCCAG ATAAGACAGG GAACACTTGT GAGCACACAG AGCAGCATCT GATGCCCTGT	1320
30	GGTGTGTC ATGTGCCCC TGTCTACTGA CCAATCAGTG TGGCATGAG CCCACGCCAC	1380
	CCAAACCTTT CACTTTCCAA AGAGCTAGCC GTCTCCACC CAGTACCATG TCCTAGCCTG	1440
	TCTGCATTG TTAGTGGTAA TATTCTTTAT GTATAATAAA TTTTATACC CAAAAAATA	1500
35	AAAAAAAAA ACTCGA	1516

40 (2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 681 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

50	GCTCCCATGT TGCTGGCTGT CCGTACATCA CCCTGTCCCC TGCAGGAGGG GGCTACAGGC	60
	CATCTCCCTC CTGTAGGCTT CTGACTCCCC TCCACTTTTG GGCCCTCAGC TTATCTCGGG	120
55	CAGGGGACCA TTGCAGCATC CTCCCTCCT CNGGACTCAA GGTGCTGAGG TATAAGCCCT	180
	GGGCCCCAGA TCCCTGRTKA CACCTTCCTG GAGAAGACTC TCAAAAGTGA CTGTATATTT	240
	GAGTTACCA GCAATAACTC CCCACACTCG AAGCAGGTCC AAACCCMAGG ATCCAGGGT	300
60	CCTTGGGCTC TGTGGCACTG TCTTCCCAAG ATCTTCTCTG TTGCACAATG GGAAACCTAA	360

GAGGAAAAAG ACAGGGGCCT GCTTGCCAG CCATGCGAGG GATTCCATGC CCACCTGCCC 420
 TCTGYCTGCC TCGCTGGAAT GTGGGCCCT GCTCCCCGTC AGGTTGTGCT GTCTCTGACC 480
 5 TATGTTTACA TCCCCGAGGG GTTCTGCCT CCTCCCCACC CAGGTCAGGG TGTGGTCCAG 540
 CAGCTTGCTG TGGGGTGCTG ACATGTGTCA CCACGCCCC CCTTGCCCC GGGGGGTCA 600
 10 TGGTCTCTC CTGGATGCTG CTCCTGAAT YTTTTTYYT GAWAAACCYT TTAMAATTAA 660
 AAAAAAAAAA AAAAACTCG A 681

15

(2) INFORMATION FOR SEQ ID NO: 190:

(i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 1014 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

GCCTCAAGCC ACGCATATGA TAATTTCTG GAACATTCAA ATTCAGTGTT TCTACAGCCA 60
 GTTAGTCTAC AAACCATGTC AGCAGCACCA TCAAACCAGA GTCTGCCACT TTTGTGTCATC 120
 30 GCTGGATGAT TGCTGGGCAA AGGTGGCCTT TTAGAGCTCT TAAAAGCCCA CAAAAAGGCT 180
 ATTCGTAGAG CCACAGTCAA CACATTGGT TATATTGCAA AGGCCATTGG CTCATGATG 240
 35 TATTGGCTAC ACTTCTGAAC AACCTCAAAG TTCAAGAAAG GCAGAACAGA GTTGTACCA 300
 CTGTAGCAAT AGCTATTGTT GCAGAAACAT GTTCACCCCT TACAGTACTC CCTGCCTTAA 360
 TGAATGAATA CAGAGTTCCT GAACTGAATG TTCAAATGG AGTGTTAAAA TCGCTTTCCT 420
 40 TCTGTGTTGA ATATATTGGT GAAATGGGAA AAGACTACAT TTATGCCGTA ACACCGTTAC 480
 TTGAAGATGC TTTAATGGAT AGAGACCTTG TACACAGACA GACGGCTAGT GCAGTGGTAC 540
 45 AGCACATGTC ACTTGGGGTT TATGGATTG GTTGTGAAGA TTCGCTGAAT CACTTGTGTA 600
 ACTATGTATG GCCCAATGTR TTTGAGACAT CTCCTCATGT AATTCAGGCA GTTATGGGAG 660
 CCCTAGAGGG CTGAGAGTT GCTATTGGAC CATGTAGAAT GTTGCAATAT TGTTTACAGG 720
 50 GTCTGTTTCA CCCAGCCCGG AAAGTCAGAG ATGTATATTG GAAAATTTAC AACTCCATCT 780
 ACATTGGTTC CCAGACGCT CTCATAGCAC ATTACCCAAG AATCTACCAA CGATGATAAG 840
 55 RACACCTATA TTCGTTATGA ACTGACTAT ATCTTATAAT TTTATGTTW ATTTKGTGKT 900
 TAATGCACAS TACTTCACAC CTAAACTTG CTTTGATTG GTGATGTAAA CTTTAAACA 960
 TTGCAGATCA GTGTAGGACT GGTCCATAGG GGAAGAGCTA GGAANTCCAT AGGC 1014
 60

(2) INFORMATION FOR SEQ ID NO: 191:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2779 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

10

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

15	TCGCAGCAGG GTGTGTCCAG ATGGTCAGTC TCTGGTGGCT AGCCTGTCCT GACAGGGGAG	60
	AGTTAAGCTC CCGYTCTCCA CCGTGCCGGC TGGCCAGGTG GGCTGAGGGT GACCGAGAGA	120
	CCAGAACTG CTTGCTGGAG CTTAGTGCTC AGAGCTGGGG AGGGAGGTTC CGCCGCTCCT	180
20	CTGCTGTGAG CGCCGGCAGC CCCTCCCGGC TTCCTTCCTT CCGCAGCCC CTGCTACTGA	240
	GAAGCTCCGG GATCCCAGCA GCCGCCACGC CCTGGCCTCA GCCTGCGGGG CTCCAGTCAG	300
	GCCAACACCG ACGCGCANTG GGAGGAAGAC AGGACCCCTG ACATCTCCAT CTGCACAGAG	360
25	GTCTTGCTG GACCGAGCAG CCTCTCTCTC CTAGGATGAC CTCACCTCC AGCTCTCCAG	420
	TTTTTCAGGTT GGAGACATTA GATGGAGGCC AAGAAGATGG CTCTGAGGCG GACAGAGGAA	480
30	AGCTGGATTT TGGGAGCGGG CTGCCCTCCA TGGAGTCACA GTTCCAGGGC GAGGACCGGA	540
	AATTCGCCCC TCAGATAAGA GTCAACCTCA ACTACCGAAA GGAACAGGT GCCAGTCAGC	600
	CGGATCCAAA CCGATTGAC CGAGATCGGC TCTTCAATGC GGTCTCCCGG GGTGTCCCCG	660
35	AGGATCTGGC TGGACTTCCA GAGTACCTGA GCAAGACCAG CAAGTACCTC ACCGACTCGG	720
	AATACACAGA GGGCTCCACA GGTAAAGACGT GCCTGATGAA GGCTGTGCTG AACCTTAAGG	780
40	ACGGGGTCAA TGCTGCATT CTGCCACTGC TGCAGATCGA CCGGGACTCT GGCAATCCTC	840
	AGCCCTGGT AAATGCCAG TGCACAGATG ACTATTACCG AGGCCACAGC GCTCTGCACA	900
	TGCCCATGGA GAAGAGGAGW CTGCAGTGTG TGAAGCTCCT GGTGGAGAAT GGGGCCAATG	960
45	TGCATGCCCC GGTCGCGGC GCTTCTTCCA GAAGGGCCAA GGGACTTGCT TTTATTTCCG	1020
	TGAGCTACCC CTCTYTTTGG CCGCTTGAC CAAGCAGTGG GATGTGGTAA GCTACCTCCT	1080
50	GGAGAACCCA CACCAGCCCG CCAGCCTGCA GGCAGTACT CCCAGGGCAA CACAGTCTG	1140
	CATGCCCTAG TGATGATCTC GGACAACTCA GCTGAGAACA TTGCACTGGT GACCAGCATG	1200
	TATGATGGGC TCCTCCAAGC TGGGGCCCGC CTCTGCCCTA CCGTGCACTG TGAGGACATC	1260
55	CGCAACCTGC AGGATCTCAC GCCTCTGAAG CTGGCCGCCA AGGAGGGCAA GATCGAGATT	1320
	TTCAAGCACA TCCTGCAGCG GGAGTTTCA GGAAGTGGCC ACCTTTCCCG AAAGTTCAAC	1380
60	GAGTGGTGCT ATGGGCCTGT CCGGGTGTG CTGTATGACC TGGCTTCTGT GGACAGCTGT	1440

GAGGAGAACT CAGTGCTGGA GATCATTGCC TTTCATTGCA AGAGCCCGCA CCGACACCGA 1500
 5 ATGGTCGTTT TGGAGCCCCCT GAACAACTG CTGCAGGCGA AATGGGATCT GCTCATCCCC 1560
 AAGTTCTTCT TAAACTTCCT GTGTAATCTG ATCTACATGT TCATCTTCAC CGCTGTTGCC 1620
 TACCATCAGC CTACCTGAA GAAGCAGGCC GCCCTCACC TGAAAGCGGA GGTGGAAC 1680
 10 TCCATGCTGC TGACGGGCCA CATCCTTATC CTGCTAGGGG GGATCTACCT CCTGCTGGGC 1740
 CAGCTGTGGT ACTTCTGGCG GCGCCACGTG TTCATCTGGA TCTCGTTCAT AGACAGCTAC 1800
 15 TTGAAATCC TCTTCTGTT CCARGCCCTG CTCACAGTGG TGTCCARGT GCTGTGTTTC 1860
 CTGGSCATCG AGTGGTACCT GCCCTGCTT GTGCTGCGC TGGTCTGGG CTGGCTGAAC 1920
 CTGCTTTACT ATACACGTGG CTCCAGCAC ACAGGCATCT ACAGTGTCTAT GATCCAGAAG 1980
 20 CCTGGTGAG OCTGAGCCAG GANNITGGCG CCCCGAAGCT OCTACAGGCC CCAATGCCAC 2040
 AGAGTCAGTG CAGCCCATGG AGGGACAGGA KGACGAKGCC AACGGGGCCC AGTACAGGGG 2100
 25 TATCCTGGAA GCCTCCTTGG AGCTCTTCAA ATTCAACATC GGCATGGGCG AGCTGGCCTT 2160
 CCAGGARCAG CTGCACTTCC GGGCATGGT GCTGCTGCTG CTGCTGGSCT ACGTGTGCT 2220
 CACCTACATC CTGCTGCTCA ACATGCTCAT CGCCTCATG AGCGAGACCG TCAACAGTGT 2280
 30 CGCCACTGAC AGCTGGAGCA TCTGGAAGCT GCAGAAAGCC ATCTCTGTCC TGGAGATGGA 2340
 GAATGGCTAT TGGTGGTGCA GGAAGAAGCA GCGGGCAGGT GTGATGCTGA CCGTTGGCAC 2400
 35 TAAGCCAGAT GGCAGCCCSG ATGAGCGCTG GTGCTTCAGG GTGGAGGAGG TGAAGTGGC 2460
 TTCATGGGAG CAGACGCTGC CTACGCTGTG TGAGGACCCG TCAGGGGCAG GTGTCCCTCG 2520
 AACTCTGAG AACCTGTCC TGGCTTCCCC TCCCAAGGAG GATGAGGATG GTGCTCTGA 2580
 40 GGAAACTAT GTGCCGTCC AGCTCCTCCA GTCCAAGTGA TGGCCAGAT GCAGCAGGAG 2640
 GCCAGAGGAC AGAGCAGAGG ATCTTTCCAA CCACATCTGC TGGCTCTGGG GTCCCACTGA 2700
 45 ATTCTGGTGG CAAATATATA TTTTCACTAA CTCAAAAAAA AAAAAAAAAA AAAAAAAAAA 2760
 AAAAAAAAAA AAAAAGGC 2779

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(2) INFORMATION FOR SEQ ID NO: 192:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1923 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

	ACCCGCTCCG CTCCGCTCCG CTCGGCCCCG CGCCGCCCCG CAACATGATC CGCTGCGGCC	60
	TGGCCTGCGA GCGCTGCCGC TGGATCCTGC CCCTGCTCCT ACTCAGCGCC ATCGCCTTCG	120
5	ACATCATCGC GCTGGCCGGC CGCGGCTGGT TGCAGTCTAG CGACCACGGC CAGACGTCCT	180
	CGCTGTGGTG GAAATGCTCC CAAGAGGGCG GCGGCAGCGG GTCCTACGAG GAGGGCTGTC	240
10	AGAGCCTCAT GGAGTACGCG TGGGGTAGAG CAGCGGCTGC CATGCTCTTC TGTGGCTTCA	300
	TCATCCTGGT GATCTGTTTC ATCCTCTCCT TCTTCGCCCT CTGTGGACCC CAGATGCTTG	360
	TCTTCCTGAG AGTGATTGGA GGTCTCCTTG CCTTGGCTGC TGTGTTCCAG ATCATCTCCC	420
15	TGGTAATTTA CCCCGTGAAG TACACCCAGA CCTTCACCCT TCATGCCAAC CSTGCTGTCA	480
	CTTACATCTA TAACTGGGCC TACGGCTTTG GGTGGGCAGC CAGGATTATC CTGATYGGCT	540
20	GTGCCTTCTT CTTCTGCTGC CTCGCCAACT ACGAAGATGA CCTTCTGGGC AATGCCAAGC	600
	CCAGGTAATT CTACACATCT GCCTAAGTGG GGAATGAATG TGGGAGAAAA TCGCTGCTGC	660
	TGAGATGGAC TCCAGAAGAA GAAACTGTTT CTCCAGGCGA CTTTGAACCC ATTTTTTGGC	720
25	AGTGTTCATA TTATTAACT AGTCAAAAAT GCTAAAATAA TTTGGGAGAA AATATTTTTT	780
	AAGTAGTGT ATAGTTTCAT GTTTATCTTT TATTATGTTT TGTGAAGTTG TGTCTTTTCA	840
30	CTAATTACCT ATACTATGCC AATATTTCTT TATATCTATC CATAACATTT ATACTACATT	900
	TGTAAGAGAA TATGCACGTG AAACCTAACA CTTTATAAGG TAAAAATGAG GTTTCCAAGA	960
	TTTAATAATC TGATCAAGTT CTGTGTTATTT CCAATAGAA TGGACTCGGT CTGTTAAGGG	1020
35	CTAAGGAGAA GAGGAAGATA AGGTAAAAAG TTGTTAATGA CCAAACATTC TAAAAGAAAT	1080
	GCAAAAAAAA AGTTTATTTT CAAGCCTTCG AACTATTTAA GGAAAGCAA ATCATTTCCT	1140
40	AAATGCATAT CATTTGTGAG AATTTCTCAT TAATATCCTG AATCATTTCAT TTCAGCTAAG	1200
	GCTTCATGTT GACTCGATAT GTCATCTAGG AAAGTACTAT TTCATGGTCC AAACCTGTTG	1260
	CCATAGTTGG TAAGGCTTTC CTTTAAGTGT GAAATATTTA GATGAAATTT TCTCTTTTAA	1320
45	AGTTCTTTAT AGGGTTAGGG TGTGGGAAAA TGCTATATTA ATAAATCTGT AGTGTTTTGT	1380
	GTTTATATGT TCAGAACCAG AGTAGACTGG ATTGAAAGAT GGACTGGGTC TAATTTATCA	1440
50	TGACTGATAG ATCTGGTTAA GTTGTGTAGT AAAGCATTAG GAGGGTCATT CTTGTCACAA	1500
	AAGTGCCACT AAAACAGCCT CAGGAGAATA AATGACTTGC TTTTCTAAAT CTCAGGTTTA	1560
	TCTGGGCTCT ATCATATAGA CAGGCTTCTG ATAGTTTGCA ACTGTAAGCA GAAACCTACA	1620
55	TATAGTTAAA ATCCTGGTCT TTCTTGGTAA ACAGATTTTA AATGTCTGAT ATAAAACATG	1680
	CCACAGGAGA ATTCCGGGAT TTGAGTTTCT CTGAATAGCA TATATATGAT GCATCGGATA	1740
60	GGTCATTATG ATTTTTTACC ATTCGACTT ACATAATGAA AACCAATTCA TTTTAAATAT	1800

	CAGATTATTA TTTTGTAAGT TGTGGAAAA GCTAATTGTA GTTTTCATTA TGAAGTTTTC	1860
	CCAATAAACC AGGTATTCTA AAAAAAAAAA AAAAAA ACTN GAGGGGGGGC CCGGTACCCA	1920
5	ATT	1923
10	(2) INFORMATION FOR SEQ ID NO: 193:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 2346 base pairs	
	(B) TYPE: nucleic acid	
15	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:	
20	AGGCTCAGGG GGACACTCTC AAAATTACAC AGCTTTTAAC AGGTGGCAGA ATGGGGTTC	60
	AGACCCAGAT CTGGGTTCAA GTCACATCATG GTGTGATTGC GGCATTCCIT CCCGCATCTG	120
25	GGCCTTGCCA TCTCTCTCTC CGAGTGGACA TGGAGAGGAC GGGGGCCCAG CAGCTGGATG	180
	GCTGCAGGGG ATCAAGTCTT CTCTGGGGCT GGGCACGTAN AAGAGCATGT GGCTGGTGGA	240
	CGGCATGCGT GGCTCCTCAC CTGGCAGTCT GCCTGCCCTG CTAACCGGCT GTCTCTGTGT	300
30	CCCCTAGTGC CCTGGGCTAG CATGACCCGC CTGATGCGWT SCCGCACAGC CTCTGGTTCC	360
	AGCGTCATTC TCTGGATGGC ACCCGCAGCC GCTCCACAC CAGCGAGGGC ACCCGAAGCC	420
35	GCTCCACAC CAGCGAGGGC ACCCGCAGCC GCTCGCACAC CAGCGAGGGG GCCCACCTGG	480
	ACATCACCCC CAACTCGGGT GCTGCTGGGA ACAGNGCCGG GCCCAAGTCC ATGGAGGTCT	540
	CCTGCTAGGC GGCTTGCCCA GCTGCGCCCC CGGACTCTG ATCTCTGTAG TGGCCCCCTC	600
40	CTCCCCGGCC CCTTTTCGCC CCCTGCCTGC CATACTGCGC CTAACCTGGT ATTAATCCAA	660
	AGCTTATTTT GTAAGAGTGA GCTCTGGTGG AGACAAATGA GGTCTATTAC GTGGGTGCCC	720
45	TCTCCAAGG CGGGGTGGCG GTGGACCAA GGAAGGAAGC AAGCATCTCC GCATCGCATC	780
	CTCTTCATT AACCACTGGC CGGTTGCCAC TCTCTCCCC TCCCTCAGAG ACACCAAAT	840
	GCCAAAACA AGACGCGTAC AGCACACACT TCACAAAGCC AAGCCTAGGC CGCCCTGAGC	900
50	ATCCTGGTTC AAACGGGTGC CTGGTCAGAA GGCCAGCCGC CCACTTCCCG TTTCTCTTTT	960
	AACTGAGGAG AAGCTGATCC AGTTTCCGGA AACAAATCC TTTTCTCATT TGGGGAGGGG	1020
55	GGTAATAGTG ACATGCAGGC ACCTCTTTTA AACAGGCAA ACAGGAAGGG GGAAAAGGTG	1080
	GGATTTCATG CGAGGCTAGA GGCATTTGGA ACAACAAATC TACGTAGTTA ACTTGAAGAA	1140
	ACCGATTTTT AAAGTTGGTG CATCTAGAAA GCTTTGAATG CAGAAGCAA CAAGCTTGAT	1200
60	TTTTCTAGCA TCCTCTTAAT GTGCAGCAA AGCAGGCRAC AAAATCTCCT GGCTTTACAG	1260

ACAAATAT TTCAGCAAAC GTTGGGCATC ATGGTTTTTG AAGGCTTAG TTCTGCTTTC 1320
 5 TGCCCTCTCT CCACAGCCCC AACCTCCAC CCTGATACA TGAGCCAGTG ATTATCTTG 1380
 TTCAGGGAGA AGATCATTTA GATTGTGTTT GCATTCCTTA GAATGGAGGG CAACATTCCA 1440
 CAGCTGCCCT GGCTGTGATG AGTGTCTTG CAGGGGCCGG AGTAGGAGCA CTGGGGTGGG 1500
 10 GGCGGAATG GGGTACTCG ATGTAAGGA TTCCTGTGTG TTGTGTGAG ATCCAGTGCA 1560
 GTTGTGATTT CTGTGGATCC CAGCTTGGT CCAGGAATTT TGTGTGATTG GCTTAAATCC 1620
 AGTTTTCAAT CTTCGACAGC TGGGCTGGAA CGTGAATCA GTAGCTGAAC CTGTCTGACC 1680
 15 CGGTACGTT CTGGATCCT CAGAACTCTT TGCTCTGTC GGGGTGGGG TGGGAATCA 1740
 CGTGGGAGC GGTGGCTGAG AAAATGTAAG GATTCTGGAA TACATATTCC ATGGGACTTT 1800
 20 CCTTCCCTCT CTGCTTCTT CTTTCTCTGC TCCCTAACCT TTCGCCGAAT GGGGCAGCAC 1860
 CACTGACGTT TCTGGCGGC CAGTGGCGCT GCCAGTTCC TGTACTACTG CCTGTACTT 1920
 TTCATTTTGG CTCACGTGG ATTTTCTCAT AGGAAGTTG GTCAGAGTGA ATTGAATATT 1980
 25 GTAAGTCAGC CACTGGGACC CGAGGATTC TGGGACCCCG CAGTTGGGAG GAGGAAGTAG 2040
 TCCAGCCTTC CAGGTGGCGT GAGAGGCAAT GACTCGTTAC CTGCCGCCA TCACCTTGGA 2100
 30 GGCCCTCCCT GGCTTGAGT AGAAAAGTCG GGGATCGGG CAAGAGAGGC TGAGTAOGGA 2160
 TGGGAACTA TTGTGCACAA GTCTTCCAG AGGAGTTTCT TAATGAGATA TTTGTATTTA 2220
 TTTCCAGACC AATAAATTG TAACTTTGCA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2280
 35 AAAAAAAAAA AAAAAAACT CGAGGGGGC CCGTACCCAA TTCGCCGTAT ATGATCGTAA 2340
 ACAATC 2346

40

(2) INFORMATION FOR SEQ ID NO: 194:

45

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3054 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

TATCTGAACC ACCCTTTATT CTACATATGA TAGGCAGCAC TGAAATATCC TAACCCCTA 60
 55 AGCTCMAGGT GCCCTGTGGN ACGAGCAACT GGAATATAGC AGGGCTGGG TCTGTCTTCC 120
 TGGTCATAGG CTCACTCTTT CCCCAAATC TTCTCTGGA GCTTTCAGC CAAGGTGCTA 180
 60 AAAGGAATAG GTAGGAGACC TCTCTATCT AATCCTTAAA AGCATAATGT TGAACATTCA 240

	TTCAACAGCT GATGCCCTAT AACCCCTGCC TGGATTCTT CCTATTAGGC TATAAGAAGT	300
	AGCAAGATCT TTACATAATT CAGAGTGGTT TCATTGCCCTT CCTACCCCTCT CTAATGGCCC	360
5	CTCCATTTAT TTGACTAAAG CATCACACAG TGGCACTAGC ATTATACCA GAGTATGAGA	420
	AATACAGTGC TTTATGGCTC TAACATTACT GCCTTCAGTA TCAAGGCTGC CTGGAGAAAG	480
10	GATGGCAGCC TCAGGGCTTC CTTATGTCTT CCACCACAAG AGCTCCTTGA TGAAGGTCAT	540
	CTTTTCCCC TATCCTGTTC TTCCCTCCC CGCTCCTAAT GGTACGTGGG TACCCAGGCT	600
	GGTCTTGGG CTAGGTAGTG GGGACCAAGT TCATTACCTC CCTATCAGTT CTAGCATAGT	660
15	AAACTACGGT ACCAGTGTTA GTGGGAAGAG CTGGGTTTTC CTAGTATACC CACTGCATCC	720
	TACTCCTACC TGGTCAACCC GCTGCTTCCA GGTATGGGAC CTGCTAAGTG TGAATTACC	780
20	TGATAAGGGA GAGGAAATA CAAGGAGGGC CTCTGGTGTT CCTGGCCTCA GCCAGCTGCC	840
	CACAAGCCAT AAACCAATAA AACAAGAATA CTGAGTCAGT TTTTATCTG GGTCTCTTTC	900
	ATTCCCACTG CACTTGGTGC TGCTTTGGCT GACTGGGAAC ACCCCATAAC TACAGAGTCT	960
25	GACAGGAAGA CTGGAGACTG *TCCACTTCTA GCTCGGAAGT TACTGTGTAA ATAAACTTTC	1020
	AGAACTGCTA CCATGAAGTG AAAATGCCAC ATTTTGCTTT ATAATTCTA CCCATGTGG	1080
30	GAAAACTGG CTTTTCCTCA GCCCTTTCCA GGGCATAAAA CTCAACCCCT TCGATAGCAA	1140
	GTCCCATCAG CCTATTATTT TTTTAAAGAA AACTTGCAGT TGTTTTCTT TTTACAGTA	1200
	CTTCTTCTT GCCCCTAAT TATAAATCTT AAGTGTAAAA AAAAGTCTT ACAACAGCTT	1260
35	CTTGCTGTGA AAAATATGTA TTATACATCT GTATTTTAA ATTCTGCTCC TGAAAAATGA	1320
	CTGTCCCAT TCCACTCAC TGCATTGGG GCCTTTCCCA TTGGTCTGCA TGTCTTTTAT	1380
40	CATTGCAGGC CAGTGACAG AGGGAGAAGG GAGAACAGGG GTCGCCAACA CTGTGTGTC	1440
	TTTCTGACTG ATCCTGAACA AGAAAGAGTA AACTGAGGC GCTCGCTCCC ATGCACAACT	1500
	CTCCAAAACA CTTATCCTCC TGCAAGAGTG GGCTTTCCAG GGTCTTTACT GGAAGCAGT	1560
45	TAAGCCCCCT CCTCACCCT TCCTTTTTC TTTCTTTACT CCTTTGGCTT CAAAGGATTT	1620
	TGGAAAAGAA ACAATATGCT TTACTCAT TTTCAATTTC TAAATTGCA GGGGATACTG	1680
50	AAAAATACGG CAGGTGGCCT AAGGCTGCTG TAAAGTTGAG GGGAGAGGAA ATCTTAAGAT	1740
	TACAAGATAA AAAACGAATC CCTTAAACAA AAAGAACAAT AGAACTGGTC TTCCATTTTG	1800
	CCACCTTTC TGTTTCATGAC AGCTACTAAC CTGGAGACAG TAACATTTCA TTAACCAAAG	1860
55	AAAGTGGGTC ACCTGACCTC TGAAGAGCTG AGTACTCAGG CCACTCCAAT CACCCTACAA	1920
	GATGCCAAGG AGGTCCCAGG AAGTCCAGCT CCTTAACTG ACGCTAGNCA ATAAACCTGG	1980
60	GCAAGTGAGG CAAGAGAAAT GAGGAAGAAT CCATCTGTGA GGTGACAGGC AAGGATGAAA	2040

	GACAAAGAAG GAAAAGAGTA TCAAAGGCAG AAAGGAGATC ATTTAGTTGG GTCTGAAAGG	2100
	AAAAGTCTTT GCTATCCGAC ATGTACTGCT AGTACCTGTA AGCATTTTAG GTCCCAGAAT	2160
5	GGAAAAAAA ATCAGCTATT GGTAATATAA TAATGTCTT TCCCTGGAGT CAGTTTTTTT	2220
	AAAAAGTTAA CTCTTAGTTT TTAATTGTTT AATTCTAAAA GAGAAGGGAG CTGAGGCCAT	2280
10	TCCCTGTAGG AGTAAAGATA AAAGGATAGG AAAAGATTCA AAGCTCTAAT AGAGTCACAG	2340
	CTTTCCCAGG TATAAACCT AAAATTAAGA AGTACAATAA GCAGAGGTGG AAAATGATCT	2400
	AGTTCTGAT AGCTACCCAC AGAGCAAGTG ATTTATAAAT TTGAAATCCA AACTACTTTC	2460
15	TTAATATCAC TTTGGTCTCC ATTTTCCCA GGACAGGAAA TATGTCCCCC CCTAACTTTC	2520
	TTGCTTCAAA AATTAAAATC CAGCATCCCA AGATCATTCT ACAAGTAATT TTGCACAGAC	2580
20	ATCTCTCAC CCGAGTGCCT GTCTGGAGCT CACCCAAGGT CACCAAACAA CTTGGTTGTG	2640
	AACNNACTG CCTTAACCTT CTGGGGGAGG GGGATTAGCT AGACTAGGAG ACCAGAAGTG	2700
	AATGGGAAAG GGTGAGGACT TCACAATGTT GGCCTGTCAG AGCTTGATTA GAAGCCAAGA	2760
25	CAGTGGCAGC AAAGGAAGAC TTGGCCCAGG AAAACCTGT GGGTTGTGCT AATTCTGTG	2820
	CAGAAATAG GGTGGACAGA AGCTTGTTGG GTGCATGGAG GAATTGGGAC CTGGTTATGT	2880
30	TGTTATTCTC GGACTGTGAA TTTTGGTGAT GTAAAACAGA ATATTCTGTA AACCTAATGT	2940
	CTGTATAAAT AATGAGCGTT AACACAGTAA AATATTCAT AAGAAGTCAA AAAAAAAAAA	3000
	AAAAAACTCG AGGGGGGCC CGGTACCCAA TTTNCCAAAT AGAGATNGTA TTAC	3054
35		

(2) INFORMATION FOR SEQ ID NO: 195:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 907 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

	GGCAGAGCTC GTGGCCGNAA CTTTTTCTGC TCCTGGCTGC CACCTACTGG CTGGCCGCGG	60
50	CCCTGGCCTG GGCCTGCACC AGCCTGCGNG CGGGCTCCCA CAGCAGCCCC CTTCCAAGCA	120
	GCGTCCCCAC ACCGCGCACC TTCTGCGGGA ACGTGCTCGC CGTGCCGGGG ACCATATGGA	180
55	CGGAAGGCTT TGTGCTCACC TACAAGCTGG GTGAGCAGGG TGCCAGCAGC CTGTTGATCC	240
	TCTTGGCTCC TGCTGGAGCA CGAGCGGCGT TTCTGCTCCC GAGTTGGGAC TGTGGAATGG	300
	TGTGGGTGCT GTGGTCTGCT CCATCGCTGG CTCTCCCTG GGTGGGACCT TGCTGGCCAA	360
60	GCACTGGAAA CTGCTGCCTC TGTAGGTCG GTGCTGCGCT TCCGCTCGG GGGCCTAGCC	420

TGTCTAGACTG CCTTGGTCTT CCACCTTGGG CACCCTGGGG GCCAGCATGG ACGCTGGCAC 480
 5 AATCTTGAGA GGGTCAGCCT TGCTGAGCCT ATGTCTGCAG CACTTCTTGG GARGCCTGGT 540
 CACCACAGTC ACCTTCACTG GGAATGATGC GCTGCAGCCA GCTGGCCCCC AGGGCCTTGC 600
 AGGCCACACA CTACAGCCTT CTGGCCACGC TGGAGCTGCT GGGGAAGCTG CTGCTGGGCA 660
 10 CTYTGGSCGG AGGGCCTGGC TGATGGGTTG GGGCCACATC CCTGCTTCTT GCTCCTGCTC 720
 ATCCTCTCTG CCTTTCCCGT TCTGTACCTG GACCTAGCAC CCAGCACCTT TCTCTGAGCT 780
 GAGTGGCTGG AGTGGTCAAT AAAGCCACAT GTGCCCTGTG GCCAAAAAA AAAAAAAA 840
 15 AAAAAAAA AAAAAACTG GAGGGGGGC CCGGTACCA AATCGCCGA TATGATCGTA 900
 AACAATC 907
 20

(2) INFORMATION FOR SEQ ID NO: 196:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1290 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

GGCACGAGGA GGGACAGGA GTGGCAAGG GGAAGAAGCA GCTTATTTGA CTAACGAGC 60
 35 CCTCTGTGGT CCACCAGCGT CTTGGCTTGG TGGGAGGGCT CTCAATCAGC AGGGCCCCAG 120
 KAGGGCAAGA AGAAGTGGG CAAAGCCTGG CGCTCGGCCG CGGTGCGGC AGCTTTCMA 180
 TCTGGAGCCA CGCCTCCTCC AGGCCATGCT CCTTGAACCT GGAAATGTCA ACCGGAGCCC 240
 40 TTAACACCAG CCCTCCAGCA TCTAATAGAC TTGAATCTAC TCTAAACGAA TATTTAATCC 300
 AACCTCAACT ACATTGTAGC TCAGTCCAAC GACTAACCTT GAAATGGGG TGTTCAGCC 360
 45 TTCAGCGAGA TGGCCAAGCG GTCCCTGGG GGCTGTGGCA GCGGGCTTAT CCTTCTCTGT 420
 TGCCAACCTT GCGTCCGAC CTCCTCGCC CCCATGCGGT GACCCCGTCC GTGTCTGTGT 480
 CTGTCCATAC GTGTGAGTCC AGCTAAAAAG ACAAACAGA ACCCGTGGGC CCAGCTCGGA 540
 50 AGGTGCGTGG AGAAGGCTCC GACGTCTCCG AAGTGCAGCC CTGGGATGG CATTCCGTTG 600
 TGTGCCTTAT TCCTGGAGAA TCTGTATACG GCTCGCCTAT AAGAAATATA GCCTCTTCAT 660
 55 GCTGTATTAA AAGGACTTTT AAAAGCAAAA AAAAAAAA AAAAACTCGA GGGGGGGCCC 720
 GTTACCAAT TCGCCCAATA GTGAGTCGTA TTACAATTCA CTGGGCCGTC STTTTAACAA 780
 CGTCGTGAAC TGGGAAAACC CTGGCGTTTA CCAACTTAA TCGCCTTGCA GCACATCCCC 840
 60

CTTTCGCCAG CTGGCGTTAA TAGCGAAAAA NGCCCGCACC CGAATCGCCC TTCCCAACAG 900
 TTTCGCCAGC CCTGAATGGC GAAATGGCAA ATTGTAAGCG TTTAATATTT TKKTTAAAAT 960
 5 TCCNCGTTWA AWTTTTGTGT TAAATCARCT CAATTTTTTTT AACCCAATAA GSCCGAAATC 1020
 CGGCAATCC CCYTTATTAA TTCAAAAAA ATAAACCSAA AAWGGGTTTG AATTTTTTKT 1080
 10 TTCCCCAYTT TTGGAACAA AWTYCCCCCT TTTTAAAAA GTTGGAACCC CCAMCCYTCC 1140
 AAAGGGGAAA AAACSYTTTT YTGCGGGGNA ANGGGGCCCC CNTACTTTNA ACAYCCCCCC 1200
 CCAAWCAATT TTTTGGGGG GTCCCNAAAG GTCCCCCTAA AANCTTTTTT CGGAACCNA 1260
 15 AGGGGANCCC CCCATTTAAA ATTTTNGGIN 1290

20 (2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1020 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

30 GGTGTGCGTG GATGGTCGTG TAGGTGAGTT TTACCAAGGA TTATGGTAAC AAATGAGTGA 60
 GACCTCTATG GAGAAAATAT TGAAGNNCAT TAAAGAAGAC CTCATANTAG GAGAGAATGT 120
 35 SCTTTGGAGG ATTTGTATG AGCTTTTACA GTATTCATTT TTCAACTCAA GGCAATGGCT 180
 TTCTACACCA ACTCTAATCC ATAAACGGGT CTTATGACAT CTATGAAGTA GTAGCAAGAC 240
 ATGCTTAGTG TGTATTTCTC TCTTGAGAC ACTGTAATTT CTACCAGAAA TTTCCAGAGC 300
 40 ATTATGTAGG TAGAAAAAAA TGCAAGCAAG CTGTTAAAGA TCTTGATCC CATTATATAG 360
 TATGTATAGC TGAAATCTGT AATTCAATCA CTTTTTCTCT TTTATCCTCT AACCAAAAAA 420
 TTGTTTAATT TTGCATCCCA AATGTTTTTA ATCTTTGTAT ATTTTITAAA AAYCCTTTTC 480
 45 TCCTCATCAT TGCCTTTTTT GTGGTTGTAA ATAGACTTAC TTGCACTTTG AAGATGAGTT 540
 ACTCCTTGTC ATCTTACAAA TATGTGATAT GGTAAATTTT ATAACAGATG TCAGTTTGA 600
 50 ACCAAGAATT GGTGATTTGT TTATAAGAAA AAAACTGGCT TCATTCTGT GAAATTGCTC 660
 TTGAAAATT TCTTTTACA CGTGAAGCC AACTGAGATA CCGTGATGGT GTTGATTCT 720
 55 TTCAATGATG CTTACCATCT ATTTTAGCCA CTGAGCCTTT TATTATTTGT CTATTGTAA 780
 AGTTTATTTG TCTTAACTCA TTTAATAAAT ATACTGTTTA TCTGTTCTG AATGGGGACT 840
 GAACTTTTTG GATATTGATA TTGATTGAA AATATTTTGG AATTTTTTCT ACTTGAAATT 900
 60 TTAGAAATCT AATGAAAAT TCTATAATGT ACTGAAAGTA WGGTTGTGTA CAGTGAKCAC 960

TCTCTAATAA TATGATGNCT TGCCCTAAAN GAGGNGGGAC ATGTCCCACT TTCCACCAG 1020

5

(2) INFORMATION FOR SEQ ID NO: 198:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 524 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

AATTCOCGAA GCTGAGGGTT GTGTGCCNTC GGGCGAGCCA AGTCTTTTGA CCGGACCCCT 60
CCCGGCGCAG AAGANCTGAA GTTGATTGA GAGCCTGTCT TTGGGGITRA GCCGAGCTGC 120
20 TGCGGGCTTY GTGCGCGGCC AGGACACAAG YTACTTGCAA CGGGGCGGCG CCTGGCTTAT 180
GATGTTCTTC AACCCAGGGG CGGCCTCTGC CCTCTACTCG TGCCAGGCCC ACTTGCCAGG 240
25 CAGGAGCCCT CCCCAAGCCT TCAGGGCTGC TCGGAGTCAC CTGTTGGAAT GGACTAAAAG 300
GACCCTTGTG TGGGAACAGG TGCTCCAAAC ACCCTGCTGC TGGCTGCCAG GCAGGCCCTC 360
TGGAAGGGAA GGGGAGGAC TCATCAGGAC CTCCCTGGAC CCTGCAGGGC AGGCAGTTGG 420
30 CCCGAGCCCA AGCATTGTC TCTGCTTGCC CCAAGGGGAC AGGAAGCCTC TTGGGCTCT 480
TCCCTTCTG GACAAGGCC CCTGCTTTG CCTCACATAA ACTG 524

35

(2) INFORMATION FOR SEQ ID NO: 199:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 332 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

GTGATACAAG GAAGGGTGAT CATCATCTGT CACCATGCAA TTCCTGCTCA CAGCCTTTCT 60
50 GTTGGTGCCA CTCTGGCTC TTTGTGATGT CCCCATATCC CTAGGCTTCT CCCCTCCTA 120
GAAGGGCTTC TTGATAGATT AGAAAATAAG AATGAGTGAC ATTCCTATG TGCATATAAG 180
AAGGAGCCAC AAGACATGTC TTTTAAATAA AAGGACAGTG TOCATCCTTT TAGCTGCCGA 240
55 ATAGAACCTT GGTCTCATCC TCCTGGAGCT AGGSCTTAAA ACAGCTTCTG TGTTCCTSAT 300
TKGTCTCART GTTTTGCCAA GGTTCCTATC GG 332

60

(2) INFORMATION FOR SEQ ID NO: 200:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 376 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

CCAGGGAAGC CCCARGCCTG TCCTGAATTG ACATCAGTGC TTCCCTGAAC TGCTCCCCC	60
15 ACCCTTGGGC ATTATCCCAG GAAACTTATG TTTTCTAGAA GCTAAGCAGC TGCTGGGACT	120
CAGGGACTGG TGCAGGTAGG CTGAGTGGCA GCTCAGTCCT AGAAGGTCTC TGAAGATCTG	180
GACTGAGGAC CYTGCTACTC COCAAGCCAG AGCCCATCAG CCAGGCCTGC TGTGAGCCAC	240
20 CTGCCTGTGG AGTGCTGAGC TCAACCAAAG GCTGGCAAGC TCTGGGCCTC ATTTAAGGGA	300
TTCTGATGAG CCGATGGGCC CTGGAGGCAG CCCATTAAAG CATCTGGCTC GTTTTGGAA	360
25 AAAAAAAAAA AAAAAG	376

30

(2) INFORMATION FOR SEQ ID NO: 201:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1192 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

40 CCCAGTATAT TTCTATAACA TTTATTTTAG TGAAC TTATA ATGTTCTTT GTATTAAATT	60
ATTAGATTAT ATCTTAGAT AATATGTGA CTNAATTAGT AGGTAATATA TATTTTATTC	120
AAAATAAAT TGTGCATCTA ATGTCTACCA ATTAATGTAC TTGTAGATGT ATCTTATCTT	180
45 AACTTGAGTC TTTGCTGCCC CTAATGAGGT GTGAAGGACT CTTCTCCCT GGGGAAGTTT	240
TTCTTTTCA GGAGGGAGGA GGGCTTTCCC AGGTAATGTG TCTAGAGTGT TGGCAGAAR	300
50 AATCTGGGAC CACACCACAC CAGTCTCTC CTTAATCCAC GTCATTGACC TTCTATCCCA	360
GCTATGTTTC CAGTGTCTC TGGGTGTTT CAAGAGCAAC AAGAAAYGAA TAAATCTCTG	420
KTGAGTGTGTT TATTTGTTCT TCACTTGTT TTACACTGTA WTTTCTGAGT TTATGGGTGT	480
55 CTGTGAATTA AAAAGGAAAA GTGAAATAA GTAAACTCA GGTGAAGGA AATATACATA	540
AATAAGATAA AGCTGACCTG TAGATATARR CAGTTATAA RAGCTTAGAG TTGTCTAAGT	600
60 TGRGTGCAAA KTTTCTCTG ATCTTCTGA TGCCGARACA AAAAAGGCAG TCATGTTTGT	660

WATGTGATTG GAATGGAACC CGARAAGAGA GCAYGCTGTG TTCTTGGGGA CAGGAAAGCT 720
5 TGYGTGCACC AAGTCTKAAC CACCACCTTC ATGGGACATA GRITATGTGC TGGAACATAT 780
TTCACACCGG CCTGGCAGTA AACACTTGTA GTGTGTGCA GTGGAACGG TCATCTCCG 840
CTAAAGCAGC GCGTGTGTG CAGCGGAAAT GGTCACTGTC TGCTAAAACA CAGCTTCCAT 900
10 CGTAATGTAT GCTCCTTACT CAAAGAGTGT GGTCCCAAAC AGCCTTTGGG AGGTCCTCCT 960
TGATTTCATG ATGAAACCTG GAACATCTTG AGGACTGAGT TAACCATAGG TCCTTAAATA 1020
ACTCTCCACA CGTTTTTCTT AGTTTATCTC TACATGCAGG GTGTGCAGCA GCCTGTTCAA 1080
15 AGTCATATTT TCTGGGAAAT ATTTCCAGTG TTTATTTGCA CTTAGCCCA CTCTGTGTAG 1140
CCTTATTTCT TCTAAACTCA CCATTAATCT GAATAATAGT CAAATTTAGG GG 1192
20

(2) INFORMATION FOR SEQ ID NO: 202:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 589 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

ATCTTGGGCT ATCTTTGACA GGGGATTCTT GCAAGTTGAT GCTTTCTACA AGTGAATATA 60
35 GTCAGTCCCC AAAGATGGAG AGCTTGAGTT CTCACAGAAT TGATGAAGAT GGAGAAAACA 120
CACAGATTGA GGATACGGAA CCCATGTCTC CAGTTCTCAA TTCTAAATTT GTTCCTGCTG 180
40 AAAATGATAG TATCCTGATG AATCCAGCAC AGGATGGTGA AGTACAACTG AGTCAGAATG 240
ATGACAAAAC AAAGGGAGAT GATACAGACA CCMGGGATGA CATTAGTATT TTAGCCACTG 300
GTTGCAAGGG CAGAGAAGAA ACGGTAGCAG AAGATGTTT TATTGATCTC ACTTGTGATT 360
45 CGGGGAGTCA GGCAGTTCCG TCACCAGCTA CTCGATCTGA GGCACCTTCT AGTGTGTTAG 420
ATCAGGAGGA AGCTATGGAA ATTAAAGAAC ACCATCCAGA GGAGGGGTCT TCAGGGTCTG 480
AGGTGAAGA AATCCCTGAG ACACCTTGTC AAAGTCAAGG AGAGGAACTC AAAGAAGAAA 540
50 ATATGGAGAG TGTTCGGTTG CACCTTCTC TGAAGTGAAC TCAGTCCCA 589

55

(2) INFORMATION FOR SEQ ID NO: 203:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 847 base pairs
60 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

5
GGCACGAGCG CAAGCTGCTG GCGCCATCA ACGCGTCCG CCAGGTGCGG CTGAAACACC 60
GGAAGCTCCG GGAACAAGTG AACTCCATGG TGGACATCTC CAAGATGCAC ATGATCCTGT 120
10 ATGACCTGCA GCAGAATCTG AGCAGCTCAC ACCGGGCCCT GGAGAAACAG ATTGACACGC 180
TGGCGGGGAA GCTGGATGCC CTGACTGAGC TGCTTAGCAC TGCCCTGGGG CCGAGCAGCT 240
TCCAGAACCC AGCCAGCAGT CCAAGTAGCT GGACCCACGA GGAGGAACCA GGCTACTTTC 300
15 CCCAGTACTG AGTGGTGGAC ATCGTCTCTG CCACTCCTGA CCAGCCTGAA CAAAGCACCT 360
CAAGTGCAAG GACCAAAGGG GGCCTGGCTT GGATGGGTG GCTTGCTGAT GCCTGCTGGA 420
20 GGGGACGCTG GCTAAAGTGG GGAGGCCTTG GCCACCTGA GGCCCCAGGT GGAACATGG 480
TCACCCCCAC TCTGCATACC CTCATCAAAA ACACTCTCAC TATGCTGCTA TGGACGACCT 540
CCAGCTCTCA GTTACAAGTG CAGGCGACTG GAGGCAGGAC TCTTGGGTCC CTGGGAAAGA 600
25 GGGTACTAGG GGCCCGGATC CAGGATTCTG GGAGGCTTCA GTTACCGCTG GCCGAGCTGA 660
AGAACTGGGT ATGAGGCTGG GCGGGGCTG GAGGTGGCG CCCTGGTGG GACAACAAAG 720
30 AGGACACCAT TTTCCAGAG CTGCAGAGAG CACCTGGTGG GGAGGAAGAA GTGTAACCTCA 780
CCAGCCTCTG CTCTTATCTT TGTAATAAAT GTTAAAGCCA GAAAAAAAAA AAAAAAAAAA 840
AAAAAAA 847
35

(2) INFORMATION FOR SEQ ID NO: 204:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 852 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

45

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

ACAAACATAC TGCAGGAAG GAGTCTCATG CTGCCCGCAG CATCAGCGCA ACNCNTGGCC 60
50 GCCATCAACG CGTTCGCCA GTGCGGCTG AAACACCGGA AGCTCCGGGA ACAAGTGAAC 120
TCCATGGTGG ACATCTCCAA GATGCACATG ATCCTGTATG ACCTGCAGCA GAATCTGAGC 180
55 AGCTCACACC GGGCCCTGGA GAAACAGATT GACACGCTGG CGGGGAAGCT GGATGCCCTG 240
ACTGAGCTGC TTAGCACTGC CCTGGGGCCG AGGCAGCTTC CAGAACCAG CCAGCAGTCC 300
AAGTAGCTGG ACCACGNAG GAGGAACCAG GCTACTTTCC CCAGTACTGA GGTGGTGGAC 360
60

ATNCGTCTCT TGCCACTCCN TGNACCCAGC CCTGAACAAA GCACCTCAAG TGCAAGGACC 420
 AAAGGGGGCC CTGGCTTGGA GTGGGTGGC TTGCTGATGG CTGCTGGAGG GGACGCTGGC 480
 5 TAAAGTGGGK AGGCCTTGGC CCACCTGAGG CCCAGGTGG GAACATGGTC ACCCCCACTC 540
 TGCATACCCCT CATCAAAAAC ACTCTCACTA TGCTGCTATG GACGACCTCC AGCTCTCAGT 600
 TACAAGTGCA GCGGACTGGA GGCAGGACTC CTGGGTCCCT GGGAAAGAGG GTACTAGGGG 660
 10 CCCGATCCA GGATTCTGGG AGGCTTCAGT TACCGCTGGC CGAGCTGAAG AACTGGGTAT 720
 GAGGTGGGG CGGGCYGGA GGTGGCGCCC CCTGGTGGGA CAACAAAGAG GACACCATTT 780
 15 TTCCAGAGCT GCAGAGAGCA CCTGGTGGGG AGGAAGAAGT GTAACCTACC AGCCTCTGCT 840
 CTTATCTTTG TA 852

20

(2) INFORMATION FOR SEQ ID NO: 205:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1354 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

GATTGCGCAC GAGGCTTGCT GGAGCAGGAG AAGTCTCTRG CCGGCTGGGC ACTGGTGCTG 60
 GCASGARCTG GCATTGGACT CATGGTGCTG CATGCAGAGA TGCTGTGGTT CGGGGGGTGC 120
 35 TGGGTGTCA ATGCCACTGG GCACCTTTCA GACACACTTT GGCTGATCCC CATCACATTC 180
 CTGACCATCG GCTATGGTGA CGTGGTGCCG GGCACCATGT GGGCAAGAT CGTYTGCCCTG 240
 40 TGCATGGAG TCATGGGTGT CTGCTGCACA GCCCTGCTGG TGGCCGTGGT GGCCCGGAAG 300
 CTGGAGTTTA ACAAGGCAGA GAAGCACGTG CACAACCTCA TGATGGATAT CCAGTATACC 360
 AAAGAGATGA AGGAGTCCG TGCCCGAGTG CTACAAGAAG CCTGGATGTT CTACAAACAT 420
 45 ACTCGCAGGA AGGAGTCTCA TGCTGCCCCG AGGCATCAGC GCAANCTGCT GGCCGCCATC 480
 AACGCGTTCC GCCAGGTGCG GCTGAAACAC CGGAAGCTCC GGAACAAGT GAACTCCATG 540
 50 GTGGACATCT CCAAGATGCA CATGATCCTG TATGACCTGC AGCAGAATCT GAGCAGCTCA 600
 CACCGGGCCC TGGAGAAACA GATTGACACG CTGGCGGGGA AGCTGGATGC CCTGACTGAG 660
 CTGCTTAGCA CTGCCCTGGG GCCGAGGCAG CTTCAGAAC CCAGCCAGCA GTCCAAGTAG 720
 55 CTGGACCCAC GAGGAGGAAC CAGGCTACTT TCCCCAGTAC TGAGGTGGTG GACATCGTCT 780
 CTGCCACTCC TGANCCAGC CCTGAACAAA GCACCTCAAG TGCAAGGACC AAAGGGGGCC 840
 60 CTGGCTTGGA GTGGGTGGC TTGCTGATGG CTGCTGGAGG GGACGCTGGC TAAAGTGGGK 900

5 AGGCCTTGGC CCACCTGAGG CCCAGGTGG GAACATGGTC ACCCCCACTC TGCATACCT 960
 CATCAAAAC ACTCTCACTA TGCTGCTATG GACGACCTCC AGCTCTCAGT TACAAGTGCA 1020
 GCGGACTGGA GGCAGGACTC YTGGGTCCCT GGGAAAGAGG GYACTAGGGG CCCGGATCCA 1080
 GGATTCTGGG AGGCTTCAGT TACCGCTGGC CGAGCTGAAG AACTGGGTAT GAGGCTGGGG 1140
 10 CGGGGCTGGA GGTGGGCCCC CCTGGTGGGA CAACAAAGAG GACACCATTT TTCCAGAGCT 1200
 GCAGAGAGCA CCTGGTGGGG AGGAAGAAGT GTAACCTACC AGCCTCTGCT CTTATCTTTG 1260
 TAATAAATGT TAAAGCCAGA AAAAAATAAA AAAAAAATAA AAAAAACTCG AGGGGGGCCC 1320
 15 AGACCCAATC TCCCTATAGT AAGNCGCCNN ANAN 1354

20

(2) INFORMATION FOR SEQ ID NO: 206:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1378 base pairs
 25 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

TCCCCAGGTG CACAGCCAGG GCCCTCCTGT CTGCAGGAGA ATTCACAGCT GGTGTGGGAC 60
 TCAGCCCCCTA GNCCATTCAA AGCCTTAATG TTGTAATCAT ATCTTACGTG TTGAAGACCT 120
 35 GACTGGAGAA ACAAATGTG CAATAACGYG AATTTTATCT TAGAGATCTG TGCAGCCTAT 180
 TTCTGTGACA AAAGTTATAT TGTCTAATAA GAGAAGTCTT AATGGCCTCT GTGAATAATG 240
 TAACTCCAGT TACACGGTGA CTTTAAATAG CATACTAGTA TTTGATGAAA GGACGTCAAA 300
 40 CAATGTGGCG ATGTCGTGGA AAGTTATCTT TCCCGCTCTT TGCTGTGGTC ATTGTGTCTT 360
 GCAGAAAGGA TGGCCCTGAT GCAGCAGCAG CGCCAGCTGT ANATAAAAAA TAATTCACAC 420
 45 TATCAGACTA GCAAGGCACT AGAAGTGGAA AAGACCACAG AAAACAAAGA ATCCAACCTT 480
 TTCATCTTAC AGGTGAACAA ACTGTGATGA TGCACATGTA TGTGTTTTGT AAGCTGTGAG 540
 CACCGTAACA AAATGTAAAT TTGCCATTAT TAGGAAGTGC TGGTGGCAGT GAAGAAGCAC 600
 50 CCAGGCCACT TGAATCCAG TCTGGTGCCC TGTCTACACC AGACAACACA GGAGCTGGGT 660
 CAGATTCCCC TCAGCTGCTT AACAAAGTTC CTCGAACAGA AAGTGCTTAC AAAGCTGCCT 720
 55 TCTCGGATAC TGAAAGGTG AGTTTCTGTA ACTGCACTGA TTTTATTGCA GTTGAAAAAA 780
 AAAAAAGCT ATTCCAAAGA TTTCAAGCTG TTCTGAGACA TCTTCTGATG GCTTTACTTC 840
 60 CTGAGAGGCA ATGTTTTTAC TTTATGCATA ATTCATGTGT GCCAAGGAAT AAAGTGAAGA 900

AACAGCACCT TTTAATATAT AGGTCTCTCT GGAAGAGACC TAAATTAGAA AGAGAAAAC 960
 GTGACAATTT TCATATTCTC ATTCTTAAAA AACACTAATC TTAAC TAACA AAAGTTCTTT 1020
 5 TGAGAATAAG TTACACACAA TGGCCACAGC AGTTTGTCTT TAATAGTATA GTGCCTATAC 1080
 TCATGTAATC GGTTACTCAC TACTGCCTTT AAAAAAAAAA ACCAGCATAT TTATTGAAAA 1140
 10 CATGAGACAG GATTATAGTG CCTTAACCGA TATATTTTGT GACTTAAAAA ATACATTTAA 1200
 AACTGCTCTT CTGCTCTAGT ACCATGCTTA GTGCAAATGA TTATTTCTAT GTACAACTGA 1260
 TGCTTGTTCT TATTTTAATA AATTATCAG AGTGAAAAA AAAAAAAAAA AAAAAAAAAA 1320
 15 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAGAA NAAAAANA 1378

20 (2) INFORMATION FOR SEQ ID NO: 207:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1166 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

30 AANCCACTGC ANTTTAAACC CCTCCCTC CAAGAAAGTT CACAACCGGC CATGGATGAC 60
 CCTCATTTTA GATGGCCNC AATATTTAAG ATGGACTGRG GACCCARAG ACTGACCTT 120
 35 GAAAGGGGA CTCAGAAGAA AGATCCTGA CATTGCCMAA CATGCTGGGC TTGTCCAACA 180
 CAGTGATGCG GCTCATCGAG AARCGGCTT TCCMAGGACA AGTACTTTAT GATAGGTGGG 240
 ATGCTGTGA CCTGTGTGT CATGTTCTC GTGGTGCAGT ACCTGACATG AGCCAGCCAC 300
 40 GCTCAGTGGC TGAACAGCAT TCCACAGCC TGCAAGTGTG TGTGTGTGTG AAAGAGAGAG 360
 GGGGCCCAGA GGCCGCTTT TGAAATGTT GCCTGTCTGA ACTGTGAAGA CACTTGGGAG 420
 45 TGATTGTGGT CTAATTTCCA ACCTGCTCTG TTTTCTGTGA CATCTTGGAG GGGGAGCTAG 480
 TGCCAMCACC ATGCGCGGTG CTTAGGAAAT GAAAGAAGTC CCGGTCTGT CTCTCTCACT 540
 CTCGCTCTCA MTGGGGGAGG GAAAGAATGG CTTTGGTGGC TTTGTTTACA CAGCTGATGC 600
 50 GTGSCCTGGG AAGGTGTCCA CAGTGAGCCC TGTGTGCAGG ACTGTCCACN ACGGTTTACA 660
 CCTGTGACAC ATCAGGCTT TCTGGCTCCT GATAGGGTGG AGCAAAAGTG GAAAGGAAAG 720
 55 GAAAGAGGCY TTTTCTTACA GCCATTATAT TAAATAGTAG GTCGATTCAC ATCYTCGTGC 780
 TCCTGGCCAC CCTCCCTGT GCCTCAGTGA CATGTAGATG ACTGACTGCC AATACTTGTC 840
 ACCATTCCCT GGAAGCAGCT ACCTAGGGGA AACAGATGT AGTGCTATTG CCGATAACAA 900
 60 GTAAGATTTT CCACACTACA GCTGGGTGTT TCTCTTTTCT AAAGTGAGGC CAGTGTTATT 960

5 TCCCGGGAGT GTTCAGTCTT GACCCTAGTC ACTGATTTT TCTAGTTGTT AATAGAGTGG 1020
TTGGGCTTTT AAGGTTTACA GACTGTGGGC TTGGGCACCT GCGCCCAGGG STTTTGTGGG 1080
GGCCTTTGCC CCTTAGRAAA GTAGCTTTTA GGGGCAAAGA TTTGTTGATT TTCCCCATTA 1140
CAGTCTTCAG CTCNAGGGTT TAAAAA 1166

10

(2) INFORMATION FOR SEQ ID NO: 208:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 697 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

TACTTCTAGG ATTATAAGGA ATTAACATTC AGATGACATT TCCATTTGAG AAGGAAAATA 60
25 GTTGCTTTCA GTGCCTTTA TTTGATTCTT GGAGAGAGCA GACTCGCACS AACATTCAAC 120
CCCAGCGCTG ATATGACAGT AATCCTCAGA GGCAGAGCCC AGCACAAAAC AGCAATGCTA 180
30 GAAAGTTACA ATTGGAAAGT TTCTGCCAG CTTCGGGAAT GACACTGCAA AGCTGATGCC 240
AGAAACTGCC AGRGTAATTC TCCTCATTAC TGCTCTACCC ACCCACTTTC AGCTCCCCAA 300
ATTAAGTAGT GCACTTGACT AATTCTCTTT ACCTTTATCA TTTARGGTGA RGCATTGCAC 360
35 AAAAAGTCTC GACTTTGCCA TATAAGGGCT GTGGTTCTCT GTGGTCCCCT GGATAAGAGG 420
CATCACCATT ATCTGGAAAC ATGCAGTAAA TGCAGATTNT TCATCTTCTC CCCAGACCTC 480
CTGAGTTAGA AATTACAAG TTCTCCAGT GATCTCATAC ATGCTAAAGT TTGAGAACCA 540
40 TTGAGTAAAG TTAATGCATT AAGAAGAGAT TAGATAGGGA TGGTGGCGTA TCTTCCTACA 600
GTTTCCTGT TAACAAGAAA GTCAGAGGTC AGTTGATCAG ACATTAGATT ATTTATTGCT 660
45 AAAACTAAAA AAAATTAAAA AAACTGGAG GGGGGCC 697

50

(2) INFORMATION FOR SEQ ID NO: 209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 932 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

60 CGTGAGTCAC CTCTCTATAG TGGGCGTGGC CGAGGCCGGG GTGACCCTGC CGAAGCCTCC 60

	GCTGCCAGAA ACCATGTTCA AGGTAATTAA AAGGTCCGTG GGGCCAGCCA GCCTGAGCTT	120
5	GCTCACCTTC AAAGTCTATG CAGCACCAAA AAAGGACTCA CCTCCCAAAA ATTCCGTGAA	180
	GGTTGATGAG CTTTCACTCT ACTCAGTTCC TGAGGGTCAA TCGAAGTATG TGGAGGAGGC	240
	AAGGAGCCAG CTTGAAGAAA GCATCTCACA GCTCCGACAC TATTGCGAGC CATAACAAC	300
10	CTGGTGTGAG GAAACGTACT CCCAAACTAA GCCCAAGATG CAAAGTTTGG TTCAATGGGG	360
	GTTAGACAGC TATGACTATC TCCAAAATGC ACCTCCTGGA TTTTTCCTGA GACTTGGTGT	420
15	TATTGGTTTT GCTGGCCTTA TTGGACTCCT TTTGGCTAGA GGTTCAAAA TAAAGAAGCT	480
	AGTGTATCCG CCTGGTTTCA TGGGATTAGC TGCTCCTCCTC TATTATCCAC AACAAGCCAT	540
	CGTGTTCGCC CAGGTCAGTG GGGAGAGATT ATATGACTGG GGTTCACGAG GATATATAGT	600
20	CATAGAAGAT TTGTGGAAGG AGAACTTTCA AAAGCCAGGA AATGTGAAGA ATTCACCTGG	660
	AACTAAGTAG AAAACTYCAT GTTCTGCCAT CTTAATCAGT TATRGGTAAA CATTGGAAC	720
25	TCCATAGAAT AAATCAGTAT TTCTACAGAA AAATGGCATA GAAGTCAGTA TTGAATGTAT	780
	TAAATGGCT TTCTTCTTCA GGAAAACTA GACCAGACCT CTGTTATCTT CTGTGAAATC	840
	ATCCTACAAG CAAACTAACC TGAATCCCT TCACCTAGAG ATAATGTACA AGCCTTAGAA	900
30	CTCCTCATTC TCATGTTGCT ATTTATGTAC CT	932

35 (2) INFORMATION FOR SEQ ID NO: 210:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 661 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

45	GTCAATCTTT AAATAAAAGC TTCCTGTTT AAAGCTTTTC AAAGGAGCAG ACCACCTTGA	60
	AGATTCCTCC TAGGGTTGAT ATGTGTCTAA TTCATTTTAT AAAAATTATT CTGTCTTCA	120
50	TTTTAAAGCT TTGGCTATAT AGTCAGAAAT GTCCTAAATA ACAAACTATT TTGTATTTAA	180
	TTTAGGGAAG ACTAAAGGA AGAAAAATGA AAAGTCAGTC TTTATGTAAG CTCCAAGGAT	240
	ATTAGGCTTT AAAGGGCTTT TCTAGTTTTA TGAGAATTG TACTACTGAT TTTTATATAT	300
55	TCCTGTTTTT GAGATGAACA GATCTCTGGG GAAATGTTG AGTTACAATG GCATTTCACT	360
	GTGATCCTCT TCAAGCTCAG ATCAGTTCTA TAACCCAATG ACAACCTGTC TCTTTGGTTT	420
60	ACTGTCCTGT GAAATGTCAG CTCAAGTTTC CCAGAAGTCG TGTGTTTATG ATGAGTCAGA	480

GTGCTTTTCC TCGGTGGGAC AGTTGCTGGC CCTCTTAATT TTGGTGTATG TGCTTCCAAG 540
 TATCTAAACC TCCAGTCTGA TCTGTATATG CTATCCTAAC TGTTAATTGT ATTATGTATT 600
 5 ATGTTGATTA TCTTGCTTGA AGGTTTCATAC TTTTCAATTT GATAGAAATA AAGTTTTTTT 660
 C 661

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(2) INFORMATION FOR SEQ ID NO: 211:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 592 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

GAAACTGACA TTGTTAAACA CACTAAAACA GAAGTACTTA CCTCTTGAAG ATTTAATATA 60
 TAATGGTTGA CATGATACAT GTACATGAAT GGAATGACCA GATGCTTATG GTCTACATTT 120
 25 TCCTTTATCC TGTTAGTATT ACCTTCCTTA ATCTTTGTTC CTTAACATGC TAAATTCCTC 180
 TTCAGTGTIT ATTTTCTAGT GACAGAATGC TAACATTTCT TACACCCTGG CAGAAGGGAG 240
 30 AGAAATGTGT TTTGGGGTGG GTAATAAAT TTTTGAGTGA AATATCATAA GATGAGAATG 300
 GAAAGAGGGA GACACAAAGA GTTATAACAA AAAACAATG GTTTTTTTAG CCATTTGACT 360
 GGCTCTTTAA ATAGTCTACA AGACATTAC GTTNAACATC ACTTTTAGTG AAATAAAATG 420
 35 TGCCATACTA GTATGTGCTT CAAAGGGCA AATGTGCTTT AGTGCCCTAA GGCTAAATTT 480
 TGGTCATTG ACATCAGAGA TGTGTAAAT ATTGCACCTA ATACGCACCT ATTTCTCAAT 540
 40 AGTGTATTT TTTGGCTAG CATTTNCTTT ACCACTAACC TTGTTGGATA GC 592

45 (2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 938 base pairs
 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

55 TGGAGTGGCT TTCCAGCTGA ATGAATCCTA TGTCTGCGT GCAGGTGGTT GGTTTTCAAT 60
 GTTCTTSCTA ATTTTTTTCC TATGGCTCT TGGGAGTTN CTTTGTTC TCCTGTGTTT 120
 60 GCCCAGCTTT AATAAAACCA GGCACAAACA AAAACCATAG CATTCGAAA CAATAGGGGG 180

	CCCACATTGG ACCCAGTATG TCACTTTAAT GGACTTCAAG AAAAAATCTG AATGGGAAAA	240
	TGACACTAGG AATGTATACT CCACACATTT TATGCCATAT AATGGTGTGT TTTCTTAATT	300
5	TTGTTTCTTG TGGCGAAATG TGGCTTTCAA ATTAAAATGM CCTTTCTTC TTKGAACTT	360
	TTTGTITKGA CTGTATAAT TAAGGGTTTG GAAAGATTCA TAATMTGAG AGAGGTTTGC	420
10	AACCAGGAGA TACAAAGAAG TCTCAGTAGT AATCTTGTTC ATGTGCTTTT ACAGCCAGCT	480
	ACATTTAAGR ATGTATTAGT TACAGAAAT ATATGTCTGT GTATGTGTCT CTACTCAATA	540
	AAGTACATGC CTCCACATAA TGCGGTGCTG TCCATCTCGG CAAATACTGG CCAAGTCCCT	600
15	TTATGACAGG CACACAGAAA CCATAGCATG GTCTGGCTTT CAGAAAATGC CTCTCATCTT	660
	TCCTGGAACC TTATTTTGCT AAATGTCTGT TTTCTTGTGA TTTGTGTGAC CTCACAGCAC	720
20	CATTGTGACC ATGGTGATGC CTCATTGCA TGATATGTAC CTTGTGTTTA ATGTGAAATA	780
	CATTTTCATT GAAGAGTCTG ATGACTTGCT AGCGTTTTAT TTTTCTGTGA AGCTCAATGT	840
	GCTGAAACCA AACCAGGCTT TTA AAAACCT GTGTAGAAGA AAACCAAAAA ATCCTGTGTG	900
25	GGTGTCTTT CCTGTCAA CTCATTAAAA ATTCCTTT	938

30 (2) INFORMATION FOR SEQ ID NO: 213:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1079 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

40	AGCCTGCCGG GAGAGTGGTG GCATCTRARA GGCTGGTCGT GGACTGTGGT TGGGGGAGGT	60
	GGGAGCTGTT TTAACCGTGT GCCCCTCTC CTGTGCKGC GTGGGCATCC CCCGGGCGAG	120
45	TGGAACGCGG GCGCTCCTCC AGCTTCCGAG TCCAGCCAGC CTGGGCGCGG GGCGCGCCCC	180
	CGAGACACCC GAGGAGTCCG TTCTCCCTG GTTACGTGGA CTGTGGAGCT GGTCTCTTGT	240
	GGCTCAGCGC CGTGCGGAGG TTGAAGCGTA CTTGCGGAGG TCGCACCAGG GGCGTGAGGA	300
50	GGAGGAGGAA GGCATGAGC CGAGCTTGAG GAATCCGTGY TCCAACTCT ACACTCAAGG	360
	RTGCMCTGCG CAACTCTGGT GCGATGGGC TGGGGCAGAT GTCCTTGAG TTCTACCAGA	420
55	AGAAGAAGTC TCGCTGGCCA TTCTCAGACG AGTGATCCC ATGGGAAGTG TGGACGGTCA	480
	AGGTGCATGT GGTAGCCCTG GCCACGGAGC AGGAGCGGCA GATCTGCCG GAGAAGGTGG	540
	GTGAGAACT CTGCGAGAAG ATCATCAACA TCGTGAGGT GATGAATCGG CATGAGTACT	600
60	TGCCCAAGAT GCCCACACAG TCGGAGGTGG ATAACGTGTT TGACACAGGC TTGCGGGACG	660

TGCAGCCCTA CCTGTACAAG ATCTCCTTCC AGATCACTGA TGCCCTGGGC ACCTCAGTCA 720
 CCACCACCAT GCGCAGGCTC ATCAAAGACA CCCTTGCCCT CTGAGCGTGG CTGGATCTCT 780
 5 GGGAGCTCCT TGATGGCTCC CAGACCTTGG CTTTGGGAA TTGCACTTT GGGCCTTTGG 840
 GCTCTGGAAC CTGCTCTGGG TCATTGGTGA GACTTGGAAG GGGCAGCCCC CGCTGGCTTC 900
 10 TTGGTTTGT GGTGCCAGC CTCAGGTCAT CCTTTTAATC TTTGCTGACG GTTCAGTCT 960
 GCCTCTACTG TCTCTCCATA GCCCTGGTGG GGTCCCCCTT CTTTCTCCAC TGTACAGAAG 1020
 15 AGCCACCACT GGGATGGGGA ATAAAGTTGA GAACATGAGT TTGGGCTGAA AAAAAAAAAA 1079

(2) INFORMATION FOR SEQ ID NO: 214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3791 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

TGAAGCAGGC GCTCTTGGCT CGCGCGGGCC CGCTGCAATC CGTGGAGGAA CGCGCGGCCG 60
 30 AGCCACCATC ATGCCTGGGC ACTTACAGGA AGGCTTCGGC TGCCTGGTCA CCAACCGATT 120
 CGACCAGTTA TTTGACGACG AATCGGACCC CTTCGAGGTG CTGAAGGCAG CAGAGAACAA 180
 35 GAAAAAAGAA GCCGGCGGGG GCGCGTTGG GGGCCCTGGG GCCAAGAGCG CATCAGGGCC 240
 GCGGCCCAGA CCAACTCCAA CGCGGCAGGC AAACAGCTGC GCAAGGAGTC CCAGAAAGAC 300
 CGCAAGAACC CGCTGCCCCC CAGCGTTGGC GTGGTTGACA AGAAAGAGGA GACGCAGCCG 360
 40 CCCGTGGCGC TTTAAGAAAG AAGGAATAAG ACGAGTTGGA AGAAGACCTG ATCAACAAC 420
 TCAGGTGAA GGGAAAATAA TTGATAGAAG ACCAGAAAGG CGACCACCTC GTGAACGAAG 480
 45 ATTCGAAAAG CCACTTGAAG AAAAGGTGA AGGAGGCGAA TTTTCAGTTG ATAGACGAT 540
 TATTGACCGA CCTATTGAG GTCGTGGTGG TCTTGAAGA GGTGAGGGG GCGGTGGACG 600
 TGAATGGGC CGAGGAGATG GATTTGATTC TCGTGGCAA CGTGAATTG ATAGGCATAG 660
 50 TGAAGTGAT AGATCTTCTT TTTCACATTA CAGTGGCTG AAGCACGAGG ACAAACGTGG 720
 AGGTAGCGGA TCTCACAAC TGGGAACGT CAAAGACGAA TTAAC TACT TGGATCAATC 780
 55 AAATGTGACT GAGGAAACAC CTGAAGGTGA AGAACATCAT CCAGTGGCAG AACTGAAAA 840
 TAAGGAGAAT GAAGTTGAAG AGGTAAAAGA GGAGGGTCCA AAAGAGATGA CTTTGGATGA 900
 GTGAAGGCT ATTCAAAATA AGGACCGGGC AAAAGTAGAA TTAAATATCC GAAAACCAA 960
 60

	TGAAGGTGCT GATGGGCAGT GGAAGAAGGG ATTTGTCTTT CATAAATCAA AGAGTGAAGA	1020
	GGCTCATGCT GAAGATTGGG TTATGGACCA TCATTTCGGG AAGCCAGCAA ATGATATAAC	1080
5	GTCTCAGCTG GAGATCAATT TTGGAGACCT TGGCCGCCCA GGACGTGGCG GCAGGGGAGG	1140
	ACGAGGTGGA CGTGGGGGTG GTGGGCGCCC AAACCGTGGC AGCAGGACCG ACAAGTCAAG	1200
10	TGCTTCTGCT CCTGATGTGG ATGACCCAGA GGCATTCCCA GCTCTGGCTT AACTGGATGC	1260
	CATAAGACAA CCTGGTTCC TTTGTGAACC CTTCTGTTCA AAGCTTTTGC ATGCTTAAGG	1320
	ATTCCAAACG ACTAAGAAAT TAAAAAATAA AAGACTGTCA TTCATACCAT TCACACCTAA	1380
15	AGACTGAATT TTATCTGTTT TAAAAATGAA CTTCTCCCGC TACACAGAAG TAACAAATAT	1440
	GGTAGTCAGT TTTGTATTTA GAAATGTATT GGTAGCAGGG ATGTTTTTCAT AATTTTCAGA	1500
20	GATTATGCAT TCTTCATGAA TACTTTTGTG TTGCTGCTTG CAAATATGCA TTTCCAAACT	1560
	TGAAATATAG GTGTGAACAG TGTGTACCAG TTAAAGCTT TCACTTCATT TGTGTTTTTT	1620
	AATTAAGGAT TTAGAAGTTC CCCCAATTAC AAACGTGTTT TAAATATTGG ACATACTGGT	1680
25	TTTAATACCT GCTTTGCATA TTCACACATG GTCAACTGGG ACATGTTAAA CTTTGATTTG	1740
	TCAAAATTTA TGCTGTGTGG AATACTAACT ATATGTATTT TAACCTAGTT TTAATATTTT	1800
30	CATTTTTGGG GAAAAATCTT TTTTCAC TTCATGATAGC TGTATATAT ATATGCTAAA	1860
	TCTTTATATA CAGAAATATC AGTACTTGAA CAAATTCAAA GCACATTTGG TTTATTAACC	1920
	CTTGCTCCIT GCATGGCTCA TTAGGTTCAA ATTATACTG ATTTACATTT TCAGCTATAT	1980
35	TTACTTTTTA AATGCTTGAG TTTCCCATTT TAAATCTAA ACTAGACATC TTAATTGGTG	2040
	AAAGTTGTTT AAACACTTTA TTGTGGTAG GCACATCGTG TCAAGTGAAG TAGTTTTATA	2100
40	GGTATGGGTT TTTTCTCCCC CTTCAACAGG GTGGGTGGAA TAAGTTGATT TGGCCAATGT	2160
	GTAATATTTA AACTGTTCTG TAAATAAGT GTCTGGCCAT TTGGTATGAT TTCTGTGTGT	2220
	GAAAGGTCCC AAAATCAAAA TGGTACATCC ATAATCAGCC ACCATTTAAC CCTTCCTTGT	2280
45	TCTAAAACAA AAACCAAAGG GCGCTGGTTG GTAGGGTGA GTGGGGGAGT ATTTTAATTT	2340
	TTGGAATTTG GGAAGCAGAC AGCTTTACTT TGTAAGGTTG GAACAGCAGC ACTATACATG	2400
50	AAATATAAAC CAAAAACCTT TACTGTTTCT AAATTCCTA GATTGCTATT ATTTGGTTGT	2460
	AAGTTGAGTA TTCCACAGAA AGTGGTAATT ATCTCTTCTC TCTTCCTCCA TTAGAAAATT	2520
	AGGTAAATAA TGGATTCCTA TAATGGGAGC ATCACCACCT ATTAACACAC ACATAGAATG	2580
55	ATGAATTAAA AAAGTTTCTT AGGATTGTCT TTTATCTGC CACATTTATT GATAAACAGT	2640
	GAAGGAATTT TTAATAAATT TTTAAGAATT GTTTGTCAG TCATTTTATG AAATGTTCTA	2700
60	CCTGTATATG GTAATGTCCA GTTTTAAAAA TATTGGACAT CTTCAATCTT AAACATTTCT	2760

	ATTTAGCTGA TTGGTTCTCA CATATACTTC TAAAAGAAAC TTTTATGTTA TAAGAGTTAC	2820
	TTTTTGGATA AGATTTATTA ATCTCAGTTA CCTACTATTC TGACATTTTA GGAAGGAGGT	2880
5	AATTGTTTTT AATGATGGAT AAACITGTGC TGGTGTGTTG GATCTTATGA TGCTGAGCAT	2940
	GTCTGCACT GGTGCTAATG TCTAATATAA TTTTATATTT ACACACATAC GTGCTACCCA	3000
10	GAGATTAATT TAGTCCATAT GAACTATTGA CCCATTGTTT ATTGAGACAG CAACATACGC	3060
	ACTCCTAAAT CAGTGTGTTT AGACTTTTCA AGTATCTAAC TCATTTCCTAA ACATGTACCA	3120
	TGTTTTATAA ACCTCTTGAT TTCCAGCAAC ATACTATAGA AAACACCTGC TACTCAAAC	3180
15	ACAACTTCTC AGTGTATCC ATTGCTGTGC TGAGAGACAA CATAGCAATA TCTGGTATGT	3240
	TGCAAGCTTT CAAGATAGCC TGAACCTAAA AAGTTGGTGC ATTAGTTGTA TCTGATGGAT	3300
20	ATAAATTTGC CTCTAGTTC ACTTTGTGTC AAGAGCTAAA ACTGTGAACC TAACTTTCTC	3360
	TTATTTGGTG GTAATACTG AAAATAAAGA TTTATTTTCA TGCTCACTTC TTAAGAATCA	3420
	TAAAACAAT CAAATAGGRT CATGTTTATT GTCATGTGTT TCCTGGKTTT TGACCTGTGT	3480
25	GCACACCCCT GTGTGTTTAT AATTTTAAA TTGAATTTTA TATGGGGTTT TTATTTGCTA	3540
	AAAACCAGGC TGTGAATCA CATTGGGAA GGGTACTTAT CTTAATGACT AATGACTTAA	3600
30	TTGGGAAAGT TGAATCTTG TAAATACAA AATCCAAGGA CTTCTGGGA TTAAATCTAA	3660
	TTGTCACTTC NTAGGCAGA TNCACTTTTT TGGATAATGG AAAGTTAAGC ATACCGAATG	3720
	CTACTTTTGG TTGACAAACG GGCCTAATAG TCCGGGGGGA AATCCCTAAC NGTAAGGNT	3780
35	CCCAAGTATG G	3791

40 (2) INFORMATION FOR SEQ ID NO: 215:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1334 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

50	CAGTGTCTCG TCCTGCTCGG GCGCTGCGG CCCCAGGCGT CGCCATGACC AGTGAGCTGG	60
	ACATCTTCGT GGGGAACAGA CCTTATCGA CGAGGACGTG TATCGCCTCT GGCTCGATGG	120
55	TTACTCGGTG ACCGACGCGG TGGCCCTGCG GGTGCGCTCG GGAATCCTGG AGCAGACTGG	180
	CGCCACGGCA GCGGTGCTNC AGAGCGACAC CATGGACCAT TACCGCACCT TCCACATGCT	240
	CGAGCGGCTG CTGCATGCGC CGCCCAAGCT ACTGCACCAG YTCATCTTCC AGATTCCGCC	300
60	CTCCCGGCAG GCACTACTCA TCGAGAGGTA CTATGCCTTT RATGAGGCCT TTGTTCCGGA	360

	GGTGCTGGGC AAGAAGCTGT CCAAAGGCAC CAAGAAAGAC CTGGATGACA TCAGCACCAA	420
	AACAGGCATC ACCCTCAAGA GCTGCCGGAG ACAGTTTGAC AACTTTAAAC GGGTCTTCAA	480
5	GGTGGTAGAG GAAATGCGGG GCTCCCTGGT GGACAATATT CAGCAACACT TCCTCCTCTC	540
	TGACCGGTTG GCCAGGGACT ATGCAGCCAT CGTCTTCTTT GCTAACAACC GCTTTGAGAC	600
10	AGGGAAGAAA AAACTGCAGT ATCTGAGCTT CGGTGACTTT GCCTTCTGCG CTGAGCTCAT	660
	GATCCAAAAC TGGACCCPTG GAGCCGTCGA CTCACAGATG GATGACATGG ACATGGACTT	720
15	AGACAAGGAA TTTCTCCAGG ACTTGAAGGA GCTCAAGGTG CTAGTGGCTG ACAAGGACCT	780
	TCTGGACCTG CACAAGAGCC TGGTGTGCAC TGCTCTCCGG GGAAAGCTGG GCGTCTTCTC	840
	TGAGATGGAA GCCAACTTCA AGAACCTGTC CCGGGGGCTG GTGAACGTGG CCGCCAAGCT	900
20	GACCCACAAT AAAGATGTCA GAGACCTGTT TGTGGACCTC GTGGAGAAGT TTGTGGAACC	960
	CTGCCGCTCC GACCACTGGC CACTCAGCGA CGTGCGGTTT TTCCTGAATC AGTATTTCAGC	1020
25	GTCTGTCCAC TCCCTCGATG GCTTCCGACA CCAGGCCTCT GGGACCGCTA CATGGGCACC	1080
	CTCCGCGGCT GCCTCCTGCG CCTGTATCAT GACTGAGGTG CCTCCCAACG CTCCGCCAC	1140
	GCTGACAATA AAGTTGCTCT GAGTTTGAG ACTGGTCTC GCTCCGGGA GCAAGTGGG	1200
30	GGCGTCAGA TGTGCTGTG TCTGTCTCTG AGCACCTGGT GTCCGTGTAC AAGGATGGAT	1260
	GTGTNCGTG GCTCCTTGGG AACTGAGACA TATCTCAGG AATGGTGTCT GTGCTCAGCC	1320
35	CATCCACCAG AAGA	1334

40 (2) INFORMATION FOR SEQ ID NO: 216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1511 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

50	GTGGCGGGGA TGCTGCGAGG GGGTCTCCTG CCCCAGGCGG GCCGGCTGCC TACCTCCAG	60
	ACTGTCCGCT ATGGCTCCAA GGCTGTTACC CGCCACCGTC GTGTGATGCA CTTTCAGCGG	120
	CAGAAGCTGA TGGCTGTGAC TGAATATATC CCCCCGAAAC CAGCCATCCA CCCATCATGC	180
55	CTGCCATCTC CTCCAGCCC CCCACAGGAG GAGATAGGCC TCATCAGGCT TCTCCGCGG	240
	GAGATAGCAG CAGTTTCCA GGACAACCGA ATGATAGCCG TCTGCCAGAA TGTGGCTCTG	300
60	AGTGCAGAGG ACAAGCTTCT TATGCGACAC CAGCTGCGGA AACACAAGAT CCTGATGAAG	360

	RTCTTCCCCA ACCAGGTCCT GAAGCCCTTC CTGGAGGATT CCAAGTACCA AAATCTGCTG	420
	CCCCTTTTTG TGGGGCACA CATGCTGCTG GTCAGTGAAG AGCCCAAGGT CAAGGAGATG	480
5	GTACGGATCT TAAGGACTGT GCCATTCTCT CGCTGCTAG GTGGCTGCAT TGATGACACC	540
	ATCCTCAGCA GGCAGGGCTT TATCAACTAC TCCAAGCTCC CCAGCCTGCC CCTGGTGCAG	600
10	GGGGAGCTTG TAGGAGGCCT CACCTGCCCT ACAGCCCAAG CCCACTCCCT GCTCCAGCAC	660
	CAGCCCTCC AGCTGACCAC CCTGTTGGAC CAGTACATCA GAGAGCAACG CGAGAAGGAT	720
	TCTGTCATGT CGGCCAATGG GAAGCCAGAT CCTGACACTG TTCGGACTC GTAGCCAGCC	780
15	TGTTTAGCCA GCCCTGCGCA TAAATACACT CTGCGTTATT GGCTGTGCTC TCCTCAATGG	840
	GACATGTGGA AGAACTTGGG GTCGGGGAGT GTGTTTGTC CTTGGTTTTT ACTAGTAATG	900
20	ATATTGTCTG GTATAGGGCC ACTTGAGAT GCAGAGGATT CCATTTTCTG TGTCTGCTAC	960
	CGGCTTGTCT CTTAGTTTTT CCAACTTGGG ACGTGATAGG AGCAAAGTCT CTCCATTCTC	1020
	CAGGTCCAAG GCAGAGATCC TGAAAAGATA GGGCTATTGT CCCCTGCCCT CTTGGTCACT	1080
25	GCCTCTTGCT GCACGGGCTC CTGAGCCACC CCCTTGGGGC ACAACCTGCC ACTGCCACAG	1140
	TAGCTCAACC AAGCAGTTGT GCTGAGAATG GCACCTGGTG AGAGCCTGCT GTGTGCCAGG	1200
30	CTTGTGCTG AGTGCTGTAC ATGTATTAGT TCCTTTACTG CTGACCACAT TGTACCCATT	1260
	TCACAGAGAA GGAGCAGAGA AATTAAAGTG CTGTCTCAAG GTCATGCAGT TAGTAAGTGG	1320
	CAGAACAGGG ACTTGAACCA AGCCCTCTGC TCTGAAGACC GCGTCTGAA TTTCTTCACT	1380
35	AGAGCTTCTT CATCAGGTTA CCCAGAAGTG GGTCCCATCC ACCATCCAGG TGTGCTTGGA	1440
	TGTTAGTTCT CCACCTCGA GGTGTACGCT GTGAAAAGTT TGGGAGCACT GCTTTATAAT	1500
40	AAAATGAAAT A	1511

45 (2) INFORMATION FOR SEQ ID NO: 217:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 642 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

55	AGGCCTTACT TTTCCTCCA CAAAGGAGTC GCAGCCACGC TAGCTCTGAC TTGCCACTGT	60
	GACAAAGTTC ACGTAGCAGG TCTAGGCAAA GACTGGGCAA TTGAGCAGAG GAGACGGACC	120
	TGTGACTCTG ACCRYGAGSC GGRCCCTTC ACCTTGGCTG GGCTGGTCCT GGTCCCTAGG	180
60	TTTTGTGAGG TTGTCCTTGT TTGGATCCCT CAACTAGGTG ATAAGCACTG GAGGGGGATG	240

5 ACCCGCCTTG GACGTGTTTC TTAACTCA TCCATATAAT AGGGCCGTGG GATGGTGTGA 300
 GAGGTAAAGC AGGATGATGG TGTTTTAAGA CCAGAGCTTG GGACCAGGGC TCCTACACCT 360
 AATTTTCTCT CTGCTAGCT GAACAAAGT CTAAATTAGC TTAACAAAAG AACAGGCTGC 420
 CGTCAGCCAG AGTTCGAAG GCCATGCTTT CAGTTTCCCT TGTGACAAT TGCTCTCCAG 480
 10 TTCTATGAA AGCACAGAGC CTTAGGGGGC CTGGCCACAG AACACAACCA TCTTAGGCCT 540
 GAGCTGTGAA CAGCAGGGG TTGTGTGTCT GTTCTGTTTC TCTGCTGCC GAACTTCTC 600
 AATAAACCTT ATTTCTTATT TTATATTAC GTNGGTGCTG GG 642
 15

(2) INFORMATION FOR SEQ ID NO: 218:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1241 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

25

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

30 GGTCCCACTG TTCCATTTTA TGCTAATAGA TTCCATTCTA GGGCCAGCC GTCTCTTGAC 60
 TGATGGTGT CCCTTTAACC CTTGGCATGT ATAATAGAAT TTTGGTGAAT GAAAGAACCC 120
 AAATAGGCCA GATAGTCCCC CCAGGCCCTG ATATCCATAA AAGGCTGGG AATGCATTAT 180
 35 GTAATTGTCC TTAGTCTTTT TGTGTTTTA GAAAAAAAAA ACAAGATGGG CTCAGATGGA 240
 TGCCTACGTA AAAATGGTTC CTAGCTGTGT ACTCATAACT TTTCTTTGAA TTGAGTAGTG 300
 AAAGGAAGGA GGAGGAAAG AAATTAAATG TCCTTCTAGT ATTCTCTGGA CTCAAGTCTG 360
 40 ACATATGRGA TAATAACCTA TATGAAATG CCAAGAATTG TATCTGAAAC AAGRGAACAG 420
 TTTGACACAT TTATCATGCC TTCATATTAC ATATTAACTG AAACCAATTA ATAAACATAT 480
 45 GAAATATCCA TGCACAAGG CAAAGGCACC TAAACCTTTT GTTCTTTTTT CTACATAGCA 540
 GAAATTGATT TTTTTTTTAT TTTTTTAGGG GAACCTATAT AATTATGACC CAGTGATGTC 600
 TTTTGGTGAC TTAAGCTTAT GAATTCAGGT TACAATTGAG TTGATTCTAG ATGGTTACTA 660
 50 CCTTGAAAG GATGTTGGTG CCTATGTGA CACGAGCCAG AGCCTGCTGG GAATAAACAA 720
 AGCAGATTCA TGCCAACACC AACTCGTAGC TTTAGTGGA GATGGGAGTG GTCACAGACT 780
 55 CCCAAATGT GGGGCTTGG ATTTCCACAC CATCCACGT GTGTGTCATC TTCTCTTTT 840
 ACACTCTTGA TGATAATTG AAAATGRTGA AATCACTCT GAATTTGCCT ATAGCATGAG 900
 CACATTCTTA TGACAACATA ACAAATAGTT CATAATGTGA ATATTAGAAA CTGTTACAGC 960
 60

CTGCAGTTAC CATAATTTTC CATGTTTGTC GAATTGATAT TGAAATAGCA GGGCTAAGGA 1020
ATTACTGGCA AGTTTTAGCC TGTGGGTAAT ACCTTAGGGT TATTTAAATA TTTGTAAATT 1080
5 TATTTAAATG TTCATGAATG TTTGAAAGGA ACAAATTAT CAGGGATGGC TCTTTGCCAT 1140
GGGTCTTATT TTCACCTCT TTTCTGTAAG AAAAAAGAAC AATGCTTAA TGTATTTTAA 1200
AAGTTTTTGG TATAGTTTCT AATCCAATT TTAATAAAG T 1241
10

(2) INFORMATION FOR SEQ ID NO: 219:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1080 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

20

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

TGTTTATGTG ACCTAAAACA TACACACATG CACACACACA TACATATCCA TTCATTCATT 60
25 CATTCAGTGT GTGTTTCCAG TGTCTGTGTG TCACTGTTTA TGCAGTTTCC ATTTCACAGT 120
GAATTATGAG TGGAGGGCAA CTTTCTAAC CAGATTGTCT TTTCAGAACA AAGACCKGGG 180
30 RAATTGAGGAA GAGTTTGGAA AGAGGGAGAG GCAAGGAAAG AGAGCTTTAA ATTGAAAGGT 240
TAATTTCTCA AGAGGAACCT GGGCTGAATG ACTACAGTGT TATACCTCC AATCTTTGCA 300
GGTGGGCATG GAACACTGCT TGTATCACTC TGTGCACGGT ATAAATCCAT ATATCCACAA 360
35 AAACACACAT CCATCCATCA ACATATACAT GGTTTGGGAT GAGCAGGTCA ATAGTTTGA 420
GAGGAGTTT GTTCTTTTCT TTTCTCATT ATACTCTTAA ATTGTGTGCA GTTATCAAAC 480
40 AAACAAACAG AAAAATTGTT TGGGAAAAAC CTGTCATACG CCTTTCTAT CMAGTGCTTT 540
AAAATATAGA CTAAATACAC ACATCCTGCC AGTTTTTCT TACAGTGACA GTATCCTTAC 600
CTGCCATTAA ATATTAGCCT CGTATTTTTC TCACGTATAT TTACCTGTGA CTTGTATTG 660
45 TTATTTAAAC AGGAAAAAAA ACATTCAAAA AAAGAAAAAT TAACTGTAGC GCTTCATTAT 720
ACTATTATAT TATTATTATT ATTGTGACAT TTTGGAATAC TGTGAAGTTT TATCTCTTGC 780
50 ATATACTTTA TACGGAAGTA TTACGCCTTA AAAATACGAA AATAAATTTT ACAAGGTTTC 840
TGTTTTGTGT GGAAGAGTAA TTGATGTTGC TAAGAATGAT GTTGTTTTTT TTGGGGTTTT 900
TGTGTTTTTT TTTTAAATG TTACCAGCAC TTTTTTTGTA AGTTTCACTT TCCGAGGTAT 960
55 TGTACAAGTT CACACTGTTT GTGAAGTTTG AATATGAAGG AATAATTAAA AAAAAAAAAA 1020
AAACCNCGGG GGGGGCCCGG TCCCATTTGN CCCAAGGGGG CGGTTACGGG GTCACGGCCG 1080
60

(2) INFORMATION FOR SEQ ID NO: 220:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1258 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

TGAATTGAGG GCTTAAAGAT AAACATATGG GRITGGAGTT GTGTGTCCAT AGGGTTTCAC	60
15 TGCCTATTTG ATTTGAGTTT ATCCCTATTA ATTTTTTACA GTGAAATTTT ATTAAAGTAT	120
AATGTACATA TATTTTCAGT GGATTTTGCT CTGAAGGTTT TCCAGTGGTC TGAACACGAG	180
20 ATAGTGGGGC TTCAGCTGTG GGATATTGCA GGGCAGGAGC GCTTCACCTC TATGACACGA	240
TGTATTATAT GGGATGCCTC TGCTGTGTTT ATTATGTTTG ACGTTACCAA TGCCACTACC	300
TTCAGCAACA GCCAGAGGTG GAAACAGGAC CTAGACAGCA AGCTCACACT ACCCAATGGA	360
25 GAGCCGGTGC CTGCGCTGCT CTGGCCCAAC AAGTGTGATC TGTCCCTTTG GGCAGTGAGC	420
CGGGASCAGA TTGACCGGTT CAGTAAAGAG AACGGTTTCA CAGGTTGGAC AGAAACATCA	480
30 GTCAAGGAGA AAAAAATAT TAATGAGGCT ATGAGAGTCC TCATTGAAAA GATGATGAGA	540
AATTCCACAG AAGATATCAT GTCTTTGTCC ACCCAAGGGG ACTACATCAA TCTACAAACC	600
AAGTCTCCCA GCTGGTCTCG CTGCTAGTAG TGTTTGGYTT ATTTTCCATC CCAGTTCTGG	660
35 GAGGTCTTTT AAGTCTCTTC CCTTTGGTTG CCCACCTGAC MATTTTATTA AGTACATTTG	720
AATTGTCTCC TGACTACTGT CCAGTAAGGA GGCCCATTTG CACTTAGAAA AGACACCTGG	780
40 AACCCAKGTG CATTTCTGCA TCTCTGGAT TAGCCTTTSA CATGTTGCTG RCTCACATTA	840
GTGCCAGTTA GTGCCTTCGG TGTAAGATCT TCTCATCAGC CCTCAATTTG TGATCCGGAA	900
TTTTGTGAGA AGGATKAGAA ATCAGCACCT GCGTTTTAGA GATCATAATT CTCACCTACT	960
45 TCTGAGCTTA TTTTTCATT TGATATTCAT TGATATCATG ACTTCCAATT GAGAGGAAAA	1020
TGAGATCAAA TGTCATTTC CAAATTTCTT GTAGGCGGTT GTTTCAGATT CTTTCTGTCT	1080
50 TGAATGTAA ACATCTGATT CTGGAATGCA GAAGGAGGGG TCTGGGCATC TGTGGATTTT	1140
TGGCTACTAG AAGTGTCCCA GAAGTCACTG TATTTTTGAA ACTTCTAACG TCATAATTAA	1200
GTTTCTCTTG TCTTGGGCAT CAAGANTAGT TCCAATTTTT TGGGCCGGGG CAGGGTGG	1258

55

(2) INFORMATION FOR SEQ ID NO: 221:

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1693 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

	CACAATATAT GAAATAGTAC CCTCTAAAAA AGAGAAAAAA AAAATCAGGC GGTCAAACCTT	60
10	AGAGCAACAT TGTCTTATTA AAGCATAGTT TATTTCACTA GAAAAAATTT AATATCAAGG	120
	ACTATTACAT ACTTCATTAC TAGGAAGTTC TTTTAAAT GACACTTAAA ACAATCACTG	180
15	AAAACCTGAT CCACATCACA CCTGTATTAT TTTCTTAAA CATCTTGGAA GCCTAAGCTT	240
	CTGAGAATCA TGTGGCAAGT GTGATGGGCA GTAAAATACC AGAGAAGATG TTTAGTAGCA	300
	ATTAAAGGCT GTTTGCACCT TTAAGGACCA GCTGGGCTGT AGTGATTCCT GGGGCCAGAG	360
20	TGGCATATATG TTTTACAAA ATAATGACAT ATGTCACATG TTTGCATGTT TGTITGCTTG	420
	TTGAATTTTT GAACAGCCAG TTGACCAATC ATAGAAAGTA TTAATTTCTT TCATATGGTT	480
25	TTTGGTTCAC TGGCTTAAGA GGTTCCTCAG AATATCTATG GCCACAGCAG CATAACAGTT	540
	TCCATCTAA TAGGAATGAA ATTAATTTTG TATCTACTGA TAACAGAATC TGGGTACAT	600
	GAAAAAAAT CATTTTATCC GTCTTTAAG TATATGTTA AAATAATAAT TTATGTGTCT	660
30	GCATATTGCA GAACAGCTCT GAGAGCAACA GTTCCCAT AACTCTTTCT GACCAATAGT	720
	GCTGGCACCG TTGCTTCTC TTTGGGAAGA GGAAGGCTG TGTGAACATG GCTAACAATC	780
35	TTCAAATACC CAAATTGTA TAGCATAAAT AAAGTATTTA TTTTATGCCT CAGTATATTA	840
	TTATTTAATT TTTTAGGTAA TGCTATCTC TTGGTCTATT AAGGAAAGAA GCAATCAGTA	900
	GAGAATTCAG GATAGTTTGT TTTAAATTCT TGCAGATTAC ATGTTTTTAC AGTGGCTGC	960
40	TATTGAGGAA AGGTATTCTT CYATACAACT TGTTTTAAACC TTTGAGAACA TTGACAGAAA	1020
	TTATGCAATG GTTGTGTGAG ATACGGACTT GATGGTGCTG TTTAATCAGT TTGCTTCCAA	1080
45	AGTGGCTTAC TCAAGAGGCC CTAAGACTGG TAGAAATTAA AAGGATTTCA AAAACTTTCT	1140
	ATTCTTTCT TAAACCTACC AGCAAACTAG GATGTGATA GCAATGAATG GTATGATGAA	1200
	GAAAGTTGA CCAATTTGT TTTTGTGTG TTGTGTGTG TTTGAATTG AAATCATTTCT	1260
50	TATTCCTTTT AAGAATGTTT ATGTATGAGT GTGAAGATGC TAGCGAACCT ATGCTCAGAT	1320
	ATTATCGTA AGTCTCCCTT CACCTGTTAC AGAGTTTCAG ATCGGTCCT GATAGTATGT	1380
55	ATTTCTTTAG TAAGAATGTG TTAAAATTAC AATGATCTTT TAAAAGATG ATGCAGTTCT	1440
	GTATTTATTG TGCTGTGTCT GGTCTAAGT GGACCAATT AAACAAGTT CATATGTATT	1500
	TTTCCAGTGT TGAATCTCAC AACTGTACT TTGAAAATTT CCTTCCATCC TGAATAACGA	1560
60	ATAGAAGAGG CCATATATAT TGCTCTCTTA TCCTTGAGAT TTCCTACCT TTATGTTAAA	1620

	AGTTGTGTAT AATGTGTTAA ATCTGTGAAA GAATAAAAAG TGGATTTAA TTAATAAAAA	1680
5	AAAAAAAA AAA	1693
10	(2) INFORMATION FOR SEQ ID NO: 222:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1196 base pairs	
	(B) TYPE: nucleic acid	
15	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:	
20	ACGCGTGGGT CGACCCACGC GTCCGCGACN TGGCGTGGTG GGGAAAGGGAG AAGGATTTGT	60
	AAACCCCGGA GCGAGGTTCT GCTTACCCGA GGCCGCTGCT GTGCGGAGAC CCCCAGGTGA	120
	AGCCACCGTC ATCATGTCTG ACCAGGAGGC AAAACCTTCA ACTGAGGACT TGGGGGATAA	180
25	GAAGGAAGGT GAATATATTA AACTCAAAGT CATTGGACAG GATAGCAGTG AGATTCACCT	240
	CAAAGTGAAA ATGACAACAC ATCTCAAGAA ACTCAAAGAA TCATACTGTC AAAGACAGGG	300
30	TGTTCCAATG AATTCACCTA GGTTCCTCTT TGAGGGTCAG AGAATTGCTG ATAATCATA	360
	TCCAAAAGAA CTGGGAATGG AGGAAGAAGA TGTGATTGAA GTTTATCAGG AACAAACGGG	420
	GGGTCACTCA ACAGTTTAGA TATTCTTTTT ATTTTTCCTT TTTTCCCTCA ATCTTTTTTT	480
35	ATTTTFAAAA ATAGTTCTTT TGTAATGTGG TGTCAAAC GGAATTGAAA ACTGGCACCC	540
	CATCTCTTTG AAACATCTGG TAATTGAAT TCTAGTGCTC ATTATTCATT ATTGTTTGT	600
40	TTCATGTGTC TGATTTTGG TGATCAAGCC TCAGTCCCTC TCATATTACC CTCTCTTTT	660
	TAAAAATTAC GTGTGCACAG AGAGGTCACC TTTTTCAGGA CATGCACTT TCAGGCTTGT	720
	GGTGATAAAT AAGATCGACC AATGCAAGTG TTCATAATGA CTTCCTCAAT GCCCTGATG	780
45	TTCTAGCATG TGATTACTTC ACTCCTGGAC TGTGACTTTC AGTGGGAGAT GGAAGTTTTT	840
	CAGAGAACTG AACTGTGGAA AAATGACCTT TCCTTAACTT GAAGCTACTT TTAATAATTG	900
50	AGGGTCTGGA CCAAAAGAAG AGGAATATCA GGTGAAGTC AAGATGACAG ATAAGGTGAG	960
	AGTAATGACT AACTCAAAG ATGGCTTCAC TGAAGAAAAG GCATTTTAAG ATTTTFAAAA	1020
	AATCTGTGCA GAAGATCCCA GAAAAGTTCT AATTTTCATT AGCAATTAAT AAAGCTATAC	1080
55	ATGCAGAAAT GAATACAACA GAACACTGCT CTTTTGATT TTATTTGTAC TTTTGGCCT	1140
	GGGATATGGG TTTTAAATGG ACATTGTCTG TACCAGCTTC ATTAAATAA ACAATA	1196
60		

(2) INFORMATION FOR SEQ ID NO: 223:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1791 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

10 TCAGGGAGGT GGCAGGAAAG GCTTGGAAACA GCTGCCGGAG TGACGGAGCG GCGGCCCCGC 60
CCGGTTGCGC TGGAGGTCGA AGCTTCCAGG TAGCGGCCCG CAGAGCCTGA CCCAGGCTCT 120
15 GGACATCCTG AGCCCAAGTC CCCACACTC AGTGCACTGA TGAGTGCGGA AGTGAAGGTG 180
ACAGGGCAGA ACCAGGAGCA ATTCTGTCTC CTAGCCAAGT CGGCCAAGGG GGCAGCGCTG 240
20 GCCCACTCA TCCATCAGGT GCTGGAGGCC CCTGGTGTCT ACGTGTITGG AGAACTGCTG 300
GACATGCCCA ATGTTAGAGA GCTGGCTGAG AGTGACTTTG CCTCTACCTT CCGGCTGCTC 360
ACAGTGTITG CTTATGGGAC ATACGCTGAC TACTTAGCTG AAGCCCGGAA TCTTCCTCCA 420
25 CTAACAGAGG CTCAGAAGAA TAAGCTTCGA CACCTCTCAG TTGTACCCCT GGCTGCTAAA 480
GTAAAGTGTA TCCCATATGC AGTGTGCTG GAGGTCTTGC CCTGCGTAAT GTGCGGCAGC 540
30 TGAAGACCT TGTGATTGAG GCTGTGTATG CTGACGTGCT TCGTGGCTCC CTGGACCAGC 600
GCAACCAGCG GCTCGAGGTT GACTACAGCA TCGGGCGGGA CATCCAGCGC CAGGACCTCA 660
GTGCCATGTC CCGAACCCTG CAGGAATGGT GTGTGGGCTG TRAGGTCTGT CTGTCAAGCA 720
35 TTGAGGAGCA GGTGAGCCGT GCCAACCAAC ACAAGGAGCA GCAGCTGGGC CTGAAGCAGC 780
AGATTGAGAG TGAGGTTGCC AACCTTAAAA AAACCATTAAG GTTACGACG GCAGCAGCAG 840
40 CCGCAGCCAC ATCTCAGGAC CCTGAGCAAC ACCTGACTGA GCTGAGGGAA CCAGCTCCTG 900
GCACCAACCA GCGCCASCCA GCAAGAAAGC CTCAAAGGGC AAGGGGCTCC GAGGGAGCGC 960
CAAGATTTGG TCCAAGTCGA ATTGAAAGRA CTGTGTTTTC CTCCCTGGGG ATGTGGGGTC 1020
45 CCAGCTGCCT GCTGCCTCT TAGGAGTCTT CAGAGAGCCT TCTGTGCCCC TGGCCAGCTG 1080
ATAATCCTAG GTTCATGACC CTTCACCTCC CCTAACCCCA AACATAGATC ACACCTTCTC 1140
50 TAGGGAGGAG KCAAATGTAG GTCATGTTTT TGTTGGTACT TTCTGTTTTT TGTGACTTCA 1200
TGTTGTCCAT TGCTCCCCGC TGCCATGCTC TCTCCCTTGT TTCTTAAGA GCTCAGCATC 1260
TGTCCTGTGTT CATTACATGT CATTGAGTAG GTGGGTAGCC CTGATGGGGG TCGCTCTGTC 1320
55 TGGAGCATAA CCCACAGGCG TTTTCTCTGC CACCCCATCC CTGCATGCCT GATCCCCAGT 1380
TCCTATACCC TACCCCTGAC CTATTGAGCA GCCTCTGAAG AGCCATAGGG CCCCCACCTT 1440
60 TACTCACACC CTGAGAATTC TGGAGCCAG TCTGCCATGC CAGGAGTCAC TGGACATGTT 1500

5 CATCCTAGAA TCCTGTCACA CTACAGTCAT TTCTTTTCCT CTCTCTGGCC CTGGGGTCCT 1560
GGGAATGCTG CTGCTTCAAC CCCAGAGCCT AAGAAATGGCA GCCGTTTCIT AACATGTTGA 1620
GAGATGATTC TTCTTGGCC CTGGCCATCT CGGGAAGCTT GATGGCAATC CTGGAAGGGT 1680
TTAATCTCCT TTGTGAGTT TGGTGGGAA GGAAGGGTA TATAGATTGT ATTAATAAAAA 1740
10 AAAAGGTATA TATGCATATA TCTATATATA ATATGACGCA GAAATAAATC T 1791

15 (2) INFORMATION FOR SEQ ID NO: 224:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 2517 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

25 ACACTAGTGG ATCCAAAGAA TTCGGCACAG CGGCACAGCA TTGTTGAGCT TTTCTGTGTG 60
TGTTGGGGCCC TCAAGCGAGC TCGACTGGTC CATCCTGGGG TAGCGASGTG GTGTTTGTGA 120
AAAAGGACGA TGCCATCACC GCATAYAAGA AGTACAACAA CCGGTGTCTG GACGGGCAGC 180
30 CGATGAAGTG CAACCTTCAC ATGAATGGGA ATGTTATCAC CTCAGACCAG CCCATCCTGC 240
TGCGGCTGAG TGACAGCCCA TCAATGAAAA AGGAGAGCGA GCTGCCTCGC AGGGTGAAC T 300
35 CTGCCTCCTC CTCCAACCCC CCTGCCGAAG TGGACCCTGA CACCATCCTG AAGGCACTCT 360
TCAAGTCCTC AGGGGCCTCT KTGACCACGC AGCCACAGA WTTCAAAATC AAGCTTTGAG 420
CAGGGGAGTR AGGCAGCCAG AAGTGGGGGC AGAGGAGGGT GGCTCTGTTT CCCCAAGGCA 480
40 AAGCTTATGA CCAATGGGCC ATCGACTGG AGACCCCTGA TTGTGGGAAG GGTGCCAGG 540
GATAAAGAGC TTCTCACTG GATGGGACCC GCCTTTCTGT GTGTGTCTCT GCCCTGTGCT 600
45 CTCTCTCTA CGTTAACGTT TCCTGTAGTA TGTTCCTTCA TCTCATCGCC AAGGTAGGCT 660
TGTTGTTTTM AGTGTGTGCC TCCCGAGCC TCAGCCCCAA GCTGATTCT TATCTGGA A 720
TGGTACACTG AATTCCTG GGTGGCTTCT TGTGGCCCCA TGGGATGCAG CGTGGGGGCT 780
50 GTCTGAAGGA CCTGCTTTT TCCAGGGGCC GAGGGGCTGC CTTTCCTTTG TGTGTATTAA 840
GCTTTTCAA CAATGGAGGG GATGGAGAGC CCTGGTGTCC TGACGGGAGC CAGGTCCGCC 900
55 TGAGAGCTGT GCGCTCCTC TGTCTGTCA GTGGAGGTGC CTGGGTGGGG AGCAGGTCTC 960
AGGCCTCTTG TCCTCTCCCC AGTGGCTCCA GGCCTCACTA GTGGCAAGGG CAGGATGAGG 1020
CTGCACCGCT GGAAGAGTC TATCTAAGCT CTGGCTTGG AGTCCCGTGT CGTCTCCRCC 1080
60

CAGAGGAAGT TCTCCAGAGT TCACCTTTCC CTTTTCCTTG AGTTGTGCTG AATGCCCCAC 1140
 CCCAGCTCTC TTTCCCTTCT GGGTGTCTTT GCTGGGAGGG GGCTGTGTG TGAGCCCTCC 1200
 5 CGGTTCTCAC CTCGCCTGGC ACTTAACCAC ACCCTGGTTT TGTGTAGCCG CCAGCTCTCT 1260
 TCTGGTTGGG CCTTTGAAAG GCTCAGCCTC CCATTGTGCA GTGCTTGGGT TTGGAGCTTA 1320
 10 TTTGAATGGA AGAGGTCAGT TTGTTCTCGG CTCTCCATTT CTGGCCTCAG TTGTCTACAG 1380
 GACAGTGGTC AGGGATGCCT GGAGGCATAT ATCCAGCTGC CACCAAGGGG CACTGTTTGT 1440
 TCCCCTTAT GTGAGTGACC CCATCCATCC ATGACCAGAG GATTATTTTC CTGCCTTGGC 1500
 15 AGAGGAGGAG GAGTCAAGGG AGCAGGGCAG CTCTACCAGG CAAGGTGTTT CCCCAGCATA 1560
 GGCGCAGACA GTTGGGACGA AACTTCAGAG CCCAGGCAGT CCCTGAATGA CCAGGCCAGT 1620
 GTTGTCACTG AGTGGTCCCC TGCTGGTTGG GAGTGAAGAG AATCCAGGCT GGCAGAGCTG 1680
 20 GAGCCAGTTG GGGAGCACGG TTCTGGGAGC TCTGCAAAAT CAGTAGCAAG TGCTGGAATA 1740
 GGCACATGCC GAAGATACTC AAGAGCTCCC AAGATTTGCT TGAGGCTAGC CCAGTGAAAA 1800
 25 AAACCAGAGA CTCATGTTTC CAGGGGTGAG TCTGTGAGG AGGAAGGACC CAGGATTTGA 1860
 ACCCAGCTTC AGTGTGCAGG CTCTGAGGCT GCCCAGGACG GGAAAGTCCA AGGAAGGGGC 1920
 CTGGTGGTGC TCCACTTGCA GTTCTTTAAA GAATGCTGCT TTTTATTCTC CTAACCCCTT 1980
 30 CAAGTGGGTG CAGACTTCTC GTTAGCAGCT GGAAGACATT CCTCCACAC TTTTCCCTTC 2040
 CTGGCCCAAG AGAGCATCCA GAAGGCAGTA GGACCTGGTT TTTCAGGTAC TGGGAGCCGG 2100
 35 GGGCTCACTG CTTGCACTGT GCTTAGGTA GGGATGGTAA ATATCCTCCC TGCATGGCTT 2160
 TATCCTCCCT CTCATCCAA AGCAGGTATC TTCTGGTTGT CACAGAGTTT CATGAGTCC 2220
 AGCTGCAGCC ACGTGGCCAT CTGGAGCTGG TGCTATAGGT GACCATCTGG TACATTGAGG 2280
 40 GGACCTGTTT GCCTCCTCCA CTCIATAAGC AGTCATCTTG GGAGACCGG AGGAGAAGGT 2340
 GGTGGGCTAG TCCTGTGTCC TCCTCCACTT CCCATGCCTC TATGTTACCC ATCTGTGTCT 2400
 45 CCTGTGCAGA AGGAGAGGAA GGGCATTAA GAGATGAAG GTGATTATGT ATTACTTATC 2460
 CATTTCTGAA TAAACATTTG TTATTCCTAA AAAAAAAAAA AAAAACTCG AGGGGGG 2517

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(2) INFORMATION FOR SEQ ID NO: 225:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2424 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

	TTGTANCTAA TCGAGGATTG ATTCTAATGA CAGAGTCTTT CAACACTTTG CACATGATGT	60
5	ATCACGAAGC TACAGCTTGC CATGTGACTG GAGATTAGT AGAACTTCTG TCAATATTTT	120
	TTTCGGTTTT GAAGTCTACA CGCCCTTATC TTCAGAGAAA AGATGTGAAA CAAGCATTAA	180
	TCCAGTGGCA GGAGCGAATT GAATTTGCC ATAACTGTT AACTCTTCTT AATTCTTATA	240
10	GTCTCCAGA ACTTAGAAAT GCCTGTATAG ATGTCTCAA GGAAGTTGTA CTTTGTAGTC	300
	CCCATGATTT TTTTCATACT CTGGTTCCCT TTCTACAACA CAACCATGT ACTTACCATC	360
15	ACAGTAATAT ACCAATGTCT CTTGGACCTT ATTTCCCTTG TCRAGAAAAT ATCAAGCTAA	420
	TAGGAGGGAA AAGCAATATT CGGCTCCGC GCCCTGAACT CAATATGTGC CTCTTGCCCA	480
	CAATGGTGGA AACCAGTAAG GGCAAAGATG ACGTTTATGA TCGTATGCTG CTAGACTACT	540
20	TCTTTTCTTA TCATCAGTTC ATCCATCTAT TATGCCGAGT TGCAATCAAC TGTGAAAAAT	600
	TTACTGAAAC ATTAGTTAAG CTGAGTGTC TAGTTGCCTA TGAAGGTTTG CCACATCATC	660
25	TTGCACTGTT CCCCAAACCT TGGACTGAGC TATGCCAGAC TCAGTCTGCT ATGTCAAAAA	720
	ACTGCATCAA GCTTTTGTGT GAAGATCCTG TTTTCGCAGA ATATATTAAA TGTATCCTAA	780
	TGGATGAAAG AACTTTTTTA AACAACAACA TTGTCTACAC GTTCATGACA CATTTCCTTC	840
30	TAAAGGTTCA AAGTCAAGTG TTTTCTGAAG CAAACTGTGC CAATTTGATC AGCACTCTTA	900
	TTACAAACTT GATAAGCCAG TATCAGAACC TACAGTCTGA TTTCTCCAAC CGAGTTGAAA	960
35	TTTCCAAAGC AAGTGCTTCT TTAATGGGG ACCTGAGGGC ACTCGCTTTG CTCCTGTCAG	1020
	TACACACTCC CAAACAGTTA AACCAGCTC TAATTCCAAC TCTGCAAGAG CTTTTAAGCA	1080
	AATGCAGGAC TTGTCTGCAA CAGAGAACT CACTCCAAGA GCAAGAAGCC AAAGAAAGAA	1140
40	AAACTAAAGA TGATGAAGGA GCAACTCCCA TTAAGAGGCG GCGTGTTAGC AGTGATGAGG	1200
	AGCACACTGT AGACAGCTGC ATCAGTGACA TGAAAACAGA AACCAGGAG GTCTGACCC	1260
45	CAACGAGCAC TTCTGACAAT GAGACCAGAG ACTCCTCAAT TATTGATCCA GGAAGTGAAC	1320
	AAGATCTTCC TTCCCCTGAA AATAGTTCTG TTAAGAATA CCGAATGGAA GTTCCATCTT	1380
	CGTTTTTCTG AGACATGTCA AATATCAGGT CACAGCATGC AGAAGAACAG TCCAACAATG	1440
50	GTAGATATGA CGATTGTAAA GAATTTAAAG ACCTCCACTG TTCCAAGGAT TCTACCCTAG	1500
	CCGAGGAAGA ATCTGAGTTC CCTTCTACTT CTATCTCTGC AGTTCTGTCT GACTTAGCTG	1560
55	ACTTGAGAAG CTGTGATGGC CAAGCTTTGC CCTCCAGGA CCTGAGGTT GCTTTATCTC	1620
	TCAGTGTGG CCATTCCAGA GGACTCTTTA GTCATATGCA GCAACATGAC ATTTTAGATA	1680
	CCCTGTGTAG GACCATTGAA TCTACAATCC ATGTCGTAC AAGGATATC TGGCAAAGGA	1740
60	AACCAAGCTG CTTCTTGACA TTAGGTGTAG CATGTCTACT TTTAAGTCCC TCACCCCAA	1800

	CCCCATGCT GTTGTATAA GTTTTGCTTA TTTGTTTTTG TGCTTCAGTT TGTCCAGTGC	1860
5	TCTCTGCTTG AATGGCAAGA TAGATTATA GGCTTAATTC TTGGTCAGGC AGAACTCCAG	1920
	ATGAAAAAAA CTGCACTCTT CAGTATACTT CCTAAAGGGC AATCAGATAA TGGATATGTT	1980
	TTATGTAATT AAGAGTTCAC TTTAGTGGCT TTCATTTAAT ATGGCTGTCT GGAAGAACA	2040
10	GGGTGCGCTA GCCCTGTACA ATGTAATTTA AACTTACAGC ATTTTACTG TGTATGATAT	2100
	GGTGTCTCT GTGCCAGTTT TGTACCTTAT AGAGGCAGAT TGCTCCGAT CGCTGTGGTT	2160
15	CTTATTATCA AAATTAAAGTT TACTTGATA CGGAACAACC ACAAGAAATT TGATTCTGTA	2220
	AAGAATCCTC TTTAGCTGTG GCCTGGCAGT ATATAAATGG TGCTTTATTT AACAGAATAC	2280
	CTGTGGAGGA AATAAAGCAC ACTTGATGTA AAAATAATTG TTTTATTTTT ATTGACATGA	2340
20	CTGATTGATT GCTATTCTGT GCACTNAATT AAACGTATTG TGATGACTTA AAAAAAAAAA	2400
	AAAAAAAAAA AAAAAAAAAA AAAA	2424

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(2) INFORMATION FOR SEQ ID NO: 226:

30	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 1080 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

	ATATAGGACG GATAATCTGT TTACATTCTG TTCTTCTCGA TGCACTCACA AGCGGGTAAC	60
40	TAGGTGACAA GAAAACAAAG ATCTTATTCA AAAGAGGTCT TACAGCAACC CAACGTCTCA	120
	TCTTCCATA GTAAAGATGA CGGCGCCTTG AGGTAAGCTA CAGGCAACAC CACTTCCGCG	180
	TTTCTCTTGC GCCCTGGTCC AAGATGGCGG ATGAAGCCAC GCGACGTGTT GTGTCTGAGA	240
45	TCCCGGTGCT GAAGACTAAC GCCCGACCCC GAGATCGTGA GTTGTGGGTG CAGCGACTGA	300
	AGGAGGAATA TCAGTCCCTT ATCCGGTATG TGGAGAACAA CAAGAATGCT GACAACGATT	360
50	GGTTCGACT GGAGTCCAAC AAGGAAGGAA CTCGGTGGTT TGGAAAATGC TGGTATATCC	420
	ATGACCTCCT GAAATATGAG TTTGACATCG AGTTTGACAT TCCTATCACA TATCCTACTA	480
	CTGCCCCAGA AATTGCAGTT CCTGAGCTGG ATGGAAAGAC AGCAAAGATG TACAGGGGTG	540
55	GCAAATATG CCTGACGGAT CATTTCAAAC CTTTGTGGGC CAGGAATGTG CCCAAATTTG	600
	GACTIONCTCA TCTCATGGCT CTGGGGCTGG GTCCATGGCT GGCAGTGGAA ATCCCTGATC	660
60	TGATTGAGAA GGGCGTCATC CAACACAAAG AGAAATGCAA CCAATGAAGA ATCAAGCCAC	720

TGAGGCAGGG CAGAGGGACC TTTGATAGGC TACGATACTA TTTTCCTGTG CATCACACTT 780
 AACTCATCTA ACTGCTTCCC CGGACACCCT CCACCTCTAG TTGTTACTAA GTAGCTGCAG 840
 5 TAGGCATTGC TGGGGAAGAA ACAAACACAC ACCAAACAGT ACTGCTACTT AGTTTCTAAG 900
 GCTGCACAGG GAAGGGAAG ACTGGGCTTT GGACAATCTA GAGGTAATTT ATATCCGCCC 960
 10 CCAGTGGAG CAACATGCCA TTCTGGAGGC ACGGGGGTAA CTGAAAGTGA GTACATATAG 1020
 TCTTCTGGT TTCTGGAGAT AACCCATCAA TAAAGCTGC TTCTCTGGG TAAAAAAAG 1080

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(2) INFORMATION FOR SEQ ID NO: 227:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 1336 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

TTGCATTAC AATTACTGGG AGGCAGGCAG GGCAGTTGC ATGCTGGGGG TGGCTGCATG 60
 GSGTCCASC TCTCTGGGT TTGAAGGATG CGGTACASCT GCTTCAGCTG AGCAACGATG 120
 30 TTATCCTTGA TGTCTGGGT TGAGATCTGC AGGCGGACAC TGCCACTATC AAAGGATCGT 180
 GTGAAATCAC CAGAAAACAT CTGCTAGATC ATCCGAGCCA CTACTGGAAT GACCTGAACC 240
 35 AAGATGAGTT TCCTTTCCAA TGGTTTCCCA TCTGGCCATT CTTCCCCAAA GCATAAGTAG 300
 ATCTCAAACG GTGGCTGCTT CTCTATCTGT CCTTTCTGGT GGGCAATGAG ATCGCTAAGG 360
 AATGTTTCCA GACAAAATAG CTTGACCTTC TTTTGTCTCT CAATCAGGTT GGGAGCAACA 420
 40 AGTGATGGGG CACATGGCCC AGACCAGTAC ACCTTGCACT GGCACAGYCT GATGGCATAA 480
 ATGGCATGAC CGCTGACCTC CAGGATCAGT CCTCTGTCCA TGACGTCCAG CAGCTTGCTA 540
 45 GTGAACAGCT TCTGCTTCTC ATTGTAATA TGCTCAGGAC CTGGGAATTT GACCTGCTCC 600
 AGNCTGACGG GACCAAAGAG CTCTCTCTGG TCAGGCATGG GACCCAGGTC CCCATAGAAG 660
 AGTCGGCAGC CCTGAGGGTT GCTCACGGTC ATGGTCCTGC CCGTACTCCT TCCCACGGTA 720
 50 CTGAAACTTG ATGTCCAGGT CAGTCATTGG GAGAGAGCTG ATCCACAGTT CTGGAGAGCT 780
 ATAGAAGGRC TGTATAGGTG CCTGGGGWAC TTCCATCTCC AGGGGTTTCTG TTTTGGGCCA 840
 CACTGCCTCC GGSCTGCAGT TGCCCACT GCAATTGCC ACCTGGCTG GCGCCATGG 900
 55 AGAACCATTG ATGTTAGGA AGGGGAAGGT GTCTGGATG GGAACATGGT GCTGCGACTG 960
 ATCCAGCTCA TCTTCTCAT CTCTTCATC CACATCATTA TCCTTCTCAT CCCAGGGAGC 1020
 60 AGACCCTGTG GATCTGGGT TAATGATCGA SCCCTGGGGC TGAGGGATGT CACACACTTG 1080

ATATATCTTC ACTGGGTTC TGGGCACCTC CCTTGGTGCC ATCCATACAT CCAGGTTGAA 1140
 TTCTCTGCTC TTATTGAGAG CACAGCGCAG CTGGGCCTTC CATTAGCTG GGTACGGGTC 1200
 5 ATCCACCCCT TCCTGGTACT TCCCTGTCTC TACAGCCAG GCCTTAAAAA TGGTATTTTC 1260
 CTCTTCTTGT TGAGGGCTAT GCCGGGTGGC ATGTTTCCAG GGAATCTGGA AGCGTTTAGA 1320
 10 GTCCCTGTGT AGCCAG 1336

15 (2) INFORMATION FOR SEQ ID NO: 228:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2043 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

25 TCAGCTGGTC CCTTCCTTGT GTCTGGGGG ACCTGCTGGC GGCTCTTCC TGGGAGCCAT 60
 GACCTCAGAC CCCACCCACA CTCCAGATCG AGACCCCTGC CTCCTCCCGG CAAATGTCCT 120
 CCCGCTGCCT TGACGCTGC ACTTGCACA TGCTACCCC CAGCACAGTC CCACTGGCCC 180
 30 CTCAMCTCCC CTTCCTGAG CTCCTTCCA AGGACTCTG GTCAGTGCCT GCTGTGCAKT 240
 CAGAGGCCCA GGTCCAGCA GCCCGSGGG AACGGGTGCT GCCTSTTCT CCAGTTAGCT 300
 35 CCAGYTCAGG TCTGAGACCC GTGTGAGTA AAGGTCTGAG CAMOGACCGT GCCCTCTGCC 360
 CAGGGCTGGG TCCTGAGCAG CTGGTTTTC TGCAGGAAGG TTGGAGCAAG CAAAGTCCTT 420
 CTCTGCCCTC AGGGTCAGCT GCCCAGACTG GGGCGGATGC AGAGAGGCAG GTGGGCTGTG 480
 40 GCTGGACTGG TCCGGAGCTG GCTTCCTTAC CAGAAAAGCC TCAGCCTTCC TCTGGAAGCA 540
 TCCCCGTTT TGGGCAAGGG GGAAGGGCTC CTTTAAGGGG TGTGCTTTC CAGTGGGGAG 600
 45 CAGTCTGGCC CTGCCCCCTA CTAAAGCCTC TGCTCTCAGC ACTTTCCTCC AAGTCTTGT 660
 AACTTGCTTG AAGGTGGGTT CTGGCTGCCA GCCAGTCCCT GGACAAACTC TCCTGCCCCCT 720
 TTTAAATTT ACTCATTTT TATAAACCCA GCAGGCTGGT GTTACTTAG CCCTGTAGCT 780
 50 TTTTTCATTT TTTCTTCCG TCTTCTTCT TGAGTTCACG GTTCAATATT GCCTCCTCGC 840
 CCTGGTGAGG GGAGGTGCTG CTTTCTGCC CCACCTGCCG GCTGGTTCCA GCAGCGCTGG 900
 55 NGCCACGCTG GGGGGCCGG ATGGGGCTT CTCTCTCTGG GAGGGGTGCA GGTGCCCTCC 960
 CCAGGCTGGG AGGGTTCCTT CCTAGCTCC CCATCTGCC CCGCTGGTGA GAGTTGGGCT 1020
 60 TCTTGGTCTT GGAAGTCCCT GGCATTGGGA ACAGAGCATT TCCAGCATTT GTTGTGTGTG 1080

	TTTACTCAC CTAACCTTA GAAAATGAAT GTTAGAAGGT GCCTGCCGAG GCGGGACAGA	1140
	GTGTTTGCTC GCGCTGGAGA AGGCTCTGCT CAGCCCTGAG AGTCCCTTCC TGCCCCACCG	1200
5	ATACTGGCAC TTAAAAAGG AAGCTGACCG CACAGTGTCC AGAOGAATTG GCGCCAGAA	1260
	GATGGGGAGT TCTGTCTGC CCTTCTGTGT CTGCGTGACC TCACCCAGCC TAGGAGGGAG	1320
10	GTGCATTGAG GGTAGATTG CCTCTATTG AAAGTTCTGG GCCTTTGGGY GGAAAACAGC	1380
	CAGCTTTGGC GCTGTTGGG AGACTCCTCC AGACCAGGAA CCCCAGAAGG AGACAGAGCC	1440
	TGCCACATCC TCCCACGCC GCGCTGGGC CAGGGTGATT GGAAGTGAAG TTTGGCCACA	1500
15	ACCAAATTGA TGCTGGCTGG AACCAGAGGC CAGAAAGCCT GGCCTTGTCC CCATGTGGGA	1560
	GCCCTGTCTT CAGCCCTCTT GTCCCTTGA GCTCAGTGAA TCCCCACCAG GTGCCCACAG	1620
20	CTCCTGGACT TCAAATTCTA TATATTGAGA GAGTTGGAGA GTATATCAGA GATATTTTGT	1680
	GAAAGGAGTT GGTCTATGCA ATGTCAGTTT GGAATCTTCT TGAAAGTTTA ATGTTTTTAT	1740
	TAGGAGATTT AAAGAAAATA AAGGTCTACA ATATCTTTAG GTTTTTTTTT TTCTCTGTTT	1800
25	ACCGCACAAA CTGACCACAT GGCATGTCTA TCAGGATGGA GGGTGTCCAT GTTCTCCTCT	1860
	GTCTTTAGGG AGGTGATAAG GAGATGGSCG RAGGGGTGTT TTTTCTTTG ACTCCCTCC	1920
30	TTTCTAACAG AATGTTGCCA CCACTGCTTG AGTGGGCTGT GTTTGTTTCT CTGTCCACGC	1980
	TCTGTGTGTA GAAAATAACA TTGTTAGGGG AACTCAGGCT AGTGTACGCG TCTTGGTTTG	2040
	GGG	2043

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(2) INFORMATION FOR SEQ ID NO: 229:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

	TAAAAAGAAG CGGAGAATC TGGGCGTCGC TCTAGAGATC GATGGGCTAG AGGAGAAGCT	60
50	GTCCCACTGT CGGAGAGACC TGGAGGCCGT GAACTCCAGA CTCCACAGCC GGGAGCTGAG	120
	CCCAGAGGCC AGGAGGTCCC TGGAGAAGGA GAAAACAGC CTAATGAACA AAGCCTCCAA	180
55	CTACGAGAAG GAACTGAAGT TTCTTCGGCA AGAGAACCGG AAGAACATGC TGCTCTCTGT	240
	GGCCATCTTT ATCCTCCTGA CGCTCGTCTA TGCCCTACTGG ACCATGTGAG CCTGGCACTT	300
	CCCCACAACC AGCACAGGCT TCCACTTGGC CCCTTGGTCA GGATCAAGCA GGCACCTCAA	360
60	GCCTCAATAG GACCAAGGTG CTGGGGTGTT CCCCTCCCAA CCTAGTGTTT AAGCATGGCT	420

TCCTGGCGGC CCAGGCTTG CCTCCCTGGC CTGCTGGGG GTTCCGGGTC TCCAGAAGGA 480
CATGGTGCTG GTCCCTCCCT TAGCCCAAGG GAGAGGCAWT AAAGACACAA AGCTGGAAAT 540

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(2) INFORMATION FOR SEQ ID NO: 230:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 448 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

AATGTGAAA TATTAGAATA TTGTTACTAT TTGACCCAAC TCAAAATCTC CATGGGAAAA 60
TACCTGTGCA TACCCACAGT ATTGTTGAAA ATAATCAGAT GCAGTATCAC AGCTGTGTCA 120
GACTCTAGTA CCAGTTGGGC AATCAAGGCA CAGCTAAAAA TTGAAAACAA AGATCTGGAC 180
AACAACACAG CCAAGGTGG GGGTCAAGAA GCTCTGACGT GTACCTAGCT GTAGAATGCT 240
ATGCACACGT GCCAGGTGTA GTGTGCATAT CCAGGAAAAA CTGCAGAGAG CCCAGTCTT 300
CAMCTCTGGT TGACCATGAG CTCTGTGTAA GCAGGAAGTG AAGGCTAAGG CAGATTTAAG 360
CTCTGAAAGC ATTCCACAAC ATACACACAA ATCGTGCAA GCATTAAGGA AATCTTGTTA 420
CTGCTAAGTG TTGCTGACCC AGGAACAA 448

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(2) INFORMATION FOR SEQ ID NO: 231:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 407 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

GTATGCTGCC CCAAACCAAT ATGTGTGGCT GCCTTTWACC TGACTTCTCC AACATGTAGC 60
CCCAAGAGGA GGCCTCTAGA CTRAGGGAGG GGCTGGTGAC CCAGGTGTGG TGGGGCTGCA 120
TGARACTACC AGAGAGACAG ACATTCTGGA ACTCACCTG GGGATCCAG TGGATCTGCC 180
TATGGTCTGG TCCACCCAG ACCTGTGAGA TGTTCCTCAT GAGGATGCAC TTGTGCTTCT 240
GCAAGTATTG CTGCAGCTTC ATAGTGACTC CCACCAGCAC CAGCAATACA GYTAGCTACC 300
TGTGGCCTTG GATCTCAGCC AGCATGGCTG GGAGAGGGAG CARCTGGGCA TGTACCCTAA 360
ATGCTGTTAC CAGGAAGGA CTCCAGAGT GAAGACAAGT AGGGACT 407

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5 (2) INFORMATION FOR SEQ ID NO: 232:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 830 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

15 GTATTGATT TCAGGCTGCT AAATGGGCTC ATTTAGCATT CATTCCTTGA TG TAGACATT 60
AAAAAAAAA CTGAATAGCA TTCTTTCCAG GNTAACTAAT AAAGCAGACA TGCTAAGCCT 120
ATAAATACAT CAGCACTGCA GCACACGTTT AAGGTTGCCA CGGACAAGGA TCACACAATA 180
20 GAGAACACTG TAGTTCGGTC TGCTCACAAG ACCCAGAACA TTGATCAGTT TTTGTGTGTG 240
GTTTATTATT TTTCTGTAA AAAATTGTGA AAAGTTTGT TTAGCTAGAT GATATTTTAA 300
25 TAGCTGCGAG TGCTTTGGAA CTATAAAGAT GTCACTACTT AACACACATA CCTTATGTTT 360
TGTTTGTGTT TGTTTTACAC TCAGTATAAA TCAGGAGAAG TTAGCCAACC ATCTAGCATT 420
TAGAATCCTC TTTTATTATG TCTTCTAAGG ATATGGATGT TCCATAACA GCAACAAAAC 480
30 AGCAACAAA ACATTTTATA AATATCACTT GATAGACTGT AAGCACCTGC TTAACCTTGT 540
GTNCCAAATA TTTAGTGTGT ATATATATAT ATATATACAC ACACACACAC ATATATATTC 600
35 AACAAATAAA GCAAAATATA ACATGCATTT CACATTTTGT CTTTCCCTGT TACGATTTTA 660
ATAGCAGAAC TGTATGACAA GTTTAGGTGA TCCTAGCATA TGTTAAATTC AAATTAATGT 720
AAAACAGATT AACACAACA AAGAACTGT CTATTGAGT GAAGTCATGC TTTCTATTAT 780
40 AATAACTTGG CTTGGTATAT CCATCAAATG CACACTTATA CTGTTATCTG 830

45

(2) INFORMATION FOR SEQ ID NO: 233:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 932 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

55 CCAGAAGAAA GACCAATCTA GAATATGGAA CTCTAATCAC TTCTAGTATT TCAACTTCCT 60
AGCAGAAATG AACTTGGCCC TAGACCTAGG GGATAAGCAA TGTTCTTTAT GTAGCCAATG 120
60 CTACGGAAC AAAAGAGGTG AAAGAGACCC TTTTITTATA CTTAATGTAC ATATATTGAC 180

	TTTTTGAGCA AGAATGCCAG AAATAGCCCT CATTTCTACC CTGCAAAATA ATCCAGATCT	240
5	GCTTTCTAAA ATGRANICAG TTTCTAAAGT GAAACATGCA ATATTTATGC TCTGACTGAC	300
	TCCTGAATTG GARGAGGAAG RACTTCTGTT TACAGAAAAC YGTATTGTTA TATATGTCAG	360
	GCTGTGTATT GTGACTATCA GCATTCTGGT GCAAATGAAC TTTTCTCCAT CATGACTGT	420
10	GGAAAATTGA TACTTTTAAA GCATATTCTT CTATGAGCAC AGGTCCTCCT AGTGAAACTT	480
	AATTGACAA AGGGTGTCT ATGCTTTTCT AACCTGAWT GTATTAACAT TCACAGAGCC	540
15	TACATTTTCT CATTAGGGTT RTGATGCTCA GTATCTTTCC AAGTGCCAGG CAGRGTTC	600
	CTTTTCTGAT CAAACATACC ATTTTTTGTA TTTCACAACT ATAGACAGTC ACTTCTGCAG	660
	TCCAATTTA AAAATGCAGA ACTGCTTTAT CCAAGAATGC TGAAAAATAC TGTCTATCC	720
20	AGGTTTCCTA AACTATAAAA GCAGATTTTG CTTTGTGTTG TTAATCATAG GCATGGCCGA	780
	GCATGTGGA TTAGCCTGAG GCTTAAATC AGATGCATGT CTGGTAAGAT GACCACTGTC	840
25	TCATATCAA GAGCCTGCAG AGCCATTTC CAGACCTGTG ATTGCCAGA ACACATAGTC	900
	CCCACGTTTC TAATTGGAG CAAATCTAAA AG	932

30

(2) INFORMATION FOR SEQ ID NO: 234:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 2786 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

	TTAGCAGGT GAGCTGTAA AACAGCACAC ATCTCTCATC CCTCTTCCT TTATCCCCC	60
	CTGGGTTTCA GAAAGGAAG ATATATGGG ACCACCTCC CCTTCTTTGA TCCAGCATC	120
45	TCAGTCCCC TCCCAACCT CCATATGGCT CTCAATGGTG CTCACTTGCT TGAAGCAGG	180
	CTCCCAATAG GGAGGGGCT GCGCTCTACA GTCTCTTTGA CTGTAAGACA GGGCTCTGTA	240
50	TCAGTGAGAC GATGAGAAA GTCCAGGCT AATGGCAGAA ATTTGCACTT TGAACATGTG	300
	TGTTTTGTG TTGTGGAACC TGAGATTCCT TATTTATTAA CAGGAAGTCT GATTTTTTTT	360
	TTTTGGAGTC TTTGTGCTA TATTTGTGG GGCTGGGAGA GAGAGATTAG ATTATTTTGA	420
55	CATGGGATCC CTTCCATAAC AGGTACTTTG AAGCAAGAC ATAGGGTTGA AGAAGCACAA	480
	CCAGCCTCTG AAATCATAGC TCTCCAGTGG CTTTTAAAGA AAGCTGGTCC TCAGCACTAA	540
60	CAAAATCACT ACAATAGCCT AGTGCTTTTT TGGAAGCCTT TTAGGGAAG AATGTTAGGT	600

	TCATGGTAAC TAGTATGCTC TTTGAGATTT TTACAGTGTT GAAACTTAAG AATTTTGAGA	660
	GGGTGAGGAG GGTGTTCAG AATCTAAATT ACAGATAGAT GATTGTTTCT TGTGAATTTG	720
5	TTTCTTTTCC TTTTTTTTTG TCCCTACCAT TTCTTACAT TTCCCTTGGG GCCCATCTCT	780
	GGCTCCTTGC TTTTGTTC TTGCTTTGCT TTATCAGTTC ATTCCAGCTC CCTGTTAGTG	840
10	AAGGACACTG CTGTTAGTGA AGGAACAAAG TCTATGAGTC CTAAAATTTT AAGTCAAAGA	900
	AAACTGCTCT GTTCCCTT TAGTAACACT TCTGAAGAGG AAAAATTCA ATAGCCAAAG	960
	TTAATAATCC TATATAATAA TTGCTTTGGC TTTCACCTAA AATTCCTGGC ATCACAATTT	1020
15	CCTTGGGATA GAGGTTGTGT TGGGAATAG ATTGCTTATT GCTGTTCACT GGAGAGAAAA	1080
	GGTAGTGT TTGTACAAGG TCATACCGCC AGAAGCCCCA AATCCTATTT TGGCTCATCT	1140
20	TCAGGTAAAG AGTAATTCCT ATCCTGTGTG CTCAGAAGC TAGAATCGAA GGCTTACCCT	1200
	ATTCAATTGT TATTGTGAGA AATGCATGAT GGCTCTTGA AAGAATGACG TTTTGCTGGA	1260
	AAAAAAAAA AGAACAGTT GTGTTTACA AACATGGCTT ATCAATTTT TCAAAGAATT	1320
25	CTTTTTCCT AAAAAGAGGA GTAACAAAT GTCATTTCTG AAAGAGGCTT ACTTTATACC	1380
	AACTAGTGT AGCATTGGG ATGCCAGGA ACAGAGAGTG AGACACCTAC AATCACCAGT	1440
30	CTCAAATGCG CTATTGTTT TTTTCAGAGT GTTGCAGATT TGCCATTTCT CCATAATATG	1500
	GGGATAGAAA ATGGAATAA GATAGAAGG ATGTAGAATA TGCTTTCTG CCAACATGGT	1560
	TTGGAGTCGA CTTTGGTATA TTGACTAGAT TTGAAAATAC AAGATTGATT AGATGAATCT	1620
35	ACAAAAAGT TGCTCTCTC TCAGTCCCT TTTACACTTT TTGACTAACT AGCATCTATA	1680
	TTCCACACTT AGCTTTTTTG TCACACTTAT CCTTTGCTC CGTAAATTTC ATTTGCAGTG	1740
40	GTTAGTCATC AGATATTTTA GCCACCTACA CAAAAGCAA CTGCATTTT AAAAATCTTT	1800
	CTGAGATGGG AGAAAATGTA TTCTCCTTTC CTATACCGCT CTCCAACAA AAAACAAC	1860
	AGTTAGTTCT ACTAATTAGA AACTTGCTGT ACTTTTCTT TTCTTTTAGG GGTCAAGGAC	1920
45	CCTCTTTATA GCTACCAITT GCCTACAATA AATTATTGCA GCAGTTTGCA ATACTAAAAT	1980
	ATTTTITATA GACTTTATAT TTTTCCTTTT GATAAAGGA TGCTGCATAG TAGAGTTGGT	2040
50	GTAATTAAAC TATCTCAGCC GTTCCCTGC TTCCCTTCT GCTCCATATG CCTCATGTG	2100
	CTTCCAGGA GCTCTTTTAA TCTTAAAGTT CTACATTTCA TGCTCTTAGT CAAATTCGT	2160
	TACCTTTTTA ATAACCTTC CCACTGCATA TTCCATCTT GAATGGTGG TTCTAAATTC	2220
55	TGAAACTGTA GTTGAGATAC AGCTATTTAA TATTTCTGGG AGATGTGCAT CCTCTTCTT	2280
	KGTGGTTGCC CAAGGTGT TTGCGTAACT GAGACTCCTT GATATGCTTC AGAGAATTTA	2340
60	GGCAAACT GGCCATGGCC GTGGAGTAC TGGAGTAAA ATAAAAATAT CGAGGTATAG	2400

ACTAGCATCC ACATAGAGCA CTTGAACCTC CTTTGTACCT GTTTGGGGAA AAAGTATAAT 2460
 GAGTGTACTA CCAATCTAAC TAAGATTATT ATAGTCTGGT TGTTTGAAAT ACCATTMTTT 2520
 5 TCTCCTTTTG TGTTTTTCCC ACTTTCCAAT GTACTCAAGA AAATGAACA AATGTAATGG 2580
 ATCAATTTAA AATATTTTAT TTCTTAAAAG CCTTTTTTGC CTGTGTGAAT GTGCAGGACC 2640
 CTTCTCCTTT CATGGGAGAG ACAGGTAGTT ACCTGAATAT AGGTTGAAAA GGTATGTAA 2700
 10 AAAGAAATTA TAATAAAGG GATACTTTGC TTTTCAAATC TTTGTTTTCT CTTATCTAG 2760
 GTAAGGCATA TTAAAAATAA ATATGT 2786

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(2) INFORMATION FOR SEQ ID NO: 235:

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- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 458 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

GGGTGCAGGA ATTCGGCACG AGAGAATGTT TGATTTTCTT TCCTATTTTA AGGATCTTCT 60
 30 CTCTGTGTA TGTTGAAAAC TTACCTTAGT GAAGATGTGT TTCAACATGC TGTGTCCCTT 120
 TACCTGCATA ATCAGAGCTA TGCATCTATT CAAAGTGATG ATCTGTGGGA TAGTTTTAAT 180
 GAGGTCAAA ACCAAACACT AGATGTAAAG AGAATGATGA AAACCTGGAC CCTGCAGAAA 240
 35 GGATTTCTTT TAGTGACTGT TCAAAGAAA GGAAAGGAAC TTTTATACA ACAAGAGAGA 300
 TTCTTTTAA ATATGAAGCC TGAAATTCAG CCTTCAGATA CAAGGTACAT GCCCTCTTTC 360
 40 TTTTCATGCC ATCTCTTTTG CACTCTCAGG TGGAAATATT TTAAAGTGT TTATAATCAT 420
 AAGTCTTGT GAAACCTAAC AAGATTATCC CTTCTTAA 458

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(2) INFORMATION FOR SEQ ID NO: 236:

50

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 591 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

AGGATGAAGA GGAAATTATC TCTTGATTG CTCTCCAGGA AATCCTTCTC TATACTTTAA 60
 60 AAGCTCTGT TCTTTCTAG GATCCAAATG TGCTGATTGC TGCTAACAGT CAGGSTACAA 120

TTAAGGTGCT AGAATTGGTA TGAAGGGTTA ACTCAAGTCA AATTGTACTT GATCCTGCTG 180
 AAATACATCT GCAGCTGACA ATGAGAGARG AACAGAAAA TGTCATGTGA TGTCCTCCCC 240
 5 CAAAGTCATC ATGGGTTTIG GATTGTGTTT GAATATTTTT TCTTTTTTTC TTKTCCCTCC 300
 TTTATGAGCC TTTGGGACAT TGGGAATACC CAGCCAACCT TCCACCATCA ATGTAACCTC 360
 10 ATGGACATTG CTGCTCTTGG TGGTGTATC TAATTTTGTG GATAGGGAAA CAAATTCCTT 420
 TGAATAAAAA TAAATAACWA AACATAAAAA GTTATTTGAG CCACAGTTGA GCTTGGAAAG 480
 TTTTGTCAA ATGCNGCAAG AGATAACTCT TTTTANGAAG TAGCATATGT GAACTATAAT 540
 15 GTAACAGTGA ATAATTTGTA AAGTTCGTAT TTCCCAACCT CTTTGGGAAT T 591

20 (2) INFORMATION FOR SEQ ID NO: 237:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1286 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

30 TCTTTTAAAG GTACAGCAGG GAAGAACTGG AAATCAGAG AAAGAACTG CCCTTCCATC 60
 TACAAAAGCT GAGTTTACTT CTCCTCCTTC TTTGTTCAAG ACTGGGCTTC CACCGAGCAG 120
 35 GAGATTACCT GGGGCAATTG ATGTTATCGG TCAGACTATA ACTATCAGCC GAGTAGAAGG 180
 CAGGCGACGG GCAAATGAGA ACAGCAACAT ACAGGTCCTT TCTGAAAGAT CTGCTACTGA 240
 AGTAGACAAC AATTTTAGCA AACCACCTCC GTTTTCCCT CCAGGAGCTC CTCCCACTCA 300
 40 CCTTCCACCT CCTCCATTTC TTCCACCTCC TCCGACTGTC AGCACTGCTC CACCTCTGAT 360
 TCCACCACCG GGTTTTCTC CTCCACCAGG CGCTCCACCT CCATCTCTTA TACCAACAAT 420
 45 AGAAAGTGGA CATTCCTCTG GTTATGATAG TSGTTCTGCA CGTGCAATTC CATATGGCAA 480
 TCGGATGAAG AACGATACAG ATACAGGGAA TATGCAGAAA GAGGTTATGA GCGTCACAGA 540
 GCAAGTCGAG AAAANGAAGA ACGACATAGA GAAAGACGAC ACAGGGAGAA AGAGGAAACC 600
 50 AGACATAAGT CTTCTCGAAG TAATAGTAGA CGTCGCCATG AAAGTGAAGA AGGAGATAGT 660
 CACAGGAGAC ACAAACACAA AAAATCTAAA AGAAGCAAAG AAGGAAAAGA AGCGGGCAGT 720
 55 GAGCCTGCCC CTGAACAGGA GAGCACCAGG GCTACACCTG CAGAATAGGC ATGGTTTGTG 780
 CCTTTGTGT ATATTAGTAC CAGAAGTAGA TACTATAAAT CTTGTTATTT TTCTGGATAA 840
 TGTTTAAGAA ATTTACCTTA AATCTGTTC TGTGTGTAG TATGAAAAGT TAACTTTTTT 900
 60 TCCAAAATAA AAGAGTGAAT TTTTCATGTT AAGTTAAAA TCTTTGTCTT GTACTATTTT 960

AAAAATAAAA AGACAGCAAT GACTTTATAT CCAAGAAAGG AATGTGAATG AGTCACTTAA 1020
5 CAGGGAATCT AAAGAGCTGT GTTAGCTGTG TACATACACA GATTATCTGA GAAAAGGTCA 1080
AGGGTTCCAC TTGGGCCACA GTTTTTTGT TAATCAAACA CCACTCTCTT AAGRGGCTGC 1140
ATCACAAARG GCAACCAARG GGGCCCTCTT ARGGCTTTGA GGATTAAAC TAGTCTTTAT 1200
10 CCATTACTGC TGTGGACACT CTGGGCTTRG TATWTTTAGG GGGGNTCCTT ACCTTTTTTTT 1260
GGTTTTCNC ACCTTTTTGG TTGGGC 1286

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(2) INFORMATION FOR SEQ ID NO: 238:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 734 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

ATGGCAGCGC AGAAGGACCA GCAGAAAGAT GCCGAGGCGG AAGGGCTGAG CGGCACGACC 60
30 CTGCTGCCGA AGCTGATTCC CTCCGGTGCA GGCCGGGAGT GGCTGGAGCG GCGCCGCGCG 120
ACCATCCGGC CCTGGAGCAC CTTCGTGGAC CAGCAGCGCT TCTCACGGCC CCGCAACCTG 180
GGAGAGCTGT GCCAGCGCCT CGTACGCAAC GTGGAGTACT ACCAGAGCAA CTATGTGTTT 240
35 GTGTTCCTGG GCCTCATCCT GTACTGTGTG GTGACGTCCC CTATGTTGCT GGTGGCTCTG 300
GCTGTCTTTT TCGGCGCCTG TTAACATTCT CTATCTGCGC ACCTTGAGT CCAAGCTTGT 360
40 CCTCTTTGGC CGAAAGGTGA GCCCAGCGCA TCATATGCTC TGGCTGGAGG CATCTCCTTC 420
CCCTTCTTCT GGCTGGCTGG TCGGGGCTCG GCCGTCTTCT GGGTGCTGGG AGCCACCTG 480
GTGGTCATCG GCTCCACGC TGCCTCCAC CAGATTGAGG CTGTGGACGG GGAGGAGCTG 540
45 CAGATGGAAC CCGTGTGAGG TGTCTTCTGG GACCTGCCGG CCTCCCGGGC CAGCTGCCCC 600
ACCCCTGCCC ATGCTGTGCC TGCACGGTCT GCTGCTCGGG CCCACAGCGC CGTCCCATCA 660
50 CAAGCCCGGG GAGGGATCCC GCCTTTGAAA ATAAAGCTGT TATGGGTGTC ATTCAAAAAA 720
AAAAAAAAAA AAAA 734

55

(2) INFORMATION FOR SEQ ID NO: 239:

60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 809 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

5
CGGGGTCTTC AGGGTACCGG GCTGGTTACA GCAGTCTTAC CCCTCACGAC GCARACATGG 60
CAGCGCAGAA GGACCAGCAG AAAGATGCCG AGGCGGAAGG GCTGAGCGGC ACGACCCTGC 120
10 TGCCGAAGCT GATTCCCTCC GGTGCAGGCC GGGAGTGGCT GGAGCGGCGC CGCGCGACCA 180
TCCGGCCCTG GAGCACCTTC GTGGACCAGC AGCGCTTCTC ACGGCCCCGC AACCTGGGAG 240
AGCTGTGCCA GCGCCTCGTA CGCAACGTGG AGTACTACCA GAGCAACTAT GTGTTCGTGT 300
15 TCCTGGGCCT CATCCTGTAC TGTGTGGTGA CGTCCCTAT GTTGTGGTG GCTCTGGCTG 360
TCTTTTTCGG CGCCTGTAC ATTCTCTATC TCGGCACCTT GGAGTCCAAG CTTGTGCTCT 420
20 TTGGCCGAGA GGTGAGCCCA GCGCATCAGT ATGCTCTGGC TGGAGGCATC TCCTTCCCTT 480
TCTTCTGGCT GGCTGGTGCG GGCTCGGCCG TCTTCTGGGT GCTGGGAGCC ACCCTGGTGG 540
TCATCGGCTC CCACGCTGCC TTCCACCAGA TTGAGGCTGT GGACGGGGAG GAGCTGCAGA 600
25 TGGAAACCGT GTGAGGTGTC TTCTGGGACC TGCCGGCCTC CCGGGCCAGC TGCCCCACCC 660
CTGCCCATGC CTGTCTGCA CGGCTCTGCT GCTCGGGCCC ACAGCGCCGT CCCATCACAA 720
30 GCCCGGGGAG GGATCCCGCC TTGAAAATA AAGCTGTTAT GGGTGTCAAT CAGGAAAAAA 780
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA 809

35

(2) INFORMATION FOR SEQ ID NO: 240:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 2201 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

TCGACCCACG CGTCCGGCAA CATGGCGGCT GCCGTGGTGC AGCGCCCGGG CTGAGCGACA 60
GCAAGTGCAG CGGGCTCCTA CCCGGGTGA GGGGTGGCCT CCGCGTGGGA TCGTGCCCTC 120
50 TTCAGCCCGC TCCTGTCCCC GACATCAGT GTATTCCGCA CGTCCCCTCC GCGCTGTGTG 180
TCTACTGAGA CGGGGAGGCG TGACAGGGCC CGGGTCCCTT CTCAGTGGTG CTCTGTGCTT 240
55 CAGGGCAAGC TCCCGTCTC CGGGCGCACT TCCCTCGCCT GTGTTCGGTC CATCCTCCTT 300
TCTCCAGCCT CCTCCCTCG CAGGCGGATG AMCCGGACGA CGGCCCAGTG CCTGGCACCC 360
CGGGGTTGCC ARGGTCCAMG GGAACCCGA AGTCCGAGGA GCCCGARGTC CCGAACCCAG 420
60

	ARGGGCTGCA GGCATCAMC GGCTGTCTC CCGGCCGTC GGCTCTCATA GTGGCGGTGC	480
	TGTGCTACAT CAATCTCCTG AACTACATGG ACCGCTTCAC CGTGGCTGGC GTCCTTCCCG	540
5	ACATCGAGCA GTTCTTCAAC ATCGGGGACA GTAGCTCTGG GCTCATCCAG ACCGTGTCA	600
	TCTCCAGTTA CATGGTGTG GCACCTGTGT TTGGCTACCT GGGTGACAGG TACAATCGGA	660
10	AGTATCTCAT GTGCGGGGC ATTGCCTTCT GGTCCCTGGT GAACTGGGG TCATCCTTCA	720
	TCCCGGAGA GCATTCTGG CTGCTCTCC TGACCGGGG OCTGGTGGG GTCGGGAGG	780
	CCAGTTATTC CACCATCGCG CCCACTCTCA TTGCCGACCT CTTGTGGCC GACCAGOGGA	840
15	COGGATGCTC AGCATCTTCT ACTTTGCCAT TCCGGTGGG AGTGGTCTGG GCTACATTGC	900
	AGGCTCCAAA GTGAAGGATA TGGCTGGAGA CTGGCACTGG GCTCTGAGG TGACACGGG	960
20	TCTAGGAGTG GTGCCGTC TGCTGCTGT CTTGGTAGTG CGGGAGCCGC CAAGGGAGC	1020
	CGTGGAGCG CACTCAGATT TGCCACCCCT GAACCCACC TCGTGGTGG CAGATCTGAG	1080
	GGCTCTGGCA AGAAATCCTA GTTTCGTCTT GTCTTCCTG GGCTTCACTG CTGTGGCCTT	1140
25	TGTCACGGG TCCCTGGCTC TGTGGGCTCC GGCATTCTG CTGCGTTCCC GCGTGGTCT	1200
	TGGGGAGACC CCACCTGCC TTCCCGAGA CTCTGCTCT TCCTCTGACA GTCTCATCTT	1260
30	TGGAATCATC AACTGCCGA CCGAGTCTT GGTGTGGG CTGGTGTGG AGATCAGCCG	1320
	CCGGCTCCGC CACTCCAACC CCGGGCTGA TCCCTGGT TGTGCCACTG GCCTCCTGGG	1380
	CTCTGCACCC TTCTCTTCC TGTCCCTTGC CTGCGCCGT GGTAGCATCG TGGCCACTTA	1440
35	TATTTTMTATC TTCAATGGAG AGACCTCTT GTCCATGAAC TGGGCCATCG TGGCCGACAT	1500
	TCTGCTGTAC GTGGTGATCC CTACCGAGC CTCCACGCC GAGGCCTTCC AGATCGTGT	1560
40	GTCCCACTG CTGGTGATG CTGGGAGCCC CTACCTCATT GGCTGATCT CTGACCGCT	1620
	GCGCCGAAC TGGCCCCCT CCTTCTTGT CGAGTTCGG GCTCTGCAGT TCTCGCTCAT	1680
	GCTCTGCGG TTTGTGGG CACTGGGCG CGCACTTTC TGGGCACCG CATCTTCATT	1740
45	GAGGCGACC GCCGGCGGC ACAGCTGCAC GTGCAGGCG TGCTGCACGA AGCAGGTCC	1800
	ACAGACGACC GGATTGTGGT GCGCCAGCG GGCCGCTCCA CCGCGTGCC CGTGGCCAGT	1860
50	GTGCTCATCT GAGARGCTG CGCTCACCTA CTGCACATC TGCCACAGCT GGCCCTGGG	1920
	CCACCCACG AAGGGCTGG GCCTAACCC TTGGCCTGG CCAGCTTCCA GAGGGACCT	1980
	GGGCCGTGTG CCAGCTCCA GAACTACMT GGTAGCTCA GGGAGGAGG TGGGGTCCA	2040
55	GGAGGGGAT CCTCTCCAC AGGGGAGCC CCAAGGCTC GTGCTATTT GTAACGAAT	2100
	AAAATTTGTA GCCAGACCC AGGTGCTGC TCTGCTTTT CTCTGGGTGG CCTCTGATCT	2160
60	TGCACCCGT CTTACCCCA GGGCTCTGA AGACTGTGG T	2201

(2) INFORMATION FOR SEQ ID NO: 241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1661 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

5	GTCTTCCCG ACATCGAGCA GTTCTTCAAC ATCGGGGACA GTAGCTCTGG GCTCATCCAG	60
15	ACCGTGTTC TCTCCAGTTA CATGGTGTGT GCACCTGTGT TTGGCTACCT GGGTGACAGG	120
	TACAATCGGA AGTATCTCAT GTGGGGGGC ATTGCCTTCT GGTCCCTGGT GACACTGGGG	180
20	TCATSCTTCA TCCCCGAGA GCATTTCTGG CTGCTCCTCC TGACCCGGGG CCTGGTGGGG	240
	GTGGGGGAGG CCAGTTATTC CACCATCGCG CCCACTCTCA TTGCCGACCT CTTTGTGGCC	300
25	GACCAGCGGA SCGGATGCTC AGCATCTTCT ACTTTGCCAT TCCGGTGGGC AGTGGTCTGG	360
	GCTACATGTC AGGCTCCAAA GTGAAGGATA TGGCTGGAGA CTGGCACTGG GCTCTGAGGG	420
	TGACACCGGG TCTAGGAGTG GTGGCCGTTT TGCTGCTGTT CCTGGTAGTG CGGGAGCCGC	480
30	CAAGGGGAGC CGTGGAGCGC CACTCAGATT TGCCACCCCT GAACCCACC TCGTGGTGGG	540
	CAGATYTGAG GGCTCTGGCA AGAAATCCTA GTTTCGTCTT GTCTTCCCTG GGCTTCACTG	600
35	CTGTGGCCTT TGTACCGGC TCCTGGCTC TGTGGGCTCC GGCAITCCTG CTGCGTCCC	660
	GCGTGTCTCT TGGGAGACC CCACCTGCC TTCCCGAGA CTCTGCTCT TCCTCTGACA	720
	GTCTCATCTT TGGACTCATC ACCTGCCTGA CCGGAGTCCT GGTGTGGGC CTGGGTGTGG	780
40	AGATCAGCCG CCGYTCCGC CACTCCAACC CCCGGGCTGA TCCCCTGGTC TGTGCCACTG	840
	GCCTCCTGGG CTCTGCACCC TTCCTCTTCC TGTCCCTTGC CTGGGCCCCG GTTAGCATCG	900
45	TGGCCACTTA TATTTTCATC TTCATTGGAG AGACCTCCT GTCCATGAAC TGGGCCATCG	960
	TGGCCGACAT TCTGCTGTAC GTGGTGATCC CTACCCGACG CTCCACCGCC GAGGCCTTCC	1020
	AGATCGTGCT GTCCACCTG CTGGGTGATG CTGGGAGCCC CTACCTCAIT GGCCTGATCT	1080
50	CTGACCGCCT GCGCCGAAC TGGCCCCCCT CCTTCTTGTC CGAGTCCCG GCTCTGCAGT	1140
	TCTCGCTCAT GCTCTGCGG TTTGTTGGG CACTGGGCG CGCACTTTCC TGGGCACCGN	1200
55	CATCTTCATT GAGGCCGACC GCCGGCGGGC ACAGCTGCAC GTGCAGGGCC TGCTGCACGA	1260
	AGCAGGGTCC ACAGACGACC GGATTGTGGT GCCCCAGCG GCGCGCTCCA CCCGCGTGCC	1320
	CGTGGCCAGT GTGCTCATCT GAGAGGCTGC CGCTCACCTA CCTGCACATC TGCCACAGCT	1380
60	KGCCCTGGGC CCACCCACG AAGGGCCTGG GCCTAACCCC TTGGCCTGGC CCAGCTTCCA	1440

5 GAGGGACCCT GGGCCGTGTG CCAGCTCCCA GACACTACMT GGGTAGCTCA GGGGAGGAGG 1500
TGGGGTCCA GGAGGGGGAT CCTCTCCAC AGGGGNCACC CCAAGGGCTC GGTGCTATTT 1560
GTAACGGAAT AAAATTGTGTA GCCAGACCCC AGGTGCCTGC TCTGCTCTTT CTCTGGGTGG 1620
CCTCTGATCT TGCACCCCGT CTTACCCCA GGGCTCCTGA A 1661

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(2) INFORMATION FOR SEQ ID NO: 242:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1146 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

NGACAGAAAA GCAGAAGATG AGACTCTGTT CATTCACTTT TCCTAGGCCC ATCCTGTGGT 60
25 CATCTTTCCC CCTCCCATCA TACCTCCTCC TTCCTGGAGC CTCTGCCGGC TTGGCTGTAA 120
TGGTGGCACT TACCTGGATA TTTCAGTGGG AGGATGAAAG GCGAGACTCA CCCTACGCGG 180
30 TGGGACAGAT GGGGAGAGGA AAAAGGCAGA GATNGCCAGG AGAGGGGTGC AGGACAAACC 240
AGAGAGGTTG GGTACGGGGA AAAGTGTNGG GAGAAAGTGG GGTGCAGGCC CTGCAGGCCG 300
GTTTAGCCAG CAGCTGCGGC CTCGCCGGGC CCTTGGCATC CAACTTCGCA GACAGGGTAC 360
35 CAGCCTCCTG GTGTGTATCA TAGGATTTGT TCACATAGTG TTATGCATGA TCTTCGTAAG 420
GTTAAGAAGC CGTGGTGGTG CACCATGACA TCCAACCCGT ATATATAAAG ATAAATATAT 480
ATATATATGT ATGTAAATTA TAGCACTGAG GGCCCTGCTG CCTGCTGGA CCAAGCAAAA 540
40 CTAAGCCTTT TGGTTTGGGT ATTATGTTTC GTTTTGTAT TTGTTTGT TTGTGGCTTG 600
TCTTATGTCG TGATAGCACA AGTGCCAGTC GGATTGCTCT GTATTACAGA ATAGTGTTTT 660
45 TAATTCATCA ATGTTCTAGT TAATGCTAC CTCAGCACCT CCTCTTAGCC TAATTTTAGG 720
AGGTGCCCA ATTTTGTTC TTCAATTTA CTGGTTACTT TTTGTACAA ATCAATCTCT 780
TTCTCTCTTT CTCTCCTCCC CACCTCTCAC CCTTGCCCTC TCCATCTCCC TCTCCGCCC 840
50 TCCCTCCTC CCTCTGGCTC CCCGTCTCAT TTCTGTCCAC TCCATTCTCT CTCCCTCTCT 900
CCTGCTCCT GCTGCCCCCT CCCAGCCCA CTTSCCCGAG TTGTGCTTGC CGCTCCTTAT 960
55 CTGTCTAGT TCCGAAGCAG TTTCACTGGA AGTTGTGCAG TCCTGGTTGC AGCTTTCCGC 1020
ATCTGCCTTC GTTTCGTGTA GATTGACGCG TTTCTTTGTA ATTTCAGTGT TTCTGACAAG 1080
ATTTAAAAA AAAAAAGGA AAAAAA AAAAAAAC TCGAGGGGGG GCCCGGTACC 1140
60

CAATTG

1146

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(2) INFORMATION FOR SEQ ID NO: 243:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 1350 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

15	AACCCACGGC TGCTGCGGCA GGGCGTGGAG GGCAGAGGGC CGCGAGGGCG CAGTTGCAAA	60
	CATGGCTCAG AGCAGAGACG GCGGAAACCC GTTCGCCGAG CCCAGCGAGC TTGACAACCC	120
20	CTTTCAGCCA CCAACCAGCT ATGAGCCTCC AGCCCCTGCC CCAITGCTTC CACCTCAGC	180
	TCCCTCCTTG CAGCCCTCGA GAAAGCTCAG CCCACAGAA CCTAAGAACT ATGGCTCATA	240
	CAGCACTCAG GCTCAGCTG CAGCAGCCAC AGCTGAGCTG CTGAAGAAAC AGGAGGAGCT	300
25	CAACCGGAAG GCAGAGGAGT TGGACCGAAG GAGNCGAGAG CTGCAGCATG CTGCCCTGGG	360
	RGGCAGAGCT ACTCGACAGA ACAATTGGCC CCCTCTACCT TCTTTTGTGTC CAGTTCAGCC	420
30	CTGCTTTTTC CAGGACATCT CCATGGAGAT CCCCCAAGAA TTTCAGAAGA CTGTATCCAC	480
	CATGTACTAC CTCTGGATGT GCAGCAGGCT GGCTCTTCTC CTGAACTTCC TCGCTGCTCT	540
	GGCCAGCTTC TGTGTGGAAA CCAACAATGG CGCAGGCTTT GGGCTTTCTA TCCTCTGGGT	600
35	CCTCCTTTTC ACTCCCTGCT CCTTTGTCTG CTGGTACCGC CCCATGTATA AGGCTTTCCG	660
	GAGTGACAGT TCATTCAATT TCTTCGTTTT CTCTTCATT TTCTTCGTCC AGGATGTGCT	720
40	CTTTGTCTTC CAGGCCATTC GTATCCAGG TTGGGGATTC AGTGGCTGGA TCTCTGCTCT	780
	GGTGGTCCCG AAGGCAACAC AGCAGTATCC GTGCTCATGC TGCTGGTCCG CCTGCTCTTC	840
	ACTGGCATTG CTGTGCTAGG AATTGTATG CTGAAACGGA TCCACTCCTT ATACCGCCGC	900
45	ACAGGTGCCA GCTTTCAGAA GCGCCAGCAA GAATTTGCTG CTGGTGTCTT CTCCAACCTT	960
	GCGGTGCGAA CCGCARTTG CCAATGCAGC CGCTGGGGCT GCTGAAAATG CCTTCCGGGC	1020
50	CCCGTGACCC CTGACTGGGA TGCCCTGGCC CTGCTACTTG AGGGAGCTGA CTTAGCTCCC	1080
	GTCCCTAAGG TCTCTGGGAC TTGGAGAGAC ATCACTAACT GATGGCTCCT CCGTAGTGCT	1140
	CCCAATCCTA TGGCCATGAC TGCTGAACCT GACAGGCGTG TGGGGAGTTC ACTGTGACCT	1200
55	AGTCCCCCA TCAGGCCACA CTGCTGCAC CTCTCACAG CCCCCACCA GCTTCCCTCT	1260
	GCTGTGCCAC GGCTGTGCT TOGGTTATTT AAATAAAAAG AAAGTGAAC TGGAAAAAA	1320
60	AAAAAAAAA AAAAAAAG GGGGNCNC	1350

5 (2) INFORMATION FOR SEQ ID NO: 244:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1529 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

15 TCCAGAGGC CGGGGGGTTT CAGCTCTGCC TGTAGCAGAG CCCTGAGGAG GAGGAGGAAG 60
AGGATGTGCT GAAATACGTC CGGGAGATCT TTTTCAGCTA GGGCATAAAC TGTGCACTGA 120
ACTGTCTGCC GAGAGCAGCT GGAGGACAGC TGAGCTTCCA CTGGTGCTGC TGGGCCGMCC 180
20 GCCTGTGGGA ATGGGGCTCT CTGTGCTCCT ACCTTTGTGC CTTCTTGGGC CTGGCAGATT 240
CACCTCAGGC CAGAAGCCCC TGGACACTCC GGGCCTTGGG GTGCCGTTCT GAGTGTGCGG 300
25 AAGGCAGGAC TCAAAATGAG ATCCCATTTG ACTCCCTCTG TATGTACTGT GCCCTCTCCT 360
GGCTCTTGAG GCTCTGGAGT CCCAATTGTC TGTGTTAGTC AGTGACCAGG TTCCAGGGAA 420
AATRATGTCA TGTGGTGGTC CAACTTACTG GAACCAAAGA GACAGTACTT TGCAAAGAAA 480
30 AGGATCACTG CCAGGTGCAC TGAATTGCT ACAGTTTAGT CCGCATGATC TCTCCTGAAG 540
GAGGAAGCCT GTTTCAAAA TAGTTTCCAT CATGAGTCTA TCAATGAGCT CCCACCTCTC 600
35 CAGCCAGCCT AGAAAGCAAA CGAGCTGCCC ACAGTTCTCT GCCCTGTCTG GGAGGTTGAG 660
GCCACAGTGT ATAGACTGGT AAGCCAGACA GGCTCCTCC CGCAAGCTGC TACCTTGCTT 720
TCACCTGTAC CTTGGTCCCC GGGCAGCTAG CTATAAGCA AGAGGGACAG GAGCCCAGAA 780
40 GAGACACTGA GGACAAGAGA TCACACCAGA GTACATGTCT CTGCCTCTGT TTTCACTGTG 840
GCTTTGGACA GGAATATATG AATAAATCAC TGCCATACAG GTTTTCCAAT ACACAAGTGC 900
45 TAGAAAATAC ACACAATTCC CCAATGCGTA AGTTGTGCTA ATGTCTTTCC AAGTTCTGGG 960
TTGGGAAGTG GAGGGTGGCA GCGTTTGTTC GTGCGCAACC GTCCAGTCTT GTTCACAGCG 1020
AGGATTTGGA GTCCTCCAGG GTCTCATCAT GGGAGTGATT TGTACAGCGA CGCCTCTGCC 1080
50 CTGTCTGGCT TCAGGTCCAG GGAAGCTTTG AAGCAGTCAA GCCTTGCTTT TGTACCCCAT 1140
GTGTCTGTTC TTTGTTGAGT CACTCAGAGA TCACTCCTGG ACCTCTGGGG TTGGAGTTCC 1200
55 AGTGATGGCT TATGGCGGCC CACTCACTAT GGTGGGCTGA GTGGAAGCTC CTTAACCATG 1260
TCCCAGAGA CACTGAGGTG CTCGCTCTTT TAATGTCCTC GTTTGTTGCC GTAAGTTCTT 1320
TGCTAGGTTT CATTTTGGCA TTTGCAAAAT CAGCCTGGAA GTCTGGCCCC ATGACAGCAA 1380
60

TCACCTCCCTC CCCACCTCC TGAAGCTAGA GGAAGATTG CTCAGATCCA TTAATTAAAG 1440
CAGGAATTGG TGTGACAATG AGCTGCATGG TTTAGGGAGT CTTTGGGAGC CTGGAAGTC 1500
5 CTGAAGGACA AACATCTTG TACTAAGAA 1529

10 (2) INFORMATION FOR SEQ ID NO: 245:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1537 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

20 GTGCGAGGTC CCCGCCAGCC CCCAGCGGCC TTCCCGGCC GGGGCGCTCC CAGAGCAAAC 60
GAGGCCCTTG AGAGCTCCAC CTAGTTCACA GGATAAAATC CCACAGCAGA ACTCGGAGTC 120
AGCAATGGCT AAGCCCCAGG TGGTTGTAGC TCCTGTATTA ATGTCTAAGC TGTCTGTGAA 180
25 TGCCCCTGAA TTTTACCCTT CAGGTTATTC TTCCAGTTAC ACAGAATCCT ATGAGGATGG 240
TTGTGAGGAT TATCCTACTC TATCAGAATA TGTTGAGGAT TTTTGAATC ATCTTACAGA 300
30 GCAGCCTGGC AGTTTGTAAA CTGAAATTGA ACAGTTTGCA GAGACCCTGA ATGGTTGTGT 360
TACAACAGAT GATGCTTTGC AAGAACTTGT GGAACATC TATCAACAGG CCACATCTAT 420
CCCAAATTTT TCTTATATGG GAGCTCGCCT GTGTAAATTAC CTGTCCCATC ATCTGACAAT 480
35 TAGCCACAG AGTGGCAACT TCCGCCAATT GCTACTTCAA AGATGTCGGA CTGAATATGA 540
AGTTAAAGAT CAAGCTGCAA AAGGGGATGA AGTTACTCGA AAACGATTTC ATGCATTTGT 600
40 ACTCTTTCTG GGAGAACTTT ATCTTAACCT GGAGATCAAG GGAACAAATG GACAGGTTAC 660
AAGAGCAGAT ATTCTTCAGG TTGGTCTTCG AGAATTGCTG AATGCCCTGT TTTCTAATCC 720
TATGGATGAC AATTTAATTT GTGCAGTAAA ATGTGTTAAAG TTGACAGGAT CAGTTTIGGA 780
45 AGATGCTTGG AAGGAAAAG GAAAGATGGA TATGGAAGAA ATTATTCAGA GAATTGAAA 840
CGTTGTCCTA GATGCAAACT GCAGTAGAGA TGTAACACAG ATGCTCTTGA AGCTTGTTAGA 900
50 ACTCGGTCA AGTAACTGGG GCAGAGTCCA TGCAACTTCA ACATATAGAG AAGCAACACC 960
AGAAAATGAT CCTAACTACT TTATGAATGA ACCAACATTT TATACATCTG ATGGTGTTC 1020
TTTCACTGCA GCTGATCCAG ATTACCAAGA GAAATACCAA GAATTACTTG AAAGAGAGGA 1080
55 CTTTTTTCCA GATTATGAAG AAAATGGAAC AGATTTATCC GGGGCTGGTG ATCCATACTT 1140
GGATGATATT GATGATGAGA TGGACCCAGA GATAGAAGAA GCTTATGAAA AGTTTTGTTT 1200
60 GGAATCAGAG CGTAAGCGAA AACAGTAAAG TTAAATTTCA GCATATCAGT TTTATAAAGC 1260

AGTTTAGGTA TGGTGATTTA GCAGAACACA AGAGAGCAAG AAAATGTGTC ACATCTATAC 1320
CAAATTRAGG ATGTTGAGTT ATGTTACTAA TGTATGCAAC TTTAATTTTG TTAAACACTA 1380
5 TCTGCCAAAA TAAACTTTAT TCCCTATAAC TTAAAAATGTG TATATATATA TAATAGTTTA 1440
TTATGTACAG TTAATCTAC TGTTTTGGCT GCAATAAAAT CGATTTTGAA ATAAAWRAAA 1500
10 AAAAAAAAAA AAGGGNGGCC GCTCTAGAGG ANCCAAG 1537

15 (2) INFORMATION FOR SEQ ID NO: 246:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 506 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

25 TGCAGGATTT GGCCAGGACC CSCCGCGGTG GCGGTGCTA TCGCTTCGCA GAACCTACTC 60
AGGCAGCCAG CTGAGAAGAG TTGAGGGAAA GTGCTGCTGC TGGGTCTGCA GACCGGATGG 120
ATAACGTGCA GCCGAAAATA AAACATCGCC CCTTCTGCTT CAGTGTGAAA GGCCACGTGA 180
30 AGATGCTGCG GCTGGATATT ATCAACTCAC TGGTAACAAC AGTATTCATG CTCATCGTAT 240
CTGTGTTGGC ACTGATACCA GAAACCACAA CATTGACAGT TGGTGGAGGG GTGTTTGCAC 300
35 TTGTGACAGC AGTATGCTGT CTGCGGACG GGGCCCTTAT TTACCGGAAG CTTCTGTTCA 360
ATCCAGCGG TCCTTACCAG AAAAAGCCTG TGCATGAAAA AAAAGAAGTT TTGTAATTTT 420
ATATTACTTT TTAGTTTGAT ACTAAGTATT AAACATATTT CTGKATTATT CCAAAAAAAAA 480
40 AAAAAAAAAA AAAAAAATT TGGTGG 506

45 (2) INFORMATION FOR SEQ ID NO: 247:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1348 base pairs
(B) TYPE: nucleic acid
50 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

55 GTCTTTCTTT TNCTGTTTTG AGTTGGTGAG TGAGTGAATA GGGTAACATG GGCCTTCAGG 60
ATGACCCCTT GGAAGTGTGC CGAGTTCCTT AAATCTCAGC TGGGATCCTG GACCTGGGAG 120
60 GCCCCTGTGA GGGCCAGCTC TGGAAAAACC TGGGAGTTGA TGCCGGAGGY TGGGAAGAAC 180

	TCTGCTCGAG GGCAGGGTGC CCTGGAACAC TGGTAGTTCT GGGGCTGGGA GGGAGAGGGG	240
5	CTCCGGCTTT CTCTGAAATG AACACTGCTC TTCAGCAGTT CAAGTACTTG TTCTCAAAAC	300
	ATTTTCTAAT TGATTGGTAG GTTTTCATAA GCATTGTTTC TTTAAGGCAT GGAAAGGGAA	360
	GAATGCTCAA GCAAGTCATG TTTGTTTTCA GTGGGATGGG CCCGCGTTCT CACTGCTGGG	420
10	GGCTTCCCTT TGCATGTGGC ACCTTTGTGC AGGGCCACCA GGCAGACTCT TCCCACCTTC	480
	TCCCCTGAA GCACCAAGGG GCTTGAACCG TAATTTGGCT AATCAGAGGC ATTTTTTTTG	540
15	TCCTAGTATC TTTCACACTT GTCCAACCGT CTTATTTTTT TAAAAGTTCT GTTGTGTGTA	600
	TTAACACGAA ACTAGAGAGA AATAGTTTCT GAAGCCAGTT TATTGTGAAG ATCCCCAAGG	660
	GGAGGTTCCG TAGAGAAAAA TAGTAAGCTG GTTTAGAAAC TGACGAGGGC AAACAGCCAG	720
20	GACGCATTGG AGAGGAATTT GCCAAAGATC TACCCTGAGA TAACGCCTGT CCAGTGTCTT	780
	CACCACGTGA ATAACCAGCG CTCCAAAGTG TTTTCTGCT TTGAAAAAA AAATTCACA	840
25	AGCTTTTAAA GGTGCATTTA AGAATCCATG TGACTTTAGA ATGGAAGTGC CGGCCCTGGC	900
	AACTGTCACG TGTGCTAGAA GGTTCGATGC CTCTGGAATG CATGTGATAC TCATCTCCAT	960
	TTTGTTCCTT TGATTGCATT TTTGTTCTTT TAGCAGATCT GTCCCTGTGG GTGGTGTCTA	1020
30	AGAAGTCGGA CACCTTGGTT TTTGTGTTAG ATTGAGCTGG GCAGCTGCAA TCAGCTTCTT	1080
	TATATGCAAA TTAGGCACGA CCCATCTGTG GTTCCCTGGT TGGTGGCTAA TGAAGTGAGG	1140
35	GGAGGGAGGG ATGTCACCCC AAAAGTAGGC CCTCCCATTG GCTTTGGCCA GGCCAGACAC	1200
	TTACATCGT TTACATGGTT CTGTGTAATT TTAAAGTTTA TGTGTATAAA GCGAAGCTGT	1260
	TTCTGTGAAA CTGTATATTT TGTAAATAAA TATATGCTA CTTTGAGAWR AAAAAAAAAA	1320
40	AAAAACTCGA GGGGGGCCCG GTACCCAA	1348

45 (2) INFORMATION FOR SEQ ID NO: 248:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1766 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

55	GTGCGAATC GGCAGAGCGG CACGAGCGGC CACGAGAGCA GCGGAGTAA AGGGACTTGA	60
	GCGAGCCAGT TGCCGGATTA TTCTATTTCC CCTCCCTCTC TCCCGCCCCG TATCTCTTTT	120
60	CACCTTCTC CCACCTCGC TCGGTASCA TGGCGGAGCG TCGCGGCCA CTCAGTCCCA	180

	TTCCATCTCC TCGTCGTCTT TCGGAGCCGA GCCGTCCGCG CCCGGCGGCG GCGGGAGCCC	240
	AGGAGCCTGC CCGCCCTGG GGACGAAGAG CTGCAGCTCC TCCTGTGCGG TGCACGATCT	300
5	GATTTTCTGG AGAGATGTGA AGAAGACTGG GTTTGTCTTT GGCACCACGC TGATCATGCT	360
	GCTTTCCCTG GCAGCTTTCA GTGTATCAG TGTGGTTTCT TACCTCATCC TGGCTCTTCT	420
10	CTCTGTCAAC ATCAGCTTCA GGATCTACAA GTCCGTATC CAAGCTGTAC AGAAGTCAGA	480
	AGAAGGCCAT CCATTCAAAG CCTACCTGGA CGTAGACATT ACTCTGTCTT CAGAAGCTTT	540
	CCATAATTAC ATGAATGCTG CCATGGTGCA CATCAACAGG GCCCTGAAAC TCATTATTG	600
15	TCTCTTCTG GTAGAAGATC TGGTTGACTC CTTGAAGCTG GCTGTCTTCA TGTGGCTGAT	660
	GACCTATGTT GGTGCTGTTT TTAACGGAAT CACCCTTCTA ATTCTGTCTG AACTGCTCAT	720
20	TTTCAGTGTG CCGATTGTCT ATGAGAAGTA CAAGACCCAG ATTGATCACT ATGTTGGCAT	780
	CGCCCGAGAT CAGACCAAGT CAATTGTTGA AAAGATCCAA GCAAAACTCC CTGGAATCGC	840
	CAAAAAAAG GCAGAATAAG TACATGGAAA CCAGAAATGC AACAGTTACT AAAACACCAT	900
25	TTAATAGTTA TAACGTCGTT ACTTGTAATA TGAAGGAAAA TACTCAGTGT CAGCTTGAGC	960
	CTGCATTCCA AGCTTTTTTT TTAATTTGGT GTTTTCTCCC ATCCTTTCCC TTAAACCTC	1020
30	AGTATCAAGC AAAAAATTG ATGGACTGAT AAAAGAACTA TCTTAGAACT CAGAAGAAGA	1080
	AAGATCAAA TTCATAGGAT AAGTCAATAC CTTAATGGTG GTAGAGCCTT TACCTGTAGC	1140
	TTGAAGGGG AAAGATTGGA GGTAAGAGAG AAAATGAAAG AACACCTCTG GGTCTTCTG	1200
35	TCCAGTTTTT AGCACTAGTC TTAATCAGCT ATCCATTATA GTTTTGCCCT TAAGAAGTCA	1260
	TGATTAACTT ATGAAAAAT TATTTGGGGA CAGGAGTGTG ATACCTTCCT TGGTTTTTTT	1320
40	TTGCAGCCCT CAAATCCTAT CTTCTGCCC CACAATGTGA GCAGCTACCC CTGATACTCC	1380
	TTTTCTTTAA TGATTAACT ATCAACTTGA TAAATAACTT ATAGGTGATA GTGATAATTC	1440
	CTGATTCCAA GAATGCCATC TGATAAAAAA GAATAGAAAT GGAAAGTGGG ACTGAGAGGG	1500
45	AGTCAGCAGG CATGCTGCGG TGGCGGTCAC TCCCTCTGCC ACTATCCCA GGAAGGAAA	1560
	RGCTCCGCCA TTTGGGAAAG TGGTTTCTAC GTCACTGGAC ACCGGTTCTG AGCAATTAGTT	1620
50	TGAGAACTCG TTCCGAATG TGCTTTCTC CTCTCCCTC GCCCACCCTA AGTTTAATAA	1680
	ATAAGGTTGT ACTTTTCTTA CTATAAAATA AAAAAAAAAA AACTCGAGGG GGGCCCGGTA	1740
	CCCAAATCGC CGGATATGAT CGTAAA	1766
55		

(2) INFORMATION FOR SEQ ID NO: 249:

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2664 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

	AGTGTCTCTCG GAGCAGGCGG AGTAAAGGGA CTTGAGCGAG CCAATTGCGG GATTATTCTA	60
10	TTTCCCCCTCC CTCTCTCCCG CCCCGTATCT CTMTTCACCC TTCTCCCACC CTCGCTCGCG	120
	TASCATGGCG GAGCGTGGC GGCCTCAG TCCCATTCCTA TCTCTCGTC GTCTTGGGA	180
	GCCGAGCCGT CCGCGCCCGG CGGCGGCGG AGCCAGGAG CCTGCCCGC CCTGGGGACG	240
15	AAGAGCTGCA GCTCTCTCTG TCGGTGCAC GATCTGATTT TCTGGAGAGA TGTGAAGAAG	300
	ACTGGGTTTG TCTTTGGCAC CACGCTGATC ATGCTGCTTT CCTGGCAGC TTTCAGTGTC	360
20	ATCAGTGTGG TTCTTACCT CATCTGGCT CTCTCTCTG TCACCATCAG CTTCAGGATC	420
	TACAAGTCCG TCATCCAAGC TGTACAGAAG TCAGAAGAAG GCCATCCATT CAAAGCCTAC	480
	CTGGACGTAG ACATTACTCT GTCTCAGAA GCTTTCCATA ATTACATGAA TGCTGCCATG	540
25	GTGCACATCA ACAGGGCCCT GAAACTCATT ATTCTCTCTT TTCTGGTAGA AGATCTGGTT	600
	GACTCTTGA AGCTGGCTGT CTTTATGTGG CTGATGACCT ATGTTGGTGC TGTTTTAAAC	660
30	GGAATCACCC TTCTAATTCT TGCTGAAGT CTCATTTTCA GTGTCCGAT TGTCTATGAG	720
	AAGTACAAGA CCCAGATTGA TCACTATGTT GGCATCGCCC GAGATCAGAC CAAGTCAATT	780
	GTTGAAAAGA TCCAAGCAAA ACTCCCTGGA ATCGCCAAA AAAAGGCAGA ATAAGTACAT	840
35	GGAAACCAGA AATGCAACAG TTAATAAAC ACCATTAAAT AGTTATAACG TCGTTACTTG	900
	TACTATGAAG GAAAATACTC AGTGTGAGCT TGAGCCTGCA TTCCAAGCTT TTTTTTAAT	960
40	TTGGTGTTTT CTCCCATCCT TTCCCTTTAA CCTCAGTAT CAAGCACAAA AATTGATGGA	1020
	CTGATAAAG AACTATCTTA GAATCAGAA GAAGAAAGAA TCAAAATCAT AGGATAAGTC	1080
	AATACCTTAA TGGTGGTAGA GCCTTTACCT GTAGCTTGAA AGGGGAAAGA TTGGAGGTAA	1140
45	GAGAGAAAAT GAAAGAACAC CTCTGGGTCC TTCTGTCCAG TTTTCAGCAC TAGTCTTACT	1200
	CAGCTATCCA TTATAGTTTT GCCCTTAAGA AGTCATGATT AACTTATGAA AAAATTATTT	1260
50	GGGGACAGGA GTGTGATACC TTCCTTGGTT TTTTPTGCA GCCCTCAAAT CCTATCTTCC	1320
	TGCCCCACAA TGTGAGCAGC TACCCTGAT ACTCCTTTTC TTTAATGATT TAACTATCAA	1380
	CTTGATAAAT AACTTATAGG TGATAGTGAT AATTCCTGAT TCCAAGAATG CCATCTGATA	1440
55	AAAAAGAATA GAAATGGAAA GTGGGACTGA GAGGGAGTCA GCAGGCATGC TCGGTGGCG	1500
	GTCACCTCCT CTGCCACTAT CCCAGGGAA GGAAARGCTC CGCCATTGG GAAAGTGGTT	1560
60	TCTACGTCAC TGGACACCGG TTCTGAGCAT TAGTTTGAGA ACTCGTTCCC GAATGTGCTT	1620

TCCTCCCTCT CCCCTGCCCA CCTCAAGTTT AATAAATAAG GTTGTACTTT TCTTACTATA 1680
 AAATAAATGT CTGTAAGTGC TGTGCACTGC TGTAAACTTG TTAGAGAAAA AAATAACCTG 1740
 5 CATGTGGGCT CCTCAGTTAT TGAGTTTTTG TGATCCTATC TCAGTCTGGG GGGGAACATT 1800
 CTCAAGAGGT GAAATACAGA AAGCCTTTTT TTCTTGATCT TTTCCCGAGA TTCAAATCTC 1860
 10 CGATTCCTAT TTGGGGGCAA GTTTTTTTCT TCACCTTCAA TATGAGAATT CAGCGAACTT 1920
 GAAAGAAAA TCATCTGTGA GTTCCTTCAG GTTCTCACTC ATAGTCATGA TCCTTCAGAG 1980
 GGAATATGCA CTGGCGAGTT TAAAGTAAGG GCTATGATAT TTGATGGTCC CAAAGTACGG 2040
 15 CAGCTGCAAA AAGTAGTGA AGGAAATTGT CTACGTGTCT TGGAAAAATT AGTTAGGAAT 2100
 TTGGATGGGT AAAAGGTACC CTTCGCTTAC TCCATCTTAT TTTCTTAGCC CCCTTTGAGT 2160
 20 GTTTTAACTG GTTTCATGTC CTAGTAGGAA GTGCATTCTC CATCCTCATC CTCTGCCCTC 2220
 CCAGGAAGTC AGTGATGTGC TTTTGGGCT TCCCCTCCAA AGGACCTTCT GCAGTGAAG 2280
 TGCCACATCC AGTTCCTTTC TTTTGTGTCT GCTGTGTTTA GATAATTGAA GAGATCTTTG 2340
 25 TGCCACACAG GATTTTTTTT TTTTTAAGA AAAACCTATA GATGAAAAAT TACTAATGAA 2400
 ACTGTGTGTA CGTGTCTGTG CGTGCAACAT AAAAATACAG TAGCACCTAA GGAGCTTGAA 2460
 30 TCTTGTTTCC TGTAAAATTT CAAATTGATG TGGTATTAAT AAAAAAAAAA AAAACAMAAA 2520
 AAAAAAAAAA AAAAGGGCGG CCGCTCTAGA GGATCCAAGC TTACGTACGC GTGCATGCGA 2580
 CGTCCATAGC TCTTCTATA GGGGTCCCCC AAATTCCATT CANCGGGCCG TCGGTTTTAN 2640
 35 AAAGGTCGTG ANTGCGGAA ANCC 2664

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(2) INFORMATION FOR SEQ ID NO: 250:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 865 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

CGTGGGAGTG AGGTACCAGA TTCAGCCCAT TTGGCCCCGA CGCCTCTKTT CTCGGAATCC 60
 GGGTGCTGCG GATTGAGGTC CCGGTTCTTA ACGGTGGGAT CGGTGTCCTC GGGATGAGAT 120
 55 TTGGCGTTTC CTCGGGGCTT TGGTGGGATC GGTGTCCTCA GGATGAGATT TAGGGTTTCC 180
 TCGGGGCTTT CGGGATCTTC ACCTAATATC CGGACTGCAA GATGGAGGAA GGCGGGAACC 240
 60 TAGGAGGCCT GATTAARATG GTCCATCTAC TGGTCTGTGC AGGTGCCTGG GGCATGCAAA 300

TGTGGGTGAC CTTGCTCTCA GGCTTCCTGC TTTTCCGAAG CCTTCCCCGA CATACCTTCG 360
 GACTAGTGCA GAGCAAATC TTCCCTTCT ACTTCCACAT CTCCATGGGC TGTGCCTTCA 420
 5 TCAACCTCTG CATCTTGGCT TCACAGCATG CTTGGGCTCA GCTCACATTC TGGGAGGCCA 480
 GCCAGCTTTA CTTGCTGTTC CTGAGCCTTA CGCTGGGCAC TGTCAACGCC CGCTGGCTGG 540
 AACCOCGCAC CACAGCTGCC ATGTGGGCCC TGCAAAOCGT GGAGAAGGAG CGAGGCTTGG 600
 10 GTGGGGAGGT ACCAGGCAGC CACCAGGGTC CCGATCCCTA CCGCCAGCTG CGAGAGAAGG 660
 ACCCAAGTA CAGTGTCTC CGCCAGAATT TCTTCCGCTA CCATGGGCTG TCCTCTCTTT 720
 15 GCAATCTGGG CTGCGTCTG AGCAATGGC TCTGTCTGC TGGCCTTGG CTGGAAATAA 780
 GGAGCCTCTA GCATGGGCCC TGCATGCTAA TAAATGCTTC TTCAGAAAAA AAAAAAAAAA 840
 AACTCGAGG GGGGCCCGT ACCCA 865
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(2) INFORMATION FOR SEQ ID NO: 251:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2082 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

TGGGGGGGN AATGGGTGTC TGGCTCANGG ATTGCCNAAT CTGGAAATTC TCCATAACTT 60
 35 GCTAGCTTGT TTTTPTTTT TTTTPTTACA CCCCCCGCC CCACCCCGG ACTTGACAA 120
 TGTCAATGA TCTCAGCAGA GTTCTTCATG TGAAACGTTG ATCACCTTTC AAGCCTGCAT 180
 40 CATTCACATA TTTTTCCTC TTCTTCCCT TCAGTTCATG AACTGGTGT CATTTCTGT 240
 GTGTGTGTGT GTTTATTTT GTTTGATT TTTTPTTAA TTTTACTTT AGAGCTTGCT 300
 GTGPTGCCCA CCTTTTTC AACCTCCACC CTCACTCCT CTCAACCCAT CTCTCCGAG 360
 45 ATGAAAGAAA AAAAAAGCA AAGTTTTTT TTCTTCTCCT GAGTCTTCA TGTGAGATTG 420
 AGCTTGCAA GGAAAAAAA ATGTGAAATG TTATAGACTT GCAGCGTGCC GAGTTCCATC 480
 50 GGGTTTTTT TTTAGCATG TTATGCTAAA ATAGAGAAA AAATGCTCAT GAACCTTCCA 540
 CAATCAAGCC TGCATCAACC TTCTGGGTGT GACTTGTGAG TTTTGGCCTT GTGATGCCAA 600
 ATCTGAGAGT TTAGTCTGCC ATTAAAAAAA CTCATTCTCA TCTCATGCAT TATTATGCTT 660
 55 GCTACTTTGT CTTAGCAACA ATGAACTATA ACTGTTTCAA AGACTTTATG GAAAAGAGAC 720
 ATTATATTAA TAAAAAAA AAGCCTGCAT GCTGGACATG TATGGTATAA TTATTTTTTC 780
 60 CTTTTTTTTT CCTTTTGGCT TGGAAATGA CGTTCGAAGA CTTATAGCAT GGCATTCATA 840

CTTTGTGTTT ATGCGCTCAT GACTTTTTTG AGTTTAGAAC AAAACAGTGC AACCGTAGAG 900
 CCTTCTTCCC ATGAAATTTT GCATCTGCTC CAAACTGCT TTGAGTTACT CAGAACTTCA 960
 5 ACCTCCCAAT GCACTGAAGG CATTCTTGT GCAAAGATAC CAGAATGGGT TACACATTTA 1020
 ACCTGCCAAA CATTGAAGAA CTCCTTATGT TTTCTTTTAA ATAAGAATGA CGCCCCACTT 1080
 10 TGGGGACTAA AATTGTGCTA TTGCCGAGAA GCAGTCTAAA ATTTATTTT TAAAAAGAGA 1140
 AACTGCCCCA TTATTTTGG TTTGTTTTAT TTTATTTTA TATTTTGGG CTTTGGTCA 1200
 TTGTCAAATG TGAATGCTC TGGGTTTCTA GTATATAATT TAATCTAGT TTTTATAATC 1260
 15 TGTTAGCCCA GTTAAATGT ATGCTACAGA TAAAGGAATG TTATAGATAA ATTTGAAAGA 1320
 GTTAGGCTCG TTAGCTGTA GATTTTTTAA ACGATTGATG CACTAAATTG TTTACTATTG 1380
 20 TGATGTTAAG GGGGTAGAG TTTGCAAGG GACTGTTTAA AAAAGTAGC TTATACAGCA 1440
 TGTGCTTGCA ACTTAAATAT AAGTTGGTA TGTGTAGTCT TTGCTATACC ACTGACTGTA 1500
 TTGAAAACCA AAGTATTAAG AGGGGAAACG CCCCTGTTA TATCTGTAGG GGTATTTTAC 1560
 25 ATTCAAAAT GTATGTTTT TTTCTTTTC AAAATTAAAG TATTTGGGAC TGAATTGCAC 1620
 TAAGATATAA CTGCAAGCA TATAATACAA AAAAAATTG CAAACTGTT TAGAACGCTA 1680
 30 ATAAATTTA TGCAGTTATA AAAATGGCAT TACTGCACAG TTTTAAGATG ATGCAGATT 1740
 TTTTACAGTT GTATTGTTT GCAGAACTGG ATTTCTGTA ACTTAAAAA AAATCCACAG 1800
 TTTTAAAGC AATAATCAGT AAATGTTATT TTCAGGACT GACATCCTGT CTTTAAAAAG 1860
 35 AAATGAAAAG TAAATCTTAC CACAATAAAT ATAAAAAAT CTGTGAGTT ACTTTTCTTT 1920
 TACATATTTT GCTGTGCAA ATTGTTTTAT ATCTTGAGTT ACTAACTAAC CACGCGTGT 1980
 40 GTTCTATGT GCTTTCTTT CATTTTCAAT TCTGGTTATA TCAAGAAAAG AATAATCTAC 2040
 AATAATAAAC GGCATTTTTT TTTGAAAAA AAAAAAAAAA AA 2082

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(2) INFORMATION FOR SEQ ID NO: 252:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1482 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

CAGGCAGGCT GGCCCCGGGG ACTTCTCTCT GGCCTGCTC CCTCCGAGCG CTCGCGCGTT 60
 60 GCCCCTGCG CCCCTACGGA GTCCTTAGCC AGGATGGAGG CTGTTGTGAA CTTGTACCAA 120

GAGGTGATGA AGCACGCAGA TCCCCGGATC CAGGGCTACC CTCTGATGGG GTCCCCCTTG 180
CTAATGACCT CCATTCTCCT GACCTACGTG TACTTCGTTC TCTCACTTGG GCCTGCGATC 240
5 ATGGCTAATC GGAAGCCCTT CCAGCTCCGT GGCTTCATGA TTGTCTACAA CTTCTCACTG 300
GTGGCACTCT CCTCTACAT TGTCTATGAG TTCTGATGT CGGGCTGGCT GAGCACCTAT 360
10 ACCTGGCGCT GTGACCTGT GGAATAITCC AACAGCCCTG AGGCACTTAG GATGGTTCGG 420
GTGGCCTGGC TCTTCCTCTT CTCCAAGTTC ATTGAGCTGA TGGACACAGT GATCTTTATT 480
CTCGAAAGA AAGACGGCA GGTGACCTTC CTACATGTCT TCCATCACTC TGTGCTTCCC 540
15 TGGAGCTGGT GGTGGGGGT AAAGATTGCC CCGGAGGAA TGGGCTCTTT CCATGCCATG 600
ATAAACTCTT CCGTGCATGT CATAATGTAC CTGTACTACG GATTATCTGC CTTTGGCCCT 660
GTGGCACAAC CCTACCTTG GTGAAAAAG CACATGACAG CCATTCAGCT GATCCAGTTT 720
20 GTCTTGGTCT CACTGCACAT CTCCAGTAC TACTTTATGT CCAGCTGTAA CTACCAGTAC 780
CCAGTCATTA TTCACCTCAT CTGGATGTAT GGCACCATCT TCTTCATGCT GTTCTCCAAC 840
25 TTCTGGTATC ACTCTTATAC CAAGGGCAAG CGGCTGCCCC GTGCACTTCA GCAAAATGGA 900
GCTCCAGGTA TTGCCAAGGT CAAGGCCAAC TGAGAAGCAT GGCCTAGATA GCGGCCACC 960
TAAGTGCTTC AGGACTGCAC CTTAGGGCAG TGTCCGTGAG TGCCCTCTCC ACCTACACCT 1020
30 GTGACCAAGG CTTATGTGGT CAGGACTGAG CAGGGGACTG GCCCTCCCTT CCCCACAGCT 1080
GCTCTACAGG GACCACGGCT TTGGTTCTCT ACCCACTTCC CCCGGGCAGC TCCAGGGATG 1140
35 TGGCCTCATT GCTGTCTGCC ACTCCAGAGC TGGGGGCTAA AAGGGCTGTA CAGTTATTTT 1200
CCCCTCCCTG CCTTAAACT TGGGAGAGGA GCACTCAGG CTGGCCCCAC AAAGGTCTC 1260
GTGGCCTTTT TCCTCACACA GAAGAGGTCA GCAATAATGT CACTGTGGAC CCAGTCTCAC 1320
40 TCCTCCACCC CACACACTGA AGCAGTAGCT TCTGGGCCAA AGGTCAGGT GGGGGGGGC 1380
CTGGAATAC AGCCTGTGA GGCTGCTTAC TCAACTGTG TCTTAATTAA AAGTGACAGA 1440
45 GGAAACCAA AAAAAAAAAA AAAAATCGA GGGGGGCCG TA 1482

50 (2) INFORMATION FOR SEQ ID NO: 253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

60 GGCACGAGCG CCGTTGCCCG CCTGGCCCTT ACGGAGTCTT TAGCCAGGAT GGAGGCTGTT 60

GTGAACTTGT ACCAAGAGGT GATGAAGCAC GCAGATCCCC GGATCCAGGG CTACCCCTCTG 120
 ATGGGGTCCC CCTTGCTAAT GACCTCCATT CTCCTGACCT ACGTGTACTT CGTCTCTCA 180
 5 CTGGGGCTC GCATCATGGC TAATCGGAAG CCCTTCCAGC TCCGTGGCTT CATGATTGTC 240
 TACAACCTCT CACTGGTGGC ACTCTCCCTC TACATTGTCT ATGAGTTCCT GATGTGGGGC 300
 10 TGGCTGAGCA CCTATACCTG GCGCTGTGAC CCTCAGGACT GCACCTTAGG GCAGTGTCCG 360
 TCAGTGGCCT CTCCAMCTAC ACCTGTGACC AAGGCTTATG TGGTCAGGAC TGAGCAGGGG 420
 ACTGGCCCTC CCCTCCCCAC AGCTGCTCTA CAGGGACCAC GGCTTTGGTT CCTCACCAC 480
 15 TTCCCCCGGG CAGCTCCAGG GATGTGGCCT CATGTCTGTC TGCCACTCCA GAGCTGGGGG 540
 CTAAAAGGGG TGTACAGTTA TTTCCTCTC CCTGCCTTAA AACTTGGGAG AGGAGCACTC 600
 20 AGGGCTGGCC CCACAAAGGG TCTCGTGGCC TTCTTCTCA CACAGAAGAG GTCAGCAATA 660
 ATGTCACGTG GGACCCAGTC TCACTCCTCC ACCCCACA CA CTGAAGCAGT AGCTTCTGGG 720
 CCAAAGGTCA GGTGGGCGG GGGCCTGGGA ATACAGCCTG TGGAGGCTGC TTA CTCAACT 780
 25 TGTGCTTAA TTAAGTGA CAGAGGAAAC CACGAAAAA AAAAAAAAAA AAAA 834

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(2) INFORMATION FOR SEQ ID NO: 254:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

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TTGAACTTTT AAATTTTAG ATCAGCAAAC TCTAAGATCC TAGAATGGAA GCTGTTCTCTC 60
 ATTCTCCAT GCTCACCTC CCAGGTCAGC GAGATGGTGA AGAAGCTGCA CGCGCAACA 120
 45 CCACCAACGT TCGGAGTGA CCTCATCAAT GAGCTTGTGG AGAACTTTGG CAGATGTCCC 180
 AAGTGGTCTG GTCGGCAAGC CTTGTCTTT GTCTGCCAGA CTGTCATTGA GGATGACTGC 240
 CTTCCCATGG ACCAGTTTGC TGTGCATCTC ATGCGCATC TGCTAACCTT AGCAAATGAC 300
 50 AGGGTTCCTA ACGTGCGAGT GCTGCTTGCA AAGACATTAA GACAACTCT ACTAGAAAAA 360
 GACTATTCTT TGGCTCTGC CAGCTGCCAC CAGGAGGCTG TGGAGCAGAC CATCATGGCT 420
 55 CTTGAGATGG ACCGTGACAG CGATGTCAAG TATTTTGCAA GCATCCACCC TGCCAGTACC 480
 AAAATCTCCG AAGATGCCAT GAGCACAGCG TCCTCAACCT ACTAGAAGGC TTGAATCTCG 540
 GTGCTTTTCC TGCTTCCATG AGAGCCGAGG TTCAGTGGGC ATTCGCCACG CATGTGACCT 600
 60

	GGGATAGCTT TCGGGGAGG AGAGACCTTC CTCTCCTGCC GACTTCATTG CAGGTGCAAG	660
	TTGCCTACAC CCAATACCAG GGATTTCAAG AGTCAAGAGA AAGTACAGTA AACACTATTA	720
5	TCTTATCTTG ACTTTAAGGG GAAATAATTT CTCAGAGGAT TATAATTGTC ACCGAAGCCT	780
	TAAATCCTTC TGTCTTCCTG ACTGAATGAA ACTTGAATTG GCAGAGCATT TTCCTTATGG	840
10	AAGGGATGAG ATTCCAGAG ACCTGCATTG CTTTCTCCTG GTTTTATTTA ACAATCGACA	900
	AATGAAATTC TTACAGCCTG AAGGCAGACG TGTGCCCAGA TGTGAAAGAG ACCTTCAGTA	960
	TCAGCCCTAA CTCTTCTCTC CCAGGAAGGA CTGTCTGGGC TCTGTGGCCA GCTGTCCAGC	1020
15	CCAGCCCTGT GTGTGAATCG TTTGTGACGT GTGCAAATGG GAAAGGAGGG GTTTTACAT	1080
	CTCCTAAAGG ACCTGATGCC AACACAAGTA GGATGACTT AAACCTTTAA GCGCAGCATA	1140
20	TTGCTGTACA CATTTACAGA ATGGTTGCTG AGTGTCTGTG TCTGATTTTT TCATGCTGGT	1200
	CATGACCTGA AGGAAATTTA TTAGACGTAT AATGTATGTC TGGTGTTTTT AACTTGATCA	1260
	TGATCAGCTC TGAGGTGCAA CTTCTTCACA TACTGTACAT ACCTGTGACC ACTCTTGGGA	1320
25	GTGCTGCAGT CTTTAATCAT GCTGTTTAA CTGTGTGGC ACAAGTCTC TTGTCCAAAT	1380
	AAAATTTATT AATAAGATCT ATAGAGAGAG ATATATACAC TTTTGATTGT TTTCTAGATG	1440
30	TCTACCAATA AATGCAATTT GTGACCTGTA TTAAAAAAA NTAAAAAAC TCGAGGGGGG	1500
	CCCGGTAC	1508

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(2) INFORMATION FOR SEQ ID NO: 255:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2514 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

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	GAGAGACTCA CACTTCTTTT CCATTATCAC TGACGATGTA GTGACATAG CAGGGGAAGA	60
	GCACCTACCT GTGTGGTGA GGTGTGTGA TGAATCTCAT AACCTAAGAG AGGAATTTAT	120
50	AGGCTTCCTG CCTTATGAAG CCGATGCAGA AATTTTGGCT GTGAAATTC AACTATGAT	180
	AACTGAGAAG TGGGGATTAA ATATGGAGTA TTGTCTGGC CAGGCTTACA TTGWTCTAG	240
55	TGGATTTTCT TCCAAAATGA AAGTTGTTC TTCTAGACTT TTAGAGAAAT ATCCCCAAGC	300
	TATCTACACA CTCTGCTCTT CCTGTGCCTT AAATATGTGG TTGGCAAAT CAGTACCTGT	360
	TATGGGAGTA TCTGTGCAT TAGGAACAAT TGAGGAAGTT TGTCTTTTTT TCCATCGATC	420
60	ACCACAAC TG CTTTATAGAAC TTGACAACGT AATTCTGTG CTTTTTCAGA ACAGTAAAGA	480

	AAGGGGTAAA GAACTGAAGG AAATCTGCCA TTCTCAGTGG ACAGGCAGGC ATGATGCTTT	540
5	TGAAATTTTA GTGGAACCTC TGCAAGCACT TGTTTATGT TTAGATGGTA TAAATAGTGA	600
	CACAAATATT AGATGGAATA ACTATATAGC TGGCCGAGCA TTTGTACTCT GCAGTGCACT	660
	GTCAGATTTT GATTTCATTG TTACTATTGT TGTTCCTAAA AATGTCCTAT CTTTACAAAG	720
10	AGCCTTTGGG AAAAACCTCC AGGGGCAAAC CTCTGATGTC TTCTTTGCGG CCGGTAGCTT	780
	GACTGCAGTA CTGCATTAC TCAACGAAGT GATTGGAATA TATTGAAGTT TATCATGAAT	840
15	TTTGGTTTGA GGAAGCCACA AATTTGGCAA CCAAACCTGA TATTCAAATG AAACCTCCCTG	900
	GGAAATTCGG CAGAGCTCAC CAGGGTAACT TGGAACTCTA GCTAACCTCT GAGAGTTACT	960
	ATAAAGAAAC CCTAAGTGTC CCAACAGTGG AGCACATTAT TCAGGAACCT AAAGATATAT	1020
20	TCTCAGAACA GCACCTCAA GCTCTTAAAT GCTTATCTCT GGTACCTCA GTCATGGGAC	1080
	AACTCAAATT CAATACGTCG GAGGAACACC ATGCTGACAT GTATAGAAGT GACTTACCCA	1140
	ATCTGACAC GCTGTCAGCT GAGCTTCATT GTTGGAGAAT CAAATGGAAA CACAGGGGGA	1200
25	AAGATATAGA GCTTCCGTC ACCATCTATG AAGCCCTCCA CCTGCCTGAC ATCAAGTTT	1260
	TTCTTAATGT GTATGCATTG CTGAAGGTCC TGTGTATTCT TCCTGTGATG AAGGTTGAGA	1320
30	ATGAGCGGTA TGAAATGGA CGAAAGCGTC TTAAAGCATA TTTGAGGAAC ACTTTGACAG	1380
	ACCAAAGGTC AAGTAACTG GCTTTGCTTA ACATAAATTT TGATATAAAA CACGACCTGG	1440
35	ATTTAATGGT GGACACATAT ATTAACTCT ATACAAGTAA GTCAGAGCTT CCTACAGATA	1500
	ATTCCGAAAC TGTGGAAAAT ACCTAAGAGA CTTTAAAAA TAGGCTTTCT TATATTTGAT	1560
	ATTTGGAAGA AAAAGCCGTA AGTGTATGTA GACCACTTAA TCACTAAATA TCTTTGCCTA	1620
40	TAGGACTCCA TTGAATACAT TAGCCATTGA TAATCTACCT GTTTAAATGG CCCCTGTTTG	1680
	AACTCTCAAG CTTTGAAGAC CTACCTGTTT TTCCAGAAGA GAACGTTGAA AGTGCCATGT	1740
	TTCTTTTGC GTGATCTCTG TTGATGGCAC TCTGGAATTG TTTCACTTAA GTCATTTTAG	1800
45	ACATAGCATT TATTATCACT GTGGATCTCT ACTTGTGGG TGTATGAAT TCTTTGAAGA	1860
	AATATATTTT GAAGAGGTGT GGGAGGAAGG AATACATTTT ATAAATGTT GTAGTGAAGC	1920
50	CCACAATGA CCTTTGACTA ATAGGAGTTT TAAGTATGTT AAAATCTAT ACTGGACAGT	1980
	TACAAGAAAT TACCGGAGAA AAGCTTGTGA GCTCACCAA CAAGGATTTT AGTGTAGATT	2040
	TTGTCTTTCT TGAACCTAAA GAAACAAATG ACAAAGTTTG AATGGAAAAG CCTGCTGTTG	2100
55	TTCCACATCT CGTTGCTGTT TACATTCTTT TGTGGAGCCT ACATCTTCCT AAGCTTTTTA	2160
	GCAGGTATAT GTTGAACACT TCTGTTTCAT GGTGAGACA GAATCAGAGG CCATGGATAC	2220
60	TGACAACTGA TTTGCTGTT TTTTCTCTCT GTCTTTTCC ATGACTCTTA TATACTGCCT	2280

CATCTTGATT TATAAGCAAA ACCTGGAAAA CCTACAAAAT AAGTGTTGTG GTTTATCTAG 2340
 5 AAAAATATGG AAAATATTGC TGTATTTTTT GGTGAAGAAA ATCAATTTTG TATAGTTTAT 2400
 TTCAATCTAA ATAAATGTG AATTTTGTGTT AAAGCTTAGG CACATTATTT TTGTGGGGT 2460
 CAAAACATTC TTGTGTAAAT TCTCTTAAAC ATTGATATAA CAGCTTCACA ATTC 2514

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(2) INFORMATION FOR SEQ ID NO: 256:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2357 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

CTGCCTTATG AAGCCGATGC AGAAATTTTG GCTGTGAAAT TTCACACTAT GATAACTGAG 60
 25 AAGTGGGGAT TAAATATGGA GTATTGTCGT GGCCAGGCTT ACATTGTCTC TAGTGGATTT 120
 TCTTCCAAAA TGAAAGTGTG TGCTTCTAGA CTTTTAGAGA AATATCCCCA AGCTATCTAC 180
 ACACTCTGCT CTTCCTGTGC CTTAAATATG TGGTTGGCAA AATCAGTACC TGTATGGGA 240
 30 GTATCTGTTG CATTAGGAAC AATTGAGGAA GTTGTCTCTT TTTTCCATCG ATCACCACAA 300
 CTGCTTTTAG AACTTGACAA CGTAATTYCT GTTCTTTTTT AGAACAGTAA AGAAAGGGGT 360
 35 AAAGAACTGA AGGAAATCTG CCATTCTCAG TGGACAGGCA GGCATGATGC TTTTGAAATT 420
 TTAGTGAAC TCCTGCAAGC ACTTGTTTTA TGTTTAGATG GTATAAATAG TGACACAAAT 480
 ATTAGATGGA ATAACTATAT AGCTGGCCGA GCATTTGTAC TCTGCAGTGC AGTGTGAGAT 540
 40 TTTGATTTCA TTGTTACTAT TGTGTGTTCT AAAAATGTCC TATCTTTTAC AAGAGCCTTT 600
 GGGAAAAACC TCCAGGGGCA AACCTCTGAT GTCTTCTTTG CGGCCGGTAG CTTGACTGCA 660
 45 GTACTGCATT CACTCAACGA AGTGANTGGA AAATATTGAA GTTTATCATG AATTTTGGTT 720
 TGAGGAAGCC ACAAATTTGG CAACCAAACT TGATATTCAA ATGAAACTCC CTGGGAAATT 780
 CCGCAGAGCT CACCAGGGTA ACTTGGAATC TCAGCTAACC TCTGAGAGTT ACTATAAAGA 840
 50 AACCCTAAGT GTCCCAACAG TGGAGCACAT TATTGAGGAA CTTAAAGATA TATTCTCAGA 900
 ACAGCACCTC AAAGCTCTTA AATGCTTATC TCTGGTACCC TCAGTCATGG GACAACCTCA 960
 55 ATTCAATACG TCGGAGGAAC ACCATGCTGA CATGTATAGA AGTGACTTAC CCAATCCTGA 1020
 CACGCTGTCA GCTGAGCTTC ATTGTTGGAG AATCAAATGG AAACACAGGG GGAAAGATAT 1080
 60 AGAGCTTCCG TCCACCATCT ATGAAGCCCT CCACCTGCCT GACATCAAGT TTTTCTCTAA 1140

TGIGTATGCA TTGCTGAAGG TCGTGTGTAT TCTTCCTGTG ATGAAGGTTG AGAATGAGOG 1200
 GTATGAAAAT GGACGAAAGC GTCTTAAAGC ATATTTGAGG AACACTTTGA CAGACCAAAG 1260
 5 GTCAAGTAAC TTGGCTTTGC TTAACATAAA TTTTGATATA AAACACGACC TGGATTTAAT 1320
 GGTTGACACA TATATTAAAC TCTATACAAG TAAGTCAGAG CTTCCTACAG ATAATTCGA 1380
 10 AACTGTGGAA AATACCTAAG AGACTTTTAA AAATAGGCTT TCTTATATTT GATATTTGGA 1440
 AGAAAAAGCC GTAAGTGTAT GTAGACCACT TAATCACTAA ATATCTTTGC CTATAGGACT 1500
 CCATTGAATA CATTAGCCAT TGATAATCTA CCTGTTTAAA TGGCCCCGTG TTGAACCTC 1560
 15 AAGCTTTGAA GACCTACCTG TTCTTCCAGA AGAGAACGTT GAAAGTGCCA TGTTTCCTTT 1620
 TCGGTGATCT CTGTGATGG CACTCTGGAA TTGTTTCAGT TAAGTCATTT TAGACATAGC 1680
 ATTTATTATC ACTGTGGATC TCTACTTGTT GGGTGTATG AATTCCTTGA AGAAATATAT 1740
 20 TTGAAGAGG TGTGGGAGGA AGGAATACAT TTTATAAAAT GTTGTAGTGA AGCCCAAT 1800
 TGACCTTTGA CTAATAGGAG TTTTAAGTAT GTTAAAAATC TATACTGGAC AGTTACAAGA 1860
 25 AATTACCGGA GAAAAGCTTG TGAGCTCACC AAACAAGGAT TTCAGTGTAG ATTTTGTCTT 1920
 TCTTGAACCT AAAGAAACAA ATGACAAAGT TTGAATGGAA AAGCCTGCTG TTGTTCCACA 1980
 TCTCGTGTCT GTTTACATTC CTTTGTGGAG CCTACATCTT CCTAAGCTTT TTAGCAGGTA 2040
 30 TATGTTGAAC ACTTCTGTTT CATGGTGTAG ACAGAATCAG AGGCCATGGA TACTGACAAC 2100
 TGATTTGTCT GTTTTTFCT TCTGTCTTTT TCCATGACTC TTATATACTG CCTCATCTTG 2160
 35 ATTTATAAGC AAAACCTGGA AAACCTACAA AATAAGTGTG GTGGTTTATC TAGAAAAATA 2220
 TGAATAATAT TGCTGTTATT TTTGGTGAAG AAAATCAATT TTGTATAGTT TATTTCAATC 2280
 40 TAAATAAAAT GTGAATTTTG TTTAAAGCTT AGGCACATTA TTTTGTGG GGTCAAAACA 2340
 TTCTTGTGTA AATCTC 2357

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(2) INFORMATION FOR SEQ ID NO: 257:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 689 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

ACTTCTCGGT GCAAAAAGAT GTTCAAGCCT TATTTTATAC TTGCCTGCCC CTTTCTCTTT 60
 CATTTATTGG AGTGAGCTGC AGCTCTAAGA AGACCTGTTT TTTTGAATGG AGAGTAGCAT 120
 60 CAGGAACCAG GATGTGGGTG CGAGGCGTGC TCCTGGCTGT TGCAGATTGC TGCACCCGGG 180

AGCTCTTAGT GGACAGAGCT AGAGGATATG TGCACGTACT TCCATCTCTC TCTCTGTCTC 240
 CGATTTTAGC CCAGCACCAC AGGGTACGTT CCAGTTTTC TCTCTTCCA TAGCTGTAAG 300
 5 GCCCTTCTG GGAATGGTTC TCATCTCCT TAATCTATTA TTGGGTCACT TTCTCTGCAT 360
 GTCCCCAGCC TCCCATCACT GCCACCCACT CCCACAGAG ATGCCCTGCT CATCCGACTG 420
 10 GGGCTTTGAC TCCCACACTG TGTACCCCTC TTGTGTGGAC GCCCTGCTGC CAAACCTTC 480
 AGCAAACAGC TTCCCAAATG GAAGTTGTCA CTGTCARGGS CTTTACAATC AGCAACAGCA 540
 AAATCTACAT GCTGCTGAGG GTCCTGCCTC ATTAAGATGC AATAAATATG TAAGTACATA 600
 15 AAAACAGCAA TAGAAGAAAC GTAATGCTTT ATTCTCAAAT ATGNATGTCT ACATAGAAAA 660
 GCCAAAATTA TTAAGAATAG TAAGGAATT 689
 20

(2) INFORMATION FOR SEQ ID NO: 258:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

TCGACCCACG CGTCCGCCGA TGTGATGATT CCTGCGTATT CCAAGAACCG GGCCTATGCC 60
 35 ATCTTCTTCA TAGTCTTCAC TGTGATAGGG GACGCCCCCG GCGCTGTGCT ATCCTGTGCC 120
 GGCCACCCCTT GCGTTGGITT TGCTGCTGTA CTGGTGCGC CCCTGACCGT GGCTGTCTCC 180
 40 TCTTGAAGGA AGCCTGTTTC TGATGAACCT GCTGACAGCC ATCATCTACA GTCAGTCCG 240
 GGGCTACCTG ATGAAATCTC TCCAGACCTC GCTGTTTCGG AGGCGGGTGG GAACCCGGCT 300
 GCCTTTGAAG TCCTATCCTC CATGGTGGGG GAGGGAGGAG CCTTCCCTCA GGCAGTTGGG 360
 45 GTGAAGCCCC AGAACTTGCT GCAGGTGCTT CAGAAGGTCC AGCTGGACAG CTCCACAGA 420
 CAGGCCATGA TGGAGAAGGT GCGTTCCTAT GGCAGTGTTC TGCTCTCAGC TGAGGAGTTT 480
 CAGAAGCTCT TCAACGAGCT TGACAGAAGT GTGGTTAAAG AGCACCCGCC GAGGCCCGAG 540
 50 TACCAGTCTC CGTTTCTGCA GAGCGNCCCA GTTCTCTTTC GGCCACTNAC TACTTTGACT 600
 ACCTGGGGAA CCTCATCGCC CTGGCAAACC TGGTGTCAT TTGCGTGTTC CTGGTGTGG 660
 55 ATGCAGATGT TGCTGCCTGC TGAGCGTGAT GACTTCATCC TGGGGGTCT CAACTGCGTC 720
 TTCATTGTGT ACTACCTGTT GGAGATGCTG GCTCAAGGTC TTTTGCCCTG GGGCCTGCGA 780
 60 RGGTACYKKT CCTAACCCCA RCAAMGTGTT TTGAACGGGC TCCTCAMEGT TTGTCTGGC 840

	TGGWKKGSM	GATCTCAACT	CTGGCTGTGT	ACCGATTGCC	ACACCCAGGC	TGGAGGCCGG	900
	ANATGGTGGG	CCTGCTGTCTG	CTGTGGGACA	TGACCCGCAT	ACTGAACATG	CTCATCGTGT	960
5	TCCGCTTCT	GCGTATCATC	CCCAGCATGA	AGCCGATGGC	CGTGGTGGCC	AGTACCGTCC	1020
	TGGGCCTGGT	GCAAAACATG	CGTCCGTTTG	GCGGGATCCT	GGTGGTGGTC	TACTACGTAT	1080
10	TTGCCATCAT	TGGGATCAAC	TTGTTTAGAG	GCGTCATTGT	GGCTCTTCCT	GGAAACAGCA	1140
	GCCTGGCCCC	TGCCAATAGG	TCCGCGCCCT	GTGGGAGCTT	CGAGCAGCTG	GAGTACTGGG	1200
	CCAACAACCT	CGATGACTTT	GCGGCTGCCC	TGGTCACTCT	GTGGAACCTG	ATGGTGGTGA	1260
15	ACAACTGGCA	GGTGTTCCTG	GATGCATATC	GGCGCTACTA	AGGCCCGTGG	TCCAAGATCT	1320
	ATTTTGTATT	GTGGTGGCTG	GTGTCTCTCT	TCATCTGGGT	CAACCTGTTT	CTGGCCCTGA	1380
20	TTCTGGAGAA	CTTCCTTCAC	AAGTGGGACC	CCCGCAGCCA	CCTGCAGCCC	CTTGCTGGGA	1440
	CCCCAGAGGC	CACCTACCAG	ATGACTGTGG	AGCTCCTGTT	CAGGGATATT	CTGGAGGAGC	1500
	CCGGGGAGGA	TGAGCTCACA	GAGAGGCTGA	GCCAGCACCC	GCACCTGTGG	CTGTGCAGGT	1560
25	GACGTCCGGG	TCTGCCATCC	CAGCAGGGGC	GGCAGGAGAG	AGAGGCTGGC	ATAACACAGG	1620
	TGCCCATCAT	GGAAGAGGCG	GCCATGCTGT	GGCCAGCCAG	GCAGGAAGAG	ACCTTTCCTC	1680
30	TGACGGACCA	CTAAGCTGGG	GACAGGAACC	AAGTCCTTTG	CGTGTGGCCC	AACAACCATT	1740
	TACAGAACAG	CTGCTGGTGC	TTCAGGGAGG	CGCCGTGCCC	TCCGCTTCTT	TTTATAGCTG	1800
	CTTCAGTGAG	AATTCCCTTG	TCGACTCCAC	AGGGACCTTT	CAGACAAAAA	TGCAAGAAGC	1860
35	AGCGGCCTCC	CCTGTCCCTT	GCAGCTTCCG	TGGTGCCTTT	GCTGCCGGCA	GCCCTTGGGG	1920
	ACCACAGGCC	TGACCAGGGC	CTGCACAGGT	TAACCGTCAG	ACTTCCGGGG	CATTACAGCTG	1980
40	GGAATGATAC	TAATACCTCC	GATTTTAGCC	CAGCACCACA	GGGTACGTTT	CAGTTTTTAT	2040
	TTCTTTCCAT	AGCTGTAAGG	CCCTTTCTGG	GAATGGTTAT	CATTCTCCTT	AATCTATTAT	2100
	TGGGTCAGTT	TTCTGTCATG	TCCCAGCCT	CCCATCACTG	CCACCCACTC	CCCACAGAGA	2160
45	TGCCCTGCTC	ATCCGACTGG	GGCTTTGACT	CCCACACTGT	GTACCCCTCT	TGTGTGGACG	2220
	CCCTGCTGCC	AAAACCTTCA	GCAAACAGCT	TTCCAAATGG	AAGTTGTAC	TGTCAGGGCC	2280
50	TTTACAATCA	GCAACAGCAA	AATCTACATG	CTGCTGAGGG	TCCTGCCTCA	TTAAGATGCA	2340
	ATAAATATGT	AAGTACATAA	AAAAAAAAAA	AAAAAAA			2377

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(2) INFORMATION FOR SEQ ID NO: 259:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1193 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

5
TCTGNTCGCC GTCGCCCCGC CCTGGCCTT TGCCCGGTCG GCGGGACTT CCTGTGTCGT 60
ATTTCCAAGG ACTCCAAGC GAGGCCGGG ACTGAAGGTG TGGGTGTGCA GCCCTCTGGC 120
10 AGAGGGTTAA CTGGGTCAA ATGCACGGAT TCTCACTCG TACAGTTAGC CTCTCCCGC 180
GCACGTCCGC GAGGMYTTGA AGTCTGAGC GCTCAAGTTT GTCCGTAGTC GAGAGAAGGC 240
CATGGAGGTG CCGCCACCGG CACCGCGGAG CTTTCTCTGT AGAGCATTTGT GCCTATTTCC 300
15 CCGAGTCTTT GCTGCCGAAG CTGTGACTGC CGATTGCGAA GTCCTTGAGG AGCGTCAGAA 360
GCGGCTTCCC TACGTCCAG AGCCTATTA CCGGAATCT GGATGGGACC GCCTCCGGGA 420
20 GCTGTTTGGC AAAGACACAG TGAACACTAG TCTGAATGTA TACCGAAATA AAGATGCCTT 480
AAGCCATTTT GTAATTGCAG GAGCTGTAC GGAAGTCTT TTTAGGATAA ACGTAGGCCT 540
GCGTGGCTGG TGGCTGGTGG CATAATTGGA GCCTTGCTGG GCACTCCTGT AGGAGGCCTG 600
25 CTGATGGCAT TTCAGAAGTA CTCTGGTGG ACTGTCAGG AAAGAAAACA GAAGGATCGA 660
AAGGCACTCC ATGAGCTAAA ACTGGAAGAG TGGAAAGGCA GACTACAAGT TACTGAGCAC 720
30 CTCCCTGAGA AAATTGAAAG TAGTTTACAG GAAGATGAAC CTGAGAATGA TGCTAAGAAA 780
ATTGAAGCAC TGCTAAACCT TCCTAGAAAC CCTTCAGTAA TAGATAAACA AGACAAGGAC 840
TGAAAGTGCT CTGAACITGA AACTCACTGG AGAGCTGAAG GGAGCTGCCA TGTCCGATGA 900
35 ATGCCAACAG ACAGGCCACT CTTGGTCAG CCTGCTGACA AATTTAAGTG CTGGTACCTG 960
TGSTGGCAGT GGCTTGCTCT TGTCTTTTC TTTCTTTT AACTAAGAAT GGGGCTGTTG 1020
40 TACTCTCACT TTACTTATCC TTAAATTTAA ATACATACTT ATGTTTGTAT TAATCTATCA 1080
ATATATGCAT ACATGAATAT ATCCACCCAC CTAGATTTTA AGCAGTAAAT AAAACATTTT 1140
GCAAAAGATT AAAGTTGAAT TTTACAGTA AAAAAAAAAA AAAAAAAAAA AAA 1193
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(2) INFORMATION FOR SEQ ID NO: 260:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1262 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

60

GAAAAACCCA AAGATGCAGA CAATCTCTTT GAACATGAAT TGGGGGCTCT CAATATGGCT 60

GCATTACTAC GAAAAGAAGA AAGAGCAAGT CTTCTTAGTA ATCTTGGCCC ATGTTGTAAG 120
GCGTGTGCT TCAGACGGGA TTCTGCAATT CGAAAGCAGC TTGTTAAAAA TGAGAAGGGC 180
5 ACCATAAAAC AAGCTTACAC GAGTSCCTCCA ATGGTAGACA ATGAATTACT TCGATTGAGT 240
CTTCGGTTAT TTAAGCGGAA GACTACTTGC CATGCTCCAG GACATGAAAA GACTGAAGAT 300
AATAAACTTT CACAGTCCAG TATCCAACAG GAACTGTGTG TGTCTTAAGA CCGAAGTTCA 360
10 ATATGGTATT TTTGGTACTG TCTTCCTTCA GCAGTGCATA TTCTTTTGCA AAGTTCTTTG 420
GTTTGACAAG CATTAGTGAC AAAGGCAGAA AAGATTTATC AGCCATGCTA AAAGAGTGAA 480
15 GAATTTTGAT CTTTAGAGAC ACTAGTTTGT GCCAACTTAA GATTTTACGT TAATTTTAC 540
ATAGTATTTG ACACTCATGC AAAATAATGT GAAAACATCT AGATTTAGTA GTTTATTCTG 600
CGCCTTTTGT TAAAACTGAA GATTTTGGAA AATGGTGTG ACTGCTCTTC CAGCCTATGA 660
20 ATATTTTGT GAAATGGAAC CATGGATTTA TGTCTGGATC ATCCATACAG AACCAACAAT 720
TTTATTCAAA AACAATGTGT TCATCAAAGT AATTGCTCAC ATTGTGCAGT ACTATGTTGT 780
25 ACAGACCACG TGAAAGGGAA TGCTGGTCTA GCTGGCGTGG TATGTTTATA GGCGAATTTC 840
AGCAGAAGGA AGCCAAAATA GTTTTTCCT TTTGAAAGTT TTTAAAAAT TATTTTCATGG 900
GTCTTTTMTT TAATTAATAT GTGTGCATTG TTACAATGTA TGTGGATGT CTMTTGACCC 960
30 TAAATGCTTT TTTTGTATC AGAGATTGTG TACTATTTT ATTTTAAATA AATGTATCTT 1020
CCCTTCTCTT GTTTTAGATT TACTTTGCTC TTCGTTAATC TTATTCCTGA TGATCTAGAA 1080
35 CATTAGTCAT CAACATTACA TGTTTCATGC TTCAGATATT TTACTGCTTG TGTCCTTATT 1140
GTGGACAGC TTAAACAGA GTTGATGGTA CTTCAAATAT AGCTCATTGA TACTTAAGGG 1200
CANCTTCTTT GGGATGTGGG CTTTTTGGAA GGAAAAAAT TNCCCCAAAG GCAAATCCCA 1260
40 GT 1262

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(2) INFORMATION FOR SEQ ID NO: 261:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1179 base pairs
50 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

GGCAAACTTT CCCCCAANGC TTCGAACTT GCAAGCCGAA ACCTTGAATC GTTAAAAGTT 60
GGGTGCGNC GCGCCCTGG CCCGAAGAAG CGCAATTGGC GTTCCGCGAA CGTTGGCCCT 120
60 CAACGGCTCG GCAGCCAGCC ATGTCTTGA CCCAGGACAG CGGCCCTGGG CTACAAGGAC 180

	CTGGACCTCA TCTTCCTGCG CCGACCTGCG CGGGGAAGGG GAGTTTCAGA CTGTGAAGGA	240
5	CGTCGTGCTG GACTGCCTGT TGGACTTCTT ACCCGAGGGG GTGAACAAAG AGAAGATCAC	300
	ACCACTCACG CTCAAGGAAG CTTATGTGCA GAAAATGGTT AAAGTGTGCA ATGACTCTGA	360
	CCGATGGAGT CTTATATCCC TGTCAAACAA CAGTGGCAAA AATGTGGAAC TGAAATTTGT	420
10	GGATTCOCTC CGGAGGCAGT TTGAATTCAG TGTAGATTCT TTTCAAATCA AATTAGACTC	480
	TCTTCTGCTC TTTTATGAAT GTTCAGAGAA CCCAATGACT GAGACATTTT ACCCCACAAT	540
15	AATCGGGGAG AGCGTCTATG GCGATTTCCA GGAAGCCTTT GATCACCTTT GTAACAAGAT	600
	CATGCCCACC AGGAACCCAG AGGAAATCCG AGGGGGAGGC CTGCTTAAGT ACTGCAACCT	660
	CTTGGTGAGG GGCTTTAGGC CCGCCTCTGA TGAAATCAAG ACCCTTCAAA GGTATATGTG	720
20	TTCCAGGTTT TTCATCGACT TCTCAGACAT TGGAGAGCAG CAGAGAAAAC TGGAGTCCTA	780
	TTTGCAGAAC CACTTTGTGG GATGGAAGA CCGCAAGTAT GAGTATCTCA TGACCCTTCA	840
25	TGGAGTGGTA AATGAGAGCA CAGTGTGCCT GATGGGACAT GAAAGAAGAC AGACTTTAAA	900
	CCTTATCACC ATGCTGGCTA TCCGGGTGTT AGCTGACCAA AATGTCATT CTAATGTGGC	960
	TAATGTCACT TGCTATTACC AGCCAGCCCC CTATGTAGCA GATGCCAACT TTAGCAATTA	1020
30	CTACATTGCA CAGGTTACAG CAGTATTCAC GTGCCAGCAA CAGACCTACT CCACTTGGCT	1080
	ACCTTGCAAT TAAGAATCAT TTA AAAAATGT CCTGTGGGGA AGCCATTTCA GACAAGACAG	1140
35	GAGAGAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAGAGC	1179

40 (2) INFORMATION FOR SEQ ID NO: 262:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1162 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

50	GGCAAACTTT CCCCCAANGC TTCGAAACTT GCAAGCCGAA ACCTTGAATC GTTAAAAGTT	60
	GGGTGCGNC GCGCCCTGG CCCGAAGAAG CGCAATGGC GTTCCGCGAA CGTTGGCCCT	120
	CAACGGCTCG GCAGCCAGCC ATGTCCTGCA CCCAGGACAG CGGCCCTGGG CTACAAGGAC	180
55	CTGGACCTCA TCTTCCTGCG CCGACCTGCG CGGGGAAGGG GAGTTTCAGA CTGTGAAGGA	240
	CGTCGTGCTG GACTGCCTGT TGGACTTCTT ACCCGAGGGG GTGAACAAAG AGAAGATCAC	300
60	ACCACTCACG CTCAAGGAAG CTTATGTGCA GAAAATGGTT AAAGTGTGCA ATGACTCTGA	360

CCGATGGAGT CTTATATCCC TGTCAAACAA CAGTGGCAAA AATGTGGAAC TGAAATTTGT 420
 GGATTCCCTC CGGAGGCAGT TTGAATTCAG TGTAGATTCT TTTCAAATCA AATTAGACTC 480
 5 TCTTCTGCTC TTTTATGAAT GTTCAGAGAA CCCAATGACT GAGACATTTT ACCCCACAAT 540
 AATCGGGGAG AGCGTCTATG GCGATTTCCA GGAAGCCTTT GATCACCTTT GTAACAAGAT 600
 10 CATTGCCACC AGGAACCCAG AGGAAATCCG AGGGGGAGGC CTGCTTAAGT ACTGCAACCT 660
 CTTGGTGAGG GGCTTTAGGC CCGCCTCTGA TGAAATCAAG ACCCTTCAAA GGTATATGTG 720
 TTCCAGGTTT TTCATCGACT TCTCAGACAT TGGAGAGCAG CAGAGAAAAC TGGAGTCCTA 780
 15 TTTGCAGAAC CACTTTGTGG GATTGGAAGA CCGCAAGTAT GAGTATCTCA TGACCCTTCA 840
 TGGAGTGGTA AATGAGAGCA CAGTGTGCCT GATGGGACAT GAAAGAAGAC AGACTTTAAA 900
 CCTTATCACC ATGCTGGCTA TCCGGGTGTT AGCTGACCAA AATGTCATTG CTAATGTGGC 960
 20 TAATGTCACT TGCTATTACC AGCCAGCCCC CTATGTAGCA GATGCCAACT TTAGCAATTA 1020
 CTACATTGCA CAGGTTGAGC CAGTATTCAC GTGCCAGCAA CAGACCTACT CCACCTGGCT 1080
 25 ACCCTGCAAT TAAGAATCAT TTAATAATGT CCTGTGGGGA AGCCATTTC AACAAGACAG 1140
 GAGAGAAAAA NAANGAAAAG AG 1162

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(2) INFORMATION FOR SEQ ID NO: 263:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 735 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

CGGGCTGGGT ATTTGCCTCG CACCATGGCG CCCAAGGGCA AAGTGGGCAC GAGAGGGAAG 60
 AAGCAGATAT TTGAAGAGAA CAGAGAGACT CTGAAGTTCT ACCTGCGGAT CATACTGGGG 120
 45 GCCAATGCCA TTTACTGCCT TGTGACGTTG GTCTTCTTTT ACTCATCTGC CTCATTTTGG 180
 GCCTGGTTGG CCTTGGGCTT TAGTCTGGCA GTGTATGGGG CCAGCTACCA CTCTATGAGC 240
 50 TCGATGGCAC GAGCAGCGTT CTCTGAGGA TGGGGCCCTG ATGGATGGTG GCACGAGCTC 300
 AACATGGAGC AGGGCATGGC AGAGCACCTT AAGGATGTGA TCCTACTGAC AGCCATCGTG 360
 CAGGTGCTCA GCTGCTTCTC TCTCTATGTC TGGTCTTCTT GGCTTCTGGC TCCAGGCCGG 420
 55 GCCCTTTACC TCCTGTGGGT GAATGTGCTG GGCCCTGGT TCACTGCAGA CAGTGGCACC 480
 CCAGCACCAG AGCACAATGA GAAACGGCAG CGCCGACAGG AGCGGCGGCA GATGAAGCGG 540
 60 TTATAGCCAT TGACATTGTG GCCACAGGCC ACTGGCCCTG GGTGGCTCTG TCAGGGTGCA 600

5 CAGCCCCTCA TGCCCTGGAGC AATGAGGGTC TAGTCCAGGG GCCAAAAGCA GTCTGAGGTA 660
TTGGGTATAC TTATACTCTA TAGGGTCGTT GAATAAATGG CTTAGAATGT GAAAAAAAAA 720
AAAAAAAAAA ATTTT 735

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(2) INFORMATION FOR SEQ ID NO: 264:

(i) SEQUENCE CHARACTERISTICS:
15 (A) LENGTH: 783 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

AAGTGCATGA GCTGCCGATG TGGTGCTTAG TGATTGCGGT TTCGGTCGCT CTCCCGTGT 60
TCCCGGGCTG GGTATTGCCC TCGCACCATG GCGCCCAAGG GCAAAGTGGG CACGAGAGGG 120
25 AAGAAGCAGA TATTTGAAGA GAACAGAGAG ACTCTGAAGT TCTACCTGCG GATCATACTG 180
GGGGCCAATG CCATTTACTG CCTTGTGACG TTGGTCTTCT TTTACTCATC TGCCTCATTT 240
TGGGCCTGGT TGGCCTGGGC TTTAGTCTGG CAGTGTATGG GGCCAGCTAC CACTCTATGA 300
30 GCTCGATGGC ACGAGCAGCG TTCTCTGAGG ATGGGGCCCT GATGGATGGT GGCATGGACC 360
TCAACATGGA GCAGGGCATG GCAGAGTGAG TGTCCCCAC CCGCAGCCCA GGCACCTTAA 420
GGATGTGATC CTA CTGACAG CCATCGTGCA GGTGCTCAGC TGCTTCTCTC TCTATGTCTG 480
GTCTTCTGCG CTCTGCTC CAGGCGGGG CCTTTACCTC CTGTGGGTGA ATGTGCTGGG 540
CCCCTGGTTC ACTGCAGACA GTGGCACCCC AGCACCAGAG CACAATGAGA AACGGCAGCG 600
40 CCGACAGGAG CGGCGGCAGA TGAAGCGGTT ATAGCCATTG ACGATTTKGC SACNRGCCAC 660
TGGCCCTGGG TGGCTCTGTC AGGGTGCACA GCCCCTCATG CCTGGAGCAA TGAGGGTCTA 720
45 GTCCAGGGGC CAAAAGCAGT CTGAGGTATT GGTATACTT ATACTCTATA GGGTCGTTGA 780
ATA 783

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(2) INFORMATION FOR SEQ ID NO: 265:

(i) SEQUENCE CHARACTERISTICS:
55 (A) LENGTH: 1638 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

	GGCAGGAGGC GCGGGCAGCG GTGGGGGCGG CGCCCCCGG CGGGAGCCGT NCCCTTTCCC	60
5	GTGCGGGAGC GCGGGGYCGG GGYCCAGGGG ANCCCGGCMC ACGGAGAGCG GGAAGAGGAT	120
	GGATTGCCCG GCGCTCCCCC CCGGATGGAA GAAGGAGGAA GTGATCCGAA AATCTGGGCT	180
	AAGTGCTGGC AAGAGCGATG TCTACTACTT CAGTCCAAGT GGTAAAGAAGT TCAGAAGCAA	240
10	GCCTCAGTTG GCAAGGTACC TGGGAAATAC TGTGTATCTC AGCAGTTTIG ACTTCAGAAC	300
	TGGAAAGATG ATGCCCTAGTA AATTACAGAA GAACAAACAG AGACTGCGAA ACGATCCTCT	360
15	CAATCAAAAT AAGGGTAAAC CAGACTTGAA TACAACATTG CCAATTAGAC AAACAGCATC	420
	AATTTTCAAA CAACCGGTAA CCAAAGTCAC AAATCATCCT AGTAATAAAG TGAAATCAGA	480
	CCCACAACGA ATGAATGAAC AGCCACGTCA GCTTTTCTGG GAGAAGAGGC TACAAGGACT	540
20	TAGTGATCA GATGTAACAG AACAAATTAT AAAAACCATG GAACTACCCA AAGGTCTTCA	600
	AGGAGTTGGT CCAGGTAGCA ATGATGAGAC CCTTTTATCT GCTGTGCGCA GTGCTTTGCA	660
25	CACAAGCTCT GCGCCAATCA CAGGGCAAGT CTCCGCTGCT GTGAAAAGA ACCCTGCTGT	720
	TTGGCTTAAC ACATCTCAAC CCTCTGCAA AGCTTTTATG GTCACAGATG AAGACATCAG	780
	GAAACAGGAA GAGCGAGTAC AGCAAGTACG CAAGAAATTG GAAGAAGCAC TGATGGCAGA	840
30	CATCTTGTCG CGAGCTGCTG ATACAGAAGA GATGGATATT GAAATGGACA GTGGAGATGA	900
	AGCCTAAGAA TATGATCAGG TAACTTTCGA CCGACTTTCC CCAAGAGAAA ATTCCTAGAA	960
35	ATTGAACAAA AATGTTTCCA CTGGCTTTTG CCTGTAAGAA AAAAATGTA CCCGAGCACA	1020
	TAGAGCTTTT TAATAGCACT AACCAATGCC TTTTITAGAT TATTTTIGAT GTATATATCT	1080
	ATTATTCAAA AAATCATGTT TATTTTGAGT CCTAGGACTT AAAATTAGTC TTTTGTAAATA	1140
40	TCAAGCAGGA CCTAAGATG AAGCTGAGCT TTTGATGCCA GTTGCAATCT ACTGGAAATG	1200
	TAGCACTTAC GTAAAACATT TGTTCCTCCC ACAGTTTAA TAAGAACAGA TCAGGAATTC	1260
45	TAAATAAATT TCCAGTTAA AGATTATGTT GACTTCACTG TATATAAACA TATTTTATA	1320
	CTTTATTGAA AGGGGACACC TGTACATCTT TCCATCRTCA CTGTAAGAC AAATAAATGA	1380
	TTATATTAC AGACTGATTG GAATTCCTTC TGTGAAAAG CACACACAAT AAAGAACCCC	1440
50	TCGTTAGCCT TCCTCTGATT TACATTCAAC TCTGATCCCG GGGCCTTAGG TTTGACATGG	1500
	GAGGTGGGAG GAAGATAGCG CATATATTG CAGTATGAAC TATTGCCTCT GGGACGTTGT	1560
55	GAGGAATTGT GCTTTCACCA GAATTTCTAA GGATTTCTGG CTTAAATATC ACCTAGCCTG	1620
	TGGTAATTTT TTTTCCCT	1638
60		

(2) INFORMATION FOR SEQ ID NO: 266:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1455 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

10 CGTGCGTACT GCCATGCAGG TACCGGGTCC GGAATTCCCA GGGTCGACCC ACGCGTCCGC 60
TCAGTTGGCA AGGTACCTGG GAAATACTGT TGATCTCAGC AGTTTTGACT TCAGAACTGG 120
15 AAAGATGATG CCTAGTAAAT TACAGAAGAA CAAACAGAGA CTGCGAAACG ATCCTCTCAA 180
TCAAAATAAG GGTAAACCAG ACTTGAATAC AACATTGCCA ATTAGACAAA CAGCATCAAT 240
TTTCAACAA CCGGTAACCA AAGTCACAAA TCATCCTAGT AATAAAGTGA AATCAGACCC 300
20 ACAACGAATG AATGAACAGC CACGTCAGCT TTTCTGGGAG AAGAGGCTAC AAGGACTTAG 360
TGCATCAGAT GTAACAGAAC AAATTATAAA AACCATGGAA CTACCCAAAG GTCTTCAAGG 420
25 AGTTGGTCCA GGTAGCAATG ATGAGACCCT TTTATCTGCT GTTGCCAGTG CTTTGACAC 480
AAGCTCTGCG CCAATCACAG GGCAAGTCTC CGCTGCTGTG GAAAAGAACC CTGCTGTTTG 540
GCTTAACACA TCTCAACCCC TCTGCAAAGC TTTTATTGTC ACAGATGAAG ACATCAGGAA 600
30 ACAGGAAGAG CGAGTACAGC AAGTACGCAA GAAATTGGAA GAAGCACTGA TGGCAGACAT 660
CTTGTCGCGA GCTGCTGATA CAGAAGAGAT GGATATTGAA ATGGACAGTG GAGATGAAGC 720
35 CTAAGAATAT GATCAGGTAA CTTTCGACCG ACTTCCCCA AGAGAAAATT CCTAGAAATT 780
GAACAAAAAT GTTCCACTG GCTTTTGCCT GTAAGAAAAA AAATGTACCC GAGCACATAG 840
AGCTTTTAA TAGCACTAAC CAATGCCTTT TTAGATGTAT TTTTGATGTA TATATCTATT 900
40 ATTCAAAAAA TCATGTTTAT TTTGAGTCTT AGGACTTAAA ATTAGTCTTT TGTAATATCA 960
AGCAGGACCC TAAGATGAAG CTGAGCTTTT GATGCCAGGT GCAATCTACT GGAAATGTAG 1020
45 CACTTACGTA AAACATTTGT TTCCCCACA GTTTTAATAA GAACAGATCA GGAATCTTAA 1080
ATAAATTTC CAGTTAAAGA TTATTGTGAC TTCACTGTAT ATAAACATAT TTTTATACTT 1140
TATTGAAAGG GGACACCTGT ACATTCTTCC ATCRTCACCTG TAAAGACAAA TAAATGATTA 1200
50 TATTACAGA CTGATTGGAA TTCTTTCTGT TGAAAAGCAC ACACAATAAA GAACCCCTCG 1260
TTAGCCTTCC TCTGATTTAC ATTCAACTCT GATCCCGGGG CCTTAGGTTT GACATGGGAG 1320
55 GTGGGAGGAA GATAGCGCAT ATATTTGCAG TATGAACAT TGCCTCTGGG ACGTTGTGAG 1380
GAATTGTGCT TTCACCAGAA TTTCTAAGGA TTTCTGGCTT AAATATCACC TAGCCTGTGG 1440
60 TAATTTTTTT TCCCT 1455

(2) INFORMATION FOR SEQ ID NO: 267:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1086 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

10

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

15	CGCCTGCAGT ACCGGTCCGG AATTCCCGGG TCGACCCACG CGTCGCTGAC CCAGGAGAAG	60
	CTGCCCTGTCT ACATCAGCCT GGGCTGCAGC GCGCTGCCGC CGCGGGGGCCG GCAGCTGAAC	120
	TATGTGCTCT TCAGGGCGGG CACCGTGTG CATTTCATCTT TGTACCCCCA GCATCTAGCA	180
20	GTGTTGGCAT GTAGTAGGCA CTCAAGAAAT GTGTGTTGAA TGAACGATGC CTGTGACAAG	240
	CAAGCGGACT TTATTCTTTC CTGACCCCTG CTCCTATGAC ACACCTCCTC CTGACTGCCA	300
	CTGTCACTCC TTCAGAGCAG AACTCCTCTA GGGAACCTGG ATGGGAAACA GCCATGGCCA	360
25	AGGACATCCT GGGTGAAGCA GGGCTACACT TTGATGAACT GAACAAGCTG AGGGTGTGTTG	420
	ACCCAGAGGT TACCCAGCAG ACCATAGAGC TGAAGGAAGA GTGCAAAGAC TTTGTGGACA	480
30	AAATTTGCCA GTTTCAGAAA ATAGTTGGTG GTTTAATTGA GCTTGTGAT CAACTTGCAA	540
	AAGAAGCAGA AAATGAAAAG ATGAAGGCCA TCGGTGCTCG GAACTTGCTC AAATCTATAG	600
	CAAAGCAGAG AGAAGCTCAA CAGCAGCAAC TTCAAGCCCT AATAGCAGAA AAGAAAATGC	660
35	AGCTAGAAAG GTATCGGGTT GAATATGAAG CTTTGTGTAA AGTAGAAGCA GAACAAAATG	720
	AATTTATTGA CCAATTATT TTTCAGAAAT GAACTGAAAA TTTGCTTTT ATAGTAGGAA	780
40	GGCAAAACAA AAAAAAGCCT CTCAAAACCA AAAAAACCTC TGTAGCATTC CAGCGGCTTG	840
	ACCAATGACC TATGTCACAA GAGGTGGCGT GTAAGGAATG CAGCCCCCTG AAGACAGCAC	900
	TACAAGTCTG GGGAGCCAG TTTTAACATC AGTGCACAGC TGCTGCTGGT GGCCCTGCAG	960
45	TGTACGTTCT CACCTCTTAT GCTTAGTTGG AACTAAGCAG TTTGTAACT TTCATCCTTT	1020
	TTTTTGTAAG TTCACAAAGC TTTGGAAGGA GARGCAATAA ATTTTGTGTT TCNAAATGGC	1080
50	TTGATG	1086

55 (2) INFORMATION FOR SEQ ID NO: 268:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1003 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

5 GGCACGGGAG CAGCCGGGCT GGTCTGCTG CGAGCCGGCG GCCCGGAGTG GGGCGGGGGA 60
GCAACATGA ACGTTGGAGT TGCCACAGT GAAGTGAATC CAAATACCG TGTCATGAAC 120
AGCCGGGGTA TGTGGCTGAC ATATGCATTG GGAGTGGCT TGCTTCATAT TGTCTTACTC 180
10 AGCATTCCTT TCTTCAGTGT TCCTGTTGCT TGGACTTTAA CAAATATTAT ACATAATCTG 240
GGGATGTACG TATTTTTCGA TGCAGTGAAA GGAACACCTT TCGAACTCC TGACCAGGGT 300
15 AAAAGCAAGG CTCCTAACTC ATTGGGAACA ACTGGACTAT GGAGTACAGT TTACATCTTC 360
ACGGAAGTTT TTCACAATTT CTCCAATAAT TCTATATTTT CTGGCAAGTT TCTATACGAA 420
GTATGATCCA ACTCACTTCA TCCTAAACAC AGCTTCTCTC CTGAGTGTAC TAATTCCCAA 480
20 AATGCCACAA CTACATGGTG TTCGGATCTT TGGAATTAAT AAGTATTGAA ATGTTTTGAA 540
ACTGAAAAAA AATTTTACAG CTACTGAATT TCTTATAAGG AAGGAGTGGT TAGTAACTG 600
25 CACTGTTTCT CTGATAATGT GAAATGAGAA GTATTTACAT TGGAGGGCCA ATGGCTGGTC 660
CTTCAAGTGC TGTTTTGAAG TGCAGATTTC CATTAAATGA TGCCTCTGTT TAATACACCT 720
GGTACATTTC TGAAGAGGGG CTTTATAAGC AGGCTGGGCA GGCCAGCTT ATAAGTTAAA 780
30 GGGCATCACA GTGAGGGTGT AGTAGATAAA TTCAAGGAAA TAAGAGATTT GTAAGAAACT 840
AGGACCAGCT TAACTTATAA TGAATGGCA TTGTGTTAAG AAAAGAACAT TTCCAGTCAT 900
35 TCAGCTGTGG TTATTTAAAG CAGACTTACA TGTAACCGG AATCCTCTCT ATACAAGTTT 960
ATTAAAGATT ATTTTATTA CCGTAAAAAA AAAAAAAAAA AAA 1003

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(2) INFORMATION FOR SEQ ID NO: 269:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1234 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

ATCAGCATCT ACAAGTAGCA TATTTGGAT GGTGTTGTG TGCTACTTCA AAGTAACTAG 60
GAAAAAATAA TCCTCGCAAC ACAGGTACCT TGTCATGTCA GAATTGGGGG TGTTAGGTTG 120
55 CCAGTTGTAT CAGTGTGAT TCATTTCATT ACTTCTTACA GAGCAAACAT GAACGTTGGA 180
GTTGCCACA GTGAAGTGAA TCCAATACC CGTGTCATGA ACAGCCGGG TATGTGGCTG 240
60 ACATATGCAT TGGGAGTTGG CTGCTTCAT ATTGCTTAC TCAGCATTC CTTCTTCAGT 300

5 GTTCCTGTTG CTTGGACTTT AACAAATATT ATACATAATC TGGGGATGTA CGTATTTTGT 360
 CATGCAGTGA AAGGAACACC TTTCGAAACT CCTGACCAGG GTAAAGCAAG GCTCCTAACT 420
 CATTGGGAAC AACTGGACTA TGGAGTACAG TTTACATCTT CACGGAAGTT TTTCACAATT 480
 TCTCCAATAA TTCTATATTT TCTGGCAAGT TTCTATACGA AGTATGATCC AACTCACTTC 540
 10 ATCCTAAACA CAGCTTCTCT CCTGAGTGTG CTAATTCCTA AAATGCCACA ACTACATGGT 600
 GTTCGGATCT TTGGAATTAA TAAGTATTGA AATGTTTTGA AACTGAAAAA AAATTTTACA 660
 GCTACTGAAT TTCTTATAAG GAAGGAGTGG TTAGTAAACT GCACTGTTTC TSTGATAATG 720
 15 TGAAATGAGA AGTATTTTACA TTGGAGGGCC AATGGCTGGT CCTTCAAGTG CTGTTTTGAA 780
 GTGCAGATTT CCATTAATG ATGCCTCTGT TTAATACACC TGGTACATTT CTGAAGAGGG 840
 20 GCTTTATAAG CARGCTGGGC AGGCCAGCT TATAAGTTAA AGGGCATCAC AGTGAGGGTG 900
 TAGTAGATAA ATTCAAGGAA ATAAGAGATT TGTAAGAAAC TAGGACCAGC TTAACCTATA 960
 ATGAATGGC ATTGTGTTAA GAAAAGAACA TTTCCAGTCA TTCAGCTGTG GTTATTTAAA 1020
 25 GCAGACTTAC ATGTAAACCG GAATCCTCTC TATACAAGTT TATTAAAGAT TATTTTTATT 1080
 ACCRTACATA TTTCKCTTGT TTTATGTAAG YGGATGTATA TCCTCTTGTT TTATACAAGC 1140
 30 CAGTCCAC TTATGAGGGT ACTTTTTTGG TTTTCTGGG CTTAATATTG TGTATTGGTC 1200
 AATGAGGCCA TTTTACANT TATTAACGTT ACAG 1234

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(2) INFORMATION FOR SEQ ID NO: 270:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 574 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

NGAGGTGCGT TCTGAGCCGT CTGTCTGCG CCAAGATGCT TCAAAGTATT ATTAAAAACA 60
 TATGGATCCC CATGAAGCCC TACTACACCA AAGTTTACCA GGAGATTGG ATAGGAATGG 120
 50 GGCTGATGGG CTTTCATGTT TATAAAATCC GGGCTGCTGA TAAAGAAAGT AAGGCTTTGA 180
 AAGCTTCAGC GCCTGCTCCT GGTCACTACT AACCAGATTT ACTTGGAGTA CATGTGAAAG 240
 55 AAAACGTCAG TCTGCCTGTA AATTTCAGCA AGCCGTGTTA GATGGGGAGC GTGGAACGTC 300
 ACTGTACACT TGTATAAGTA CCGTTTACTT CATGGCATGA ATAAATGGAT CTGTGAGATG 360
 60 CACTGCTACC TGSTACTGCT TTCAGTGTGT TCCCCCTCAG CCCTCCGGCG TGTGAGGCAT 420

ACTCTGAGTA GATAATTTGT CATGCAGCGC ATGCAATCAG AATCTCACTG AGCCACCCAT 480
 CATTTGTGAAA TAATTACCTC AGTTGTACAG GACTTGGTGA TCAGGATCCA GGCACCTCACT 540
 5 TGTATTCTAC TGCTCAATAA ACGTTTATTA AACT 574

10 (2) INFORMATION FOR SEQ ID NO: 271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1731 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

20 GCTGCAAGGT GGCCTCTGTG CCGCTGCAGA TCCAGCTCAC TACCCCTGGGA AATCTTACAC 60
 CTTCAAGCAC TGTGTTTTTC TGCTGTGATA TGCAGGAAAG GTTCAGACCA GCCATCAAGT 120
 ATTTTGGGGA TATTATTAGC GTGGGACAGA GATTGTTGCA AGGGGCCCCG ATTTTAGGAA 180
 25 TTCTGTGTAT TGTAACAGAA CAATACCCTA AAGGTCTTGG GAGCACGGTT CAAGAAATG 240
 ATTTAACAGG TGTAACACTG GTACTTCCAA AGACCAAGTT TTCAATGGTA TTACCAGAAG 300
 TAGAAGCGGC ATTAGCAGAG ATTCCCGGAG TCAGGAGTGT TGTATTATTT GGAGTAGAAA 360
 CTCATGTGTG CATCCAACAA ACTGCCCTGG AGCTAGTTGG CCGAGGAGTC GAGGTTTACA 420
 TTGTTGTGTA TGCCACCTCA TCAAGAAGCA TGATGGACAG GATGTTTGCC CTCGAGCGTC 480
 35 TCGCTCRARC CNGGGATCAT AGTGACCACG AGTGNAGGCT GTTCTGCTTC AGCTGGTAGC 540
 TGATAAGGAC CATCCAAAAT TCAAGGAAAT TCAGAATCTA ATTAAGGCGA GTGCTCCAGA 600
 40 GTCGGGCTCG CTTTCCAAAG TATAGGACAT TTGAAGAACT GGTATGCTAC TCACTGGTGA 660
 AGGACAGTCA GGTGAAGGAC TGTAAGCCCA CACAAGCTCT TCTTATCTCT ACTAGAATTA 720
 AAATGTTAAG TCAAAAACGG CTCCTTTTTT GCGCCTCCTA GTGAACITAA CCAGCTAGAC 780
 45 CATTTGAGTA CCAGCATTTA GTTACAAACG TCAAAGGCTT CCGGTGCTGC TTACCTTCCT 840
 TTTTGTGTAA TGTGCTTTTA TTTATTAAAA AAAATTACAA TGAAGATGCC TGTTTTGTCT 900
 50 CTACTGTGTA CTCTGATCGT ATCTTTCCAA AGTGCAGACT CTGTGGAAGT TTTCTTAAAT 960
 TGTTCACITTT AAAGAAAATG ACGTACCAAC AATGATTTGG CTTTTATATT ACTGTAAGAT 1020
 GTTATAATGT TAATGTGGAT GTACTGCTTT TACTTTACAG ATTGATTGGA ATAAGATTAT 1080
 55 TGCATATGAA TTTACCCACA GGACTCTGAA TCATGTTACC CACTCCOCTC ACAATGTTGT 1140
 CCACCTAGTG AGTTGCATTG ATCTATCCGT ACCAAATGAT GTGAATAAT TACATATCTT 1200
 60 TCTKGACTAT ACTGATTTCT TATTTTGGTC ACTATTACTA AATCTCTGTT AATATTCTCT 1260

CTTTAACTG AAAAGGGATG GGATAGAAGG GTTTGCAATG CCATATTATT GGTGGAGGGC 1320
 5 TGTMTTAAACA TCTTTGAAGT ATGGCTTGCT GAATATCTTT ACCAACATCT TGAATATATA 1380
 TTCTAGTGTC CACAAGATTT AGCAAAAAGA TAAAGCTTGG GTGGAATATC ATTTTAAAAT 1440
 GTTCATGTTC TGTTCTATAT TTTCTTCACC TACTCTCCAA ATATTGTAAT GCAAAAAGTC 1500
 10 TCAGTAATGA TTTGGTAGTA TTAATTTTGT GGTCAITGTT TCTCTTCGAT AAATTTATTT 1560
 TCATTAAATA CTTRTTAGAG GGTTTTGAAA TGTTTTTCAA ATATGTGAAA TGTGAAACTG 1620
 CTGTCTTTTA TATTAAAGTA ATTAAAGAAA ATGTATTGTG ATTGAAATTA TTTTGNCCCTC 1680
 15 CACAAGATGG CTCTATGAGT ATTCTTCCAG GGATTCCTAAT ATTTATTTAA G 1731

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(2) INFORMATION FOR SEQ ID NO: 272:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1320 base pairs
 25 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

CTGCTTAGGA AGAGAAGGTC AGAGTTGCGG GGGGCAGAGG CATTCCTGCC GCTGGCCCAG 60
 TCACTATGTA GTGGAGGGGC AGACACCCTC CCGCAAATTC TGGAAGGTTT TTAGTCTCGA 120
 35 CTAGGGCAGT AGCCCAGGAC TOCTAGTCGC CGGCTTCAGG TCACTGCCGG CTGAACGGAG 180
 CTGCCGTGCG CATGTTTGGC TGCTTGGTGG CGGGAGGCT GGTGCAAACA GCTGCACAGC 240
 AAGTGGCAGA GGATAAATTT GTTTTGGACT TACCTGATTA TGAAAGTATC AACCATGTTG 300
 40 TGGTTTTTAT GCTGGGAACA ATCCCATTTT CTGAGGGAAT GGGAGGATCT GTCTACTTTT 360
 CTTATCCTGA TTCAAATGGA ATGCCAGTAT GGMAACTCCT AGGATTTGTC ACGAATGGGA 420
 45 AGCCAAGTGC CATCTTCAAA ATTTCAAGTC TTAATCTGG AGAAGGAAGC CAACATCCTT 480
 TTGGAGCCAT GAATATTGTC CGAACTCCAT CTGTTGCTCA GATTGGAATT TCAGTGGAAAT 540
 TATTAGACAG TATGGCTCAG CAGACTCCTG TAGGTAATGC TGCTGTATCC TCAGTTGACT 600
 50 CATTCACCTCA GTTCACACAA AAGATGTTGG ACAATTTCTA CAATTTTGCT TCATCATTTG 660
 CTGTCTCTCA GGCCAGATG ACACCAAGCC CATCTGAAAT GTTCATTCCG GCAAATGTGG 720
 55 TTCTGCAAAT GGTATGAGGC ATNTCTGTC TCCAATATTA AGGCTTTTTA TAACTGAATA 780
 TCTATTTTGT CTATGAATAT ATTCTTTTTT TGACATTTAA ACATATTTCT TTATTGTGAA 840
 CATCAGCACT GCATGCCATT AAAGTATGTA CTATAGAGAT CTGATGAGAA ACAGTTCTTA 900
 60

CCCTAAATAT TTTGTTATAT TGTCGCCATT ATGAATTTAT AAAGACAGGA AAATATAGTT 960
 GCCTATGTTT TAGGGACCAC TATTAAAGCT TATAAATATT TGTTATTTT CATTTAGAAG 1020
 5 TACCATCTAT GAGAGTAGTT TATACTGCAC TGTGTACATG AATGGCTAAT GAATCTATTT 1080
 TCCAACFTTC CCGTGTTTTA TAGATATFTC TTTTCACTTT GAGTATCCTA GAGATGGGAG 1140
 GATGCCTAGG AAGAGTTTGT TGAGAAGTGG TACCATGGTG TAGCATGGGA GAGCATTGGG 1200
 10 AATGCACTAG GTTTGAATTT GGCATAATGG TAGCTATGTG ACCCTGAGCA AATTTCTCTC 1260
 ATCTGCTCAT CTGANGAATG AGGAAATAGG AGTGAATTG ATMTTTCCTA GGTCCNTCTA 1320

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(2) INFORMATION FOR SEQ ID NO: 273:

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- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 515 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

CCCTGGAGAG GGGCTGCTGT GCCAGCTTGG GGAGGGTCTG GGATGGGGCT GCCCCTGATG 60
 30 GCCCTGATGT GGAGTACCTT GCCAGCATCT GCTGGGGTGA ACTTTATTTT AGCCCTTCCC 120
 TTGTTGTYCT TATGAAGAAC AGAGGAGGGG TGGGCAGGTC AGTGATGTCA GCAGTGAGTA 180
 TTCCAGCAC AGCGGCTCTG GAAGAGGCAT GAGGCATFTC TTTTCAAGAA TGRTCAATTAT 240
 35 TCAGCCAGAA GGCATTCATT AAGTAAGTCC TGACTTTGTG CCCAGCTCTG TGTATAGGC 300
 CCTTGGCGAG ACTCAGGAGG GGCARAGGAC GCTAGKTTKT AGWTAACACG GAACCTCARA 360
 40 GGWTATATGG TCCAAGAAGA CCGGGGGCG GTGAAAACCC TGTGGACTAA TGCTCACGGG 420
 AGCCCGAGGT CACACTTTGA CTTTGCTACC ATGGGCTGTG TCTANGNACG TATATATGCT 480
 GCGTAATTAT TACAGAGGCA GTCCATGTGC ATTGT 515

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(2) INFORMATION FOR SEQ ID NO: 274:

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- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2995 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

TGACACCCAT AAGGAATTCA TGAAGAAAGT AGAAGAAAAG CGAGTGGACG TTAACTCAGC 60

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	AGTAGCCATG GGAGAAGTCA TCCTGGCTGT CTGCCACCCC GATTGCATCA CAACCATCAA	120
	ACACTGGATC ACCATCATCC GAGCTCGCTT CGAGGAGGTC CTGACATGGG CTAAGCAGCA	180
5	CCAGCAGCGT CTTGAAACGG CCTTGTGAGA ACTGGTGGCT AATGCTGAGC TCCTGGAAGA	240
	ACTTCTGGCA TGGATCCAGT GGGCTGAGAC CACCCTCATT CAGCGGGATC AGGAGCCAAT	300
10	CCCGCAGAAC ATTGACCGAG TTAAAGCCCT TATCGCTGAG CATCAGACAT TTATGGAGGA	360
	GATGACTCGC AAACAGCCTG ACGTGGACCG GGTCACCAAG ACATACAAAA GGAAAAACAT	420
	AGAGCCTACT CACGCGCCTT TCATAGAGAA ATCCCGCAGC GGAGGCAGGA AATCCCTAAG	480
15	TCAGCCAACC CTCCTCCCA TGCCAATCCT TTCACAGTCT GAAGCAAAAA ACCCAGGAT	540
	CAACCAGCTT TCTGCCCGCT GGCAGCAGGT GTGGCTGTTA GCACTGGAGC GGCAAGGAA	600
20	ACTGAATGAT GCCTTGGATC GGCTGGAGGA GTTGAAAGAA TTTGCCAACT TTGACTTTGA	660
	TGTCTGGAGG AAAAAGTATA TGCCTTGGAT GAATCACAAA AAGTCTCGAG TGATGGATTT	720
	CTTCGGGCGC ATTGATAAGG ACCAGGATGG GAAGATAACA CGTCAGGAGT TTATCGATGG	780
25	CATTTTAGCA TCCAAGTCC CCACCACCAA GTTAGAGATG ACTGCTGTGG CTGACATTTT	840
	CGACCGAGAT GGGGATGGTT ACATTGATTA TTATGAATTT GTGGCTGCTC TTCATCCCAA	900
30	CAAGGATGCG TATCGACCAA CAACCGATGC AGATAAAATC GAAGATGAGG TTACAAGACA	960
	AGTGGCTCAG TGCAAATGTG CAAAAGGTT TCAGGTGGAG CAGATCGGAG AGAATAAATA	1020
	CCGGTCTCTC CTCGGCAATC AGTTTGGGGA TTCTCAGCAG TTGCGGCTGG TCCGTATTCT	1080
35	GCGCAACCGT GATGGTTCGC GTTGGTGGAG GATGGATGGC CTTGGATGAA TTTTTAGTGA	1140
	AAAATGATCC CTGCCGAGCA CGAGGTAGAA CTAACATTGA ACTTAGAGAG AAATTCATCC	1200
40	TACCAGAGGG AGCATCCCAG GGAATGACCC CCTTCCGCTC ACGGGGTCGA AGGTCCAAAC	1260
	CATCTTCCCG GGCAGCTTCC CCTACTCGTT CCAGCTCCAG TGCTAGTCAG AGTAACCACA	1320
	GCTGTACATC CATGCCATCT TCTCCAGCCA CCCCAGCCAG TGAACCAAG GTTATCCCAT	1380
45	CATCAGGTAG CAAGTTGAAA CGAACAACAC CAACTTTTCA TTCTAGTCGG ACATCCCTTG	1440
	CTGGTGATAC CAGCAATTAG TTCTTCCCGG GCCTCCACAG GTGCCAAAAC TAATCGGGCA	1500
50	GACCCATAAA AGTCTGCCAG TCGCCCTGGG AGTCGGGCTG GGAGTCGAGC CGGGAGTCGA	1560
	GCCAGCAGCC GGCAGGAAG TGACGCTTCT GACTTTGACC TCTTAGAGAC GCATTGCTTG	1620
	TTCCGACACT TCAGAAAGCA GCGCTGCAGG GGGCCAAGGC AACTCCAGGA GAGGGCTAAA	1680
55	CAAACCTTCC AAAATCCCAA CCATGTCTAA GAAGACCACC ACTGCCTCCC CCAGGACTCC	1740
	AGGTCCCAAG CGATAACACT GTCTAAGCAC CCCCAGCCA CTATCCACTT TGAATCCTGC	1800
60	TCCATACATT GGGTGATAT TTATTCTGAA CGGGAGAAGT TATATTGTTA AAAGTGTAAG	1860